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(54) **Title:** INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS

(57) **Abstract:** This invention uses our knowledge of the mechanisms by which antigen is recognized by T cells to identify and prepare human immunodeficiency virus (HIV) epitopes, and to develop epitope-based vaccines directed towards HIV. More specifically, this application communicates our discovery of pharmaceutical compositions and methods of use in the prevention and treatment of HIV infection.

INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

The present application claims priority to U.S. Application No. 09/412,863 filed October 5, 1999, which is herein incorporated by reference.

FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

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INDEX

I. BACKGROUND OF THE INVENTION

Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.

The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant virus. Moreover, replication competent HIV persists in the lymphoid tissue of patients who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV infection.

Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections in vivo (Oldstone *et al.*, Nature 321:239, 1989; Jamieson et al., J. Virol. 61:3930, 1987; Yap et al, Nature 273:238, 1978; Lukacher et al., J. Exp. Med. 160:814, 1994; McMichael et al., N. Engl. J. Med. 309:13, 1983; Sethi et al., J. Gen. Virol. 64:443, 1983; Watari et al., J. Exp. Med. 165:459, 1987; Yasukawa et al., J. Immunol. 143:2051, 1989; Tigges et al., J. Virol. 66:1622, 1993; Reddenhase et al., J. Virol. 55:263, 1985; Quinnan et al., N. Engl. J. Med. 307:6, 1982). HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens, epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of interferon, that inhibit viral replication.

While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, *Nature* 370:463, 1994; Walker *et al.*, *Proc. Natl.*

Acad. Sci. 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g.*, Tsubota *et al.*, *J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al.*, *Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g.*, Borrow e*t al.*, *Nature Med.* 3:205-211, 1997; Price *et al.*, *Proc. Nat. Acad. Sci.* 94:12890-1895, 1997; Koenig *et al.*, *Nature Med.* 1:330-336, 1995; and Haas *et al.*, *J. Immunol.* 157:4212-4221, 1996)

Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in $CD4^+$ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al.*, *New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g.*, Rosenberg *et al.*, *Science* 278:1447, 1997).

A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like other retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape anti-viral therapy and immune recognition (Borrow et al., Nature Med. 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g.*, Lukashov *et al.*, *AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of sufficient breadth and vigor to prevent and/or clear HIV infection.

The epitope approach, as we have described, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine compositions. Such a composition may

simultaneously target multiple dominant and subdominant epitopes and thereby be used to achieve effective immunization in a diverse population.

The information provided in this section is intended to disclose the presently understood state of the art as of the filing date of the present application. Information is included in this section which was generated subsequent to the priority date of this application. Accordingly, information in this section is not intended, in any way, to delineate the priority date for the invention.

II. SUMMARY OF THE INVENTION

This invention applies our knowledge of the mechanisms by which antigen is recognized by T cells, for example, to develop epitope-based vaccines directed towards HIV. More specifically, this application communicates our discovery of specific epitope pharmaceutical compositions and methods of use in the prevention and treatment of HIV infection.

Upon development of appropriate technology, the use of epitope-based vaccines has several advantages over current vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The epitopes for inclusion in an epitope-based vaccine may be selected from conserved regions of viral or tumor-associated antigens, which thereby reduces the likelihood of escape mutants. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

An additional advantage of an epitope-based vaccine approach is the ability to combine selected epitopes (CTL and HTL), and further, to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion

of epitopes from multiple antigens from the pathogen in a vaccine composition. In the case of HIV, epitopes derived from multiple strains may also be included. A "pathogen" may be an infectious agent or a tumor associated molecule.

One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics, however, has been the extreme polymorphism of HLA molecules. To date, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used that are specific for HLA molecules corresponding to each individual HLA allele. Impractically large numbers of epitopes would therefore have to be used in order to cover ethnically diverse populations. Thus, there has existed a need for peptide epitopes that are bound by multiple HLA antigen molecules for use in epitope-based vaccines. The greater the number of HLA antigen molecules bound, the greater the breadth of population coverage by the vaccine.

Furthermore, as described herein in greater detail, a need has existed to modulate peptide binding properties, *e.g.*, so that peptides that are able to bind to multiple HLA antigens do so with an affinity that will stimulate an immune response. Identification of epitopes restricted by more than one HLA allele at an affinity that correlates with immunogenicity is important to provide thorough population coverage, and to allow the elicitation of responses of sufficient vigor to prevent or clear an infection in a diverse segment of the population. Such a response can also target a broad array of epitopes. The technology disclosed herein provides for such favored immune responses.

In a preferred embodiment, epitopes for inclusion in vaccine compositions of the invention are selected by a process whereby protein sequences of known antigens are evaluated for the presence of motif or supermotif-bearing epitopes. Peptides corresponding to a motif- or supermotif-bearing epitope are then synthesized and tested for the ability to bind to the HLA molecule that recognizes the selected motif. Those peptides that bind at an intermediate or high affinity *i.e.*, an IC_{50} (or a K_D value) of 500 nM or less for HLA class I molecules or an IC_{50} of 1000 nM or less for HLA class II molecules, are further evaluated for their ability to induce a CTL or HTL response. Immunogenic peptide epitopes are selected for inclusion in vaccine compositions.

Supermotif-bearing peptides may additionally be tested for the ability to bind to multiple alleles within the HLA supertype family. Moreover, peptide epitopes may be analogued to modify binding affinity and/or the ability to bind to multiple alleles within an HLA supertype.

The invention also includes embodiments comprising methods for monitoring or evaluating an immune response to HIV in a patient having a known HLA-type. Such methods comprise incubating a T lymphocyte sample from the patient with a peptide composition comprising an HIV epitope that has an amino acid sequence described in Tables VII to Table XX which binds the product of at least one HLA allele present in the patient, and detecting for the presence of a T lymphocyte that binds to the peptide. A CTL peptide epitope may, for example, be used as a component of a tetrameric complex for this type of analysis.

An alternative modality for defining the peptide epitopes in accordance with the invention is to recite the physical properties, such as length; primary structure; or charge, which are correlated with binding to a particular allele-specific HLA molecule or group of allele-specific HLA molecules. A further modality for defining peptide epitopes is to recite the physical properties of an HLA binding pocket, or properties shared by several allele-specific HLA binding pockets (*e.g.* pocket configuration and charge distribution) and reciting that the peptide epitope fits and binds to the pocket or pockets.

As will be apparent from the discussion below, other methods and embodiments are also contemplated. Further, novel synthetic peptides produced by any of the methods described herein are also part of the invention.

III. BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Figure 1 provides a graph of total frequency of genotypes as a function of the number of PF candidate epitopes bound by HLA-A and B molecules, in an average population.

Figure 2: Figure 2 illustrates the position of peptide epitopes in an experimental model minigene construct.

IV. DETAILED DESCRIPTION OF THE INVENTION

The peptide epitopes and corresponding nucleic acid compositions of the present invention are useful for stimulating an immune response to HIV by stimulating the production of CTL or HTL responses. The peptide epitopes, which are derived directly or indirectly from native HIV protein amino acid sequences, are able to bind to HLA molecules and stimulate an immune response to HIV. The complete sequence of the HIV proteins to be analyzed can be obtained from Genbank. Peptide epitopes and analogs thereof can also be readily determined from sequence information that may subsequently

be discovered for heretofore unknown variants of HIV, as will be clear from the disclosure provided below.

The peptide epitopes of the invention have been identified in a number of ways, as will be discussed below. Also discussed in greater detail is that analog peptides have been derived and the binding activity for HLA molecules modulated by modifying specific amino acid residues to create peptide analogs exhibiting altered immunogenicity. Further, the present invention provides compositions and combinations of compositions that enable epitope-based vaccines that are capable of interacting with HLA molecules encoded by various genetic alleles to provide broader population coverage than prior vaccines.

IV.A. Definitions

The invention can be better understood with reference to the following definitions, which are listed alphabetically:

A "computer" or "computer system" generally includes: a processor; at least one information storage/retrieval apparatus such as, for example, a hard drive, a disk drive or a tape drive; at least one input apparatus such as, for example, a keyboard, a mouse, a touch screen, or a microphone; and display structure. Additionally, the computer may include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.

A "construct" as used herein generally denotes a composition that does not occur in nature. A construct can be produced by synthetic technologies, *e.g.*, recombinant DNA preparation and expression or chemical synthetic techniques for nucleic or amino acids. A construct can also be produced by the addition or affiliation of one material with another such that the result is not found in nature in that form.

"Cross-reactive binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.

A "cryptic epitope" elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein which comprises the epitope is used as an antigen.

A "dominant epitope" is an epitope that induces an immune response upon immunization with a whole native antigen (*see, e.g.*, Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.

With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vivo* or *in vitro*, an epitope is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

It is to be appreciated that protein or peptide molecules that comprise an epitope of the invention as well as additional amino acid(s) are still within the bounds of the invention. In certain embodiments, there is a limitation on the length of a peptide of the invention which is not otherwise a construct. An embodiment that is length-limited occurs when the protein/peptide comprising an epitope of the invention comprises a region (i.e., a contiguous series of amino acids) having 100% identity with a native sequence. In order to avoid the definition of epitope from reading, *e.g.*, on whole natural molecules, there is a limitation on the length of any region that has 100% identity with a native peptide sequence. Thus, for a peptide comprising an epitope of the invention and a region with 100% identity with a native peptide sequence (and is not otherwise a construct), the region with 100% identity to a native sequence generally has a length of: less than or equal to 600 amino acids, often less than or equal to 500 amino acids, often less than or equal to 400 amino acids, often less than or equal to 250 amino acids, often less than or equal to 100 amino acids, often less than or equal to 85 amino acids, often less than or equal to 75 amino acids, often less than or equal to 65 amino acids, and often less than or equal to 50 amino acids. In certain embodiments, an "epitope" of the invention is comprised by a peptide having a region with less than 51 amino acids that has 100% identity to a native peptide sequence, in any increment of (49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5) down to 5 amino acids.

Accordingly, peptide or protein sequences longer than 600 amino acids are within the scope of the invention, so long as they do not comprise any contiguous sequence of more than 600 amino acids that have 100% identity with a native peptide sequence, if they are not otherwise a construct. For any peptide that has five contiguous residues or

less that correspond to a native sequence, there is no limitation on the maximal length of that peptide in order to fall within the scope of the invention. It is presently preferred that a CTL epitope be less than 600 residues long in any increment down to eight amino acid residues.

"Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g.*, Stites, *et al.*, IMMUNOLOGY, 8^{TH} ED., Lange Publishing, Los Altos, CA (1994).

An "HLA supertype or family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where xx denotes a particular HLA type), are synonyms.

Throughout this disclosure, results are expressed in terms of "IC_{50}'s." IC_{50} is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. Assays for determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205. It should be noted that IC_{50} values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC_{50} of a given ligand.

Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC_{50}'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC_{50} of the reference peptide increases 10-fold, the IC_{50} values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC_{50}, relative to the IC_{50} of a standard peptide.

Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, *Nature* 339:392, 1989; Christnick *et al.*, *Nature* 352:67, 1991; Busch *et al.*, *Int. Immunol.* 2:443, 19990; Hill *et al.*, *J. Immunol.* 147:189, 1991; del Guercio *et al.*, *J. Immunol.* 154:685, 1995), cell free systems using detergent lysates (*e.g.*,

Cerundolo *et al.*, *J. Immunol.* 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890, 1994; Marshall *et al.*, *J. Immunol.* 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425, 1993); high flux soluble phase assays (Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476, 1990; Schumacher *et al.*, *Cell* 62:563, 1990; Townsend *et al.*, *Cell* 62:285, 1990; Parker *et al.*, *J. Immunol.* 149:1896, 1992).

As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50}, or K_D value, of 50 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM.

The terms "identical" or percent "identity," in the context of two or more peptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T cell response, or a helper T cell response, to the antigen from which the immunogenic peptide is derived.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment.

"Link" or "join" refers to any method known in the art for functionally connecting peptides, including, without limitation, recombinant fusion, covalent bonding, disulfide bonding, ionic bonding, hydrogen bonding, and electrostatic bonding.

"Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses.

In humans, the MHC complex is also known as the HLA complex. For a detailed description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3^{RD} ED., Raven Press, New York, 1993.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.

A "non-native" sequence or "construct" refers to a sequence that is not found in nature, *i.e.*, is "non-naturally occurring". Such sequences include, *e.g.*, peptides that are lipidated or otherwise modified, and polyepitopic compositions that contain epitopes that are not contiguous in a native protein sequence.

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α-amino and carboxyl groups of adjacent amino acids. The preferred CTL-inducing peptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues. The preferred HTL-inducing oligopeptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues.

"Pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition.

A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment, for example, the primary anchor

residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 9-residue peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif are set forth in Table 1. For example, analog peptides can be created by altering the presence or absence of particular residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif.

"Promiscuous recognition" is where a distinct peptide is recognized by the same T cell clone in the context of various HLA molecules. Promiscuous recognition or binding is synonymous with cross-reactive binding.

A "protective immune response" or "therapeutic immune response" refers to a CTL and/or an HTL response to an antigen derived from an infectious agent or a tumor antigen, which prevents or at least partially arrests disease symptoms or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.

The term "residue" refers to an amino acid or amino acid mimetic incorporated into an oligopeptide by an amide bond or amide bond mimetic.

A "secondary anchor residue" is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst bound peptides than would be expected by random distribution of amino acids at one position. The secondary anchor residues are said to occur at "secondary anchor positions." A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of a peptide comprising a particular motif or supermotif.

A "subdominant epitope" is an epitope which evokes little or no response upon immunization with whole antigens which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole protein is used to recall the response *in vitro* or *in vivo*.

A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

"Synthetic peptide" refers to a peptide that is man-made using such methods as chemical synthesis or recombinant DNA technology.

As used herein, a "vaccine" is a composition that contains one or more peptides of the invention. There are numerous embodiments of vaccines in accordance with the invention, such as by a cocktail of one or more peptides; one or more epitopes of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such peptides or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150, e.g., at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40 , 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I-binding peptides of the invention can be admixed with, or linked to, HLA class II-binding peptides, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. Vaccines can also comprise peptide-pulsed antigen presenting cells, *e.g.*, dendritic cells.

The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G. Symbols for the amino acids are shown below.

Single Letter Symbol	Three Letter Symbol	Amino Acids
A	Ala	Alanine
C	Cys	Cysteine
D	Asp	Aspartic Acid
E	Glu	Glutamic Acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
Y	Tyr	Tyrosine

IV.B. Stimulation of CTL and HTL responses

The mechanism by which T cells recognize antigens has been delineated during the past ten years. Based on our understanding of the immune system we have developed efficacious peptide epitope vaccine compositions that can induce a therapeutic or prophylactic immune response to HIV in a broad population. For an understanding of the value and efficacy of the claimed compositions, a brief review of immunology-related technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P.

et al., Nature 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601, 1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are described herein and are set forth in Tables I, II, and III (*see* also, *e.g.*, Southwood, *et al., J. Immunol.* 160:3363, 1998; Rammensee, *et al., Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via web at : http://134.2.96.221/scripts.hlaserver.dll/home.htm; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al., Cell* 74:929-937, 1993; Kondo *et al., J. Immunol.* 155:4307-4312, 1995; Sidney *et al., J. Immunol.* 157:3480-3490, 1996; Sidney *et al., Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics*, in press, 1999).

Furthermore, x-ray crystallographic analysis of HLA-peptide complexes has revealed pockets within the peptide binding cleft of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (*See, e.g.*, Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al., Immunity* 4:203, 1996; Fremont *et al., Immunity* 8:305, 1998; Stern *et al., Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al., Nature* 364:33, 1993; Guo, H. C. *et al., Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al., Nature* 360:364, 1992; Silver, M. L. *et al., Nature* 360:367, 1992; Matsumura, M. *et al., Science* 257:927, 1992; Madden *et al., Cell* 70:1035, 1992; Fremont, D. H. *et al., Science* 257:919, 1992; Saper, M. A., Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that have the potential of binding particular HLA antigen(s).

The present inventors have found that the correlation of binding affinity with immunogenicity, which is disclosed herein, is an important factor to be considered when evaluating candidate peptides. Thus, by a combination of motif searches and HLA-peptide binding assays, candidates for epitope-based vaccines have been identified. After determining their binding affinity, additional confirmatory work can be performed to

select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, antigenicity, and immunogenicity.

Various strategies can be utilized to evaluate immunogenicity, including:

1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.*, Wentworth, P. A. *et al., Mol. Immunol.* 32:603, 1995; Celis, E. *et al., Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al., J. Immunol.* 158:1796, 1997; Kawashima, I. *et al., Human Immunol.* 59:1, 1998); This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the peptide become activated during this time and are detected using, *e.g.*, a ^{51}Cr-release assay involving peptide sensitized target cells.

2) Immunization of HLA transgenic mice (*see, e.g.*, Wentworth, P. A. *et al., J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al., Int. Immunol.* 8:651, 1996; Alexander, J. *et al., J. Immunol.* 159:4753, 1997); In this method, peptides in incomplete Freund's adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr-release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.

3) Demonstration of recall T cell responses from immune individuals who have effectively been vaccinated, recovered from infection, and/or from chronically infected patients (*see, e.g.*, Rehermann, B. *et al., J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al., Immunity* 7:97, 1997; Bertoni, R. *et al., J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al., J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al., J. Virol.* 71:6011, 1997); In applying this strategy, recall responses are detected by culturing PBL from subjects that have been naturally exposed to the antigen, for instance through infection, and thus have generated an immune response "naturally", or from patients who were vaccinated against the infection. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays for T cell activity including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

The following describes the peptide epitopes and corresponding nucleic acids of the invention.

IV.C. Binding Affinity of Peptide Epitopes for HLA Molecules

As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to vaccine development. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules.

CTL-inducing peptides of interest for vaccine compositions preferably include those that have an IC_{50} or binding affinity value for class I HLA molecules of 500 nM or better (*i.e.*, the value is ≤ 500 nM). HTL-inducing peptides preferably include those that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, (*i.e.*, the value is ≤ 1,000 nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or vaccines.

As disclosed herein, higher HLA binding affinity is correlated with greater immunogenicity. Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to be immunogenic, as contrasted with about 50% of the peptides which bind with intermediate affinity. Moreover, higher binding affinity peptides lead to more vigorous immunogenic responses. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used. Thus, in preferred embodiments of the invention, high affinity binding epitopes are particularly useful.

The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens has been determined for the first time in the art by the present inventors. The correlation between binding affinity and immunogenicity was analyzed in two different experimental approaches (*see, e.g.*, Sette, *et al., J. Immunol.* 153:5586-5592, 1994). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the shaping of T cell responses (*see, e.g.,* Schaeffer *et al. Proc. Natl. Acad. Sci. USA* 86:4649-4653, 1989).

An affinity threshold associated with immunogenicity in the context of HLA class II DR molecules has also been delineated (*see, e.g.*, Southwood *et al. J. Immunology* 160:3363-3373,1998, and co-pending U.S.S.N. 09/009,953 filed 1/21/98). In order to define a biologically significant threshold of DR binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the motif) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC_{50} of 1000 nM or greater. Thus, 1000 nM can be defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

The binding affinity of peptides for HLA molecules can be determined as described in Example 1, below.

IV.D. Peptide Epitope Binding Motifs and Supermotifs

Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues

required for allele-specific binding to HLA molecules have been identified. The presence of these residues correlates with binding affinity for HLA molecules. The identification of motifs and/or supermotifs that correlate with high and intermediate affinity binding is an important issue with respect to the identification of immunogenic peptide epitopes for the inclusion in a vaccine. Kast *et al.* (*J. Immunol.* 152:3904-3912, 1994) have shown that motif-bearing peptides account for 90% of the epitopes that bind to allele-specific HLA class I molecules. In this study all possible peptides of 9 amino acids in length and overlapping by eight amino acids (240 peptides), which cover the entire sequence of the E6 and E7 proteins of human papillomavirus type 16, were evaluated for binding to five allele-specific HLA molecules that are expressed at high frequency among different ethnic groups. This unbiased set of peptides allowed an evaluation of the predictive value of HLA class I motifs. From the set of 240 peptides, 22 peptides were identified that bound to an allele-specific HLA molecule with high or intermediate affinity. Of these 22 peptides, 20 (*i.e.* 91%) were motif-bearing. Thus, this study demonstrates the value of motifs for the identification of peptide epitopes for inclusion in a vaccine: application of motif-based identification techniques will identify about 90% of the potential epitopes in a target antigen protein sequence.

Such peptide epitopes are identified in the Tables described below.

Peptides of the present invention may also comprise epitopes that bind to MHC class II DR molecules. A greater degree of heterogeneity in both size and binding frame position of the motif, relative to the N and C termini of the peptide, exists for class II peptide ligands. This increased heterogeneity of HLA class II peptide ligands is due to the structure of the binding groove of the HLA class II molecule which, unlike its class I counterpart, is open at both ends. Crystallographic analysis of HLA class II DRB*0101-peptide complexes showed that the major energy of binding is contributed by peptide residues complexed with complementary pockets on the DRB*0101 molecules. An important anchor residue engages the deepest hydrophobic pocket (*see, e.g.*, Madden, D.R. *Ann. Rev. Immunol.* 13:587, 1995) and is referred to as position 1 (P1). P1 may represent the N-terminal residue of a class II binding peptide epitope, but more typically is flanked towards the N-terminus by one or more residues. Other studies have also pointed to an important role for the peptide residue in the 6th position towards the C-terminus, relative to P1, for binding to various DR molecules.

In the past few years evidence has accumulated to demonstrate that a large fraction of HLA class I and class II molecules can be classified into a relatively few

supertypes, each characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus, peptides of the present invention are identified by any one of several HLA-specific amino acid motifs (*see, e.g.*, Tables I-III), or if the presence of the motif corresponds to the ability to bind several allele-specific HLA antigens, a supermotif. The HLA molecules that bind to peptides that possess a particular amino acid supermotif are collectively referred to as an HLA "supertype."

The peptide motifs and supermotifs described below, and summarized in Tables I-III, provide guidance for the identification and use of peptide epitopes in accordance with the invention.

Examples of peptide epitopes bearing a respective supermotif or motif are included in Tables as designated in the description of each motif or supermotif below. The Tables include a binding affinity ratio listing for some of the peptide epitopes. The ratio may be converted to IC_{50} by using the following formula: IC_{50} of the standard peptide/ratio = IC_{50} of the test peptide (*i.e.*, the peptide epitope). The IC_{50} values of standard peptides used to determine binding affinities for Class I peptides are shown in Table IV. The IC_{50} values of standard peptides used to determine binding affinities for Class II peptides are shown in Table V. The peptides used as standards for the binding assays described herein are examples of standards; alternative standard peptides can also be used when performing binding studies.

To obtain the peptide epitope sequences listed in each Table, protein sequence data for all of the HIV-1 isolates present in the 1999 Los Alamos database (http://hiv-web.lanl.gov) were evaluated for the presence of the designated supermotif or motif. A listing of the strains is provided in Table XXVI. Nine HIV-1 structural and regulatory proteins, gag, pol, env, nef, rev, tat, vif, vpr, and vpu, were included in the analysis. Peptide epitopes were additionally evaluated on the basis of their conservancy (*i.e.*, the amount of variance) among the available protein sequences for each HIV antigen. A criterion for conservancy used to generate the peptides set out in Tables VII-XX requires that the entire sequence of an HLA class I binding peptide be totally conserved in 15% of the sequences available for a specific HIV antigen. Similarly, a criterion for conservancy requires that the entire 9-mer core region of an HLA class II binding peptide be totally conserved in 15% of the sequences available for a specific protein. The percent conservancy of the selected peptide epitopes is indicated on the Tables. The frequency, *i.e.* the number of sequences of the HIV protein antigen in which the totally conserved

peptide sequence was identified, is also shown. The "pos" (position) column in the Tables designates the amino acid position in the HIV protein that corresponds to the first amino acid residue of the epitope. The "number of amino acids" indicates the number of residues in the epitope sequence.

HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes:

The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs delineated below are summarized in Table I. The HLA class I motifs set out in Table I(a) are those most particularly relevant to the invention claimed here. Primary and secondary anchor positions are summarized in Table II. Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table VI. In some cases, peptide epitopes may be listed in both a motif and a supermotif Table. The relationship of a particular motif and respective supermotif is indicated in the description of the individual motifs.

IV.D.1. HLA-A1 supermotif

The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A*0101, A*2601, A*2602, A*2501, and A*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in Table VI. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A1 supermotif are set forth in Table VII.

IV.D.2. HLA-A2 supermotif

Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993) and

cross-reactive binding among HLA-A2 and -A28 molecules have been described. (*See, e.g.*, Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table VI. As explained in detail below, binding to each of the individual allele-specific HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise an A2 supermotif are set forth in Table VIII. The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.3. HLA-A3 supermotif

The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (*see*, *e.g.*, Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-specific HLA molecules predicted to be members of the A3 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A3 supermotif are set forth in Table IX.

IV.D.4. HLA-A24 supermotif

The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sette and Sidney, *Immunogenetics*, in press, 1999). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e.*, the A24 supertype) includes at least A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A24 supermotif are set forth in Table X.

IV.D.5. HLA-B7 supermotif

The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e.*, the HLA-B7 supertype) is comprised of at least twenty six HLA-B proteins including: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g.,* Sidney, *et al., J. Immunol.* 154:247, 1995; Barber, *et al., Curr. Biol.* 5:179, 1995; Hill, *et al., Nature* 360:434, 1992; Rammensee, *et al., Immunogenetics* 41:178, 1995 for reviews of relevant data). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B7 supermotif are set forth in Table XI.

IV.D.6. HLA-B27 supermotif

The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.*, the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B27 supermotif are set forth on Table XII.

IV.D.7. HLA-B44 supermotif

The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.*, the B44 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

IV.D.8. HLA-B58 supermotif

The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in

press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.*, the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific HLA molecules predicted to be members of the B58 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B58 supermotif are set forth on Table XIII.

IV.D.9. HLA-B62 supermotif

The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.*, the B62 supertype) include at least: B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B62 supermotif are set forth on Table XIV.

IV.D.10. HLA-A1 motif

The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, J. Immunol., 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data).

Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise either A1 motif are set forth on Table XV. Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also included in the listing of HLA-A1 supermotif-bearing peptide epitopes listed in Table VII, as these residues are a subset of the A1 supermotif primary anchors.

IV.D.11. HLA-A*0201 motif

An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g.*, Hunt *et al.*, Science 255:1261-1263, March 6, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g.*, Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Ruppert *et al.*, *Cell* 74:929-937, 1993; Sidney *et al.*, *Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g.*, Ruppert *et al.*, *Cell* 74:929-937, 1993). These are shown in Table II. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise an A*0201 motif are set forth on Table VIII. The A*0201 motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.12. HLA-A3 motif

The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, *Proc. Natl. Acad. Sci USA* 90:1508, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A3 motif are set forth on Table XVI. Those peptide epitopes that also comprise the A3 supermotif are also listed in Table IX. The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.

IV.D.13. HLA-A11 motif

The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Zhang *et al.*, *Proc. Natl. Acad. Sci USA* 90:2217-2221, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A11 motif are set forth on Table XVII; peptide epitopes comprising the A3 allele-specific motif are also present in this Table because of the extensive overlap between the A3 and A11 motif primary anchor specificities. Further, those peptide epitopes that comprise the A3 supermotif are also listed in Table IX.

IV.D.14. HLA-A24 motif

The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kondo et al., J. Immunol.* 155:4307-4312, 1995; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or

secondary anchor positions; preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A24 motif are set forth on Table XVIII. These epitopes are also listed in Table X, which sets forth HLA-A24-supermotif-bearing peptide epitopes, as the primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.

Motifs Indicative of Class II HTL Inducing Peptide Epitopes

The primary and secondary anchor residues of the HLA class II peptide epitope supermotifs and motifs delineated below are summarized in Table III.

IV.D.15. HLA DR-1-4-7 supermotif

Motifs have also been identified for peptides that bind to three common HLA class II allele-specific HLA molecules: HLA DRB1*0401, DRB1*0101, and DRB1*0701 (*see, e.g.*, the review by Southwood *et al. J. Immunology* 160:3363-3373,1998). Collectively, the common residues from these motifs delineate the HLA DR-1-4-7 supermotif. Peptides that bind to these DR molecules carry a supermotif characterized by a large aromatic or hydrophobic residue (Y, F, W, L, I, V, or M) as a primary anchor residue in position 1, and a small, non-charged residue (S, T, C, A, P, V, I, L, or M) as a primary anchor residue in position 6 of a 9-mer core region. Allele-specific secondary effects and secondary anchors for each of these HLA types have also been identified (Southwood *et al., supra*). These are set forth in Table III. Peptide binding to HLA-DRB1*0401, DRB1*0101, and/or DRB1*0701 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Conserved 9-mer core regions (*i.e.*, sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis), comprising the DR-1-4-7 supermotif, wherein position 1 of the supermotif is at position 1 of the nine-residue core, are set forth in Table XIXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in section "a" of the Table. Cross-reactive binding data for exemplary 15-residue supermotif-bearing peptides are shown in Table XIXb.

IV.D.16. HLA DR3 motifs

Two alternative motifs (*i.e.*, submotifs) characterize peptide epitopes that bind to HLA-DR3 molecules (*see, e.g.*, Geluk *et al.*, *J. Immunol.* 152:5742, 1994). In the first motif (submotif DR3A) a large, hydrophobic residue (L, I, V, M, F, or Y) is present in anchor position 1 of a 9-mer core, and D is present as an anchor at position 4, towards the carboxyl terminus of the epitope. As in other class II motifs, core position 1 may or may not occupy the peptide N-terminal position.

The alternative DR3 submotif provides for lack of the large, hydrophobic residue at anchor position 1, and/or lack of the negatively charged or amide-like anchor residue at position 4, by the presence of a positive charge at position 6 towards the carboxyl terminus of the epitope. Thus, for the alternative allele-specific DR3 motif (submotif DR3B): L, I, V, M, F, Y, A, or Y is present at anchor position 1; D, N, Q, E, S, or T is present at anchor position 4; and K, R, or H is present at anchor position 6. Peptide binding to HLA-DR3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Conserved 9-mer core regions (*i.e.*, those sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) corresponding to a nine residue sequence comprising the DR3A submotif (wherein position 1 of the motif is at position 1 of the nine residue core) are set forth in Table XXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in Table XXa. Table XXb shows binding data of exemplary DR3 submotif A-bearing peptides.

Conserved 9-mer core regions (*i.e.*, those that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) comprising the DR3B submotif and respective exemplary 15-mer peptides comprising the DR3 submotif-B epitope are set forth in Table XXc. Table XXd shows binding data of exemplary DR3 submotif B-bearing peptides.

Each of the HLA class I or class II peptide epitopes set out in the Tables herein are deemed singly to be an inventive aspect of this application. Further, it is also an inventive aspect of this application that each peptide epitope may be used in combination with any other peptide epitope.

IV.E. Enhancing Population Coverage of the Vaccine

Vaccines that have broad population coverage are preferred because they are more commercially viable and generally applicable to the most people. Broad population coverage can be obtained using the peptides of the invention (and nucleic acid compositions that encode such peptides) through selecting peptide epitopes that bind to HLA alleles which, when considered in total, are present in most of the population. Table XXI lists the overall frequencies of the HLA class I supertypes in various ethnicities (Table XXIa) and the combined population coverage achieved by the A2-, A3-, and B7-supertypes (Table XXIb). The A2-, A3-, and B7 supertypes are each present on the average of over 40% in each of these five major ethnic groups. Coverage in excess of 80% is achieved with a combination of these supermotifs. These results suggest that effective and non-ethnically biased population coverage is achieved upon use of a limited number of cross-reactive peptides. Although the population coverage reached with these three main peptide specificities is high, coverage can be expanded to reach 95% population coverage and above, and more easily achieve truly multispecific responses upon use of additional supermotif or allele-specific motif bearing peptides.

The B44-, A1-, and A24-supertypes are each present, on average, in a range from 25% to 40% in these major ethnic populations (Table XXIa). While less prevalent overall, the B27-, B58-, and B62 supertypes are each present with a frequency >25% in at least one major ethnic group (Table XXIa). Table XXIb summarizes the estimated prevalence of combinations of HLA supertypes that have been identified in five major ethnic groups. The incremental coverage obtained by the inclusion of A1,- A24-, and B44-supertypes to the A2, A3, and B7 coverage and coverage obtained with all of the supertypes described herein, is shown.

The data presented herein, together with the previous definition of the A2-, A3-, and B7-supertypes, indicates that all antigens, with the possible exception of A29, B8, and B46, can be classified into a total of nine HLA supertypes. By including epitopes from the six most frequent supertypes, an average population coverage of 99% is obtained for five major ethnic groups..

IV.F. Immune Response-Stimulating Peptide Analogs

In general, CTL and HTL responses are not directed against all possible epitopes. Rather, they are restricted to a few "immunodominant" determinants (Zinkernagel, *et al., Adv. Immunol.* 27:5159, 1979; Bennink, *et al., J. Exp. Med.* 168:19351939, 1988; Rawle,

et al., J. Immunol. 146:3977-3984, 1991). It has been recognized that immunodominance (Benacerraf, *et al., Science* 175:273-279, 1972) could be explained by either the ability of a given epitope to selectively bind a particular HLA protein (determinant selection theory) (Vitiello, *et al., J. Immunol.* 131:1635, 1983); Rosenthal, *et al., Nature* 267:156-158, 1977), or to be selectively recognized by the existing TCR (T cell receptor) specificities (repertoire theory) (Klein, J., IMMUNOLOGY, THE SCIENCE OF SELFNONSELF DISCRIMINATION, John Wiley & Sons, New York, pp. 270-310, 1982). It has been demonstrated that additional factors, mostly linked to processing events, can also play a key role in dictating, beyond strict immunogenicity, which of the many potential determinants will be presented as immunodominant (Sercarz, *et al., Annu. Rev. Immunol.* 11:729-766, 1993).

The concept of dominance and subdominance is relevant to immunotherapy of both infectious diseases and cancer. For example, in the course of chronic viral disease, recruitment of subdominant epitopes can be important for successful clearance of the infection, especially if dominant CTL or HTL specificities have been inactivated by functional tolerance, suppression, mutation of viruses and other mechanisms (Franco, *et al., Curr. Opin. Immunol.* 7:524-531, 1995). In the case of cancer and tumor antigens, CTLs recognizing at least some of the highest binding affinity peptides might be functionally inactivated. Lower binding affinity peptides are preferentially recognized at these times, and may therefore be preferred in therapeutic or prophylactic anti-cancer vaccines.

In particular, it has been noted that a significant number of epitopes derived from known non-viral tumor associated antigens (TAA) bind HLA class I with intermediate affinity (IC_{50} in the 50-500 nM range). For example, it has been found that 8 of 15 known TAA peptides recognized by tumor infiltrating lymphocytes (TIL) or CTL bound in the 50-500 nM range. (These data are in contrast with estimates that 90% of known viral antigens were bound by HLA class I molecules with IC_{50} of 50 nM or less, while only approximately 10% bound in the 50-500 nM range (Sette, *et al., J. Immunol.*, 153:558-5592, 1994). In the cancer setting this phenomenon is probably due to elimination or functional inhibition of the CTL recognizing several of the highest binding peptides, presumably because of T cell tolerization events.

Without intending to be bound by theory, it is believed that because T cells to dominant epitopes may have been clonally deleted, selecting subdominant epitopes may allow existing T cells to be recruited, which will then lead to a therapeutic or prophylactic

response. However, the binding of HLA molecules to subdominant epitopes is often less vigorous than to dominant ones. Accordingly, there is a need to be able to modulate the binding affinity of particular immunogenic epitopes for one or more HLA molecules, and thereby to modulate the immune response elicited by the peptide, for example to prepare analog peptides which elicit a more vigorous response. This ability would greatly enhance the usefulness of peptide epitope-based vaccines and therapeutic agents.

Although peptides with suitable cross-reactivity among all alleles of a superfamily are identified by the screening procedures described above, cross-reactivity is not always as complete as possible, and in certain cases procedures to increase cross-reactivity of peptides can be useful; moreover, such procedures can also be used to modify other properties of the peptides such as binding affinity or peptide stability. Having established the general rules that govern cross-reactivity of peptides for HLA alleles within a given motif or supermotif, modification (*i.e.,* analoging) of the structure of peptides of particular interest in order to achieve broader (or otherwise modified) HLA binding capacity can be performed. More specifically, peptides which exhibit the broadest cross-reactivity patterns, can be produced in accordance with the teachings herein. The present concepts related to analog generation are set forth in greater detail in co-pending U.S.S.N. 09/226,775 filed 1/6/99.

In brief, the strategy employed utilizes the motifs or supermotifs which correlate with binding to certain HLA molecules. The motifs or supermotifs are defined by having primary anchors, and in many cases secondary anchors. Analog peptides can be created by substituting amino acid residues at primary anchor, secondary anchor, or at primary and secondary anchor positions. Generally, analogs are made for peptides that already bear a motif or supermotif. Preferred secondary anchor residues of supermotifs and motifs that have been defined for HLA class I and class II binding peptides are shown in Tables II and III, respectively.

For a number of the motifs or supermotifs in accordance with the invention, residues are defined which are deleterious to binding to allele-specific HLA molecules or members of HLA supertypes that bind the respective motif or supermotif (Tables II and III). Accordingly, removal of such residues that are detrimental to binding can be performed in accordance with the present invention. For example, in the case of the A3 supertype, when all peptides that have such deleterious residues are removed from the population of peptides used in the analysis, the incidence of cross-reactivity increased from 22% to 37% (*see, e.g.,* Sidney, J. *et al.,* *Hu. Immunol.* 45:79, 1996). Thus, one

strategy to improve the cross-reactivity of peptides within a given supermotif is simply to delete one or more of the deleterious residues present within a peptide and substitute a small "neutral" residue such as Ala (that may not influence T cell recognition of the peptide). An enhanced likelihood of cross-reactivity is expected if, together with elimination of detrimental residues within a peptide, "preferred" residues associated with high affinity binding to an allele-specific HLA molecule or to multiple HLA molecules within a superfamily are inserted.

To ensure that an analog peptide, when used as a vaccine, actually elicits a CTL response to the native epitope *in vivo* (or, in the case of class II epitopes, elicits helper T cells that cross-react with the wild type peptides), the analog peptide may be used to immunize T cells *in vitro* from individuals of the appropriate HLA allele. Thereafter, the immunized cells' capacity to induce lysis of wild type peptide sensitized target cells is evaluated. It will be desirable to use as antigen presenting cells, cells that have been either infected, or transfected with the appropriate genes, or, in the case of class II epitopes only, cells that have been pulsed with whole protein antigens, to establish whether endogenously produced antigen is also recognized by the relevant T cells.

Another embodiment of the invention is to create analogs of weak binding peptides, to thereby ensure adequate numbers of cross-reactive cellular binders. Class I binding peptides exhibiting binding affinities of 500-5000 nM, and carrying an acceptable but suboptimal primary anchor residue at one or both positions can be "fixed" by substituting preferred anchor residues in accordance with the respective supertype. The analog peptides can then be tested for crossbinding activity.

Another embodiment for generating effective peptide analogs involves the substitution of residues that have an adverse impact on peptide stability or solubility in, *e.g.*, a liquid environment. This substitution may occur at any position of the peptide epitope. For example, a cysteine (C) can be substituted out in favor of α-amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α-amino butyric acid for C not only alleviates this problem, but actually improves binding and crossbinding capability in certain instances (*see*, *e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999). Substitution of cysteine with α-amino butyric acid may occur at any residue of a peptide epitope, *i.e.* at either anchor or non-anchor positions.

IV.G. Computer Screening of Protein Sequences from Disease-Related Antigens for Supermotif- or Motif-Bearing Peptides

In order to identify supermotif- or motif-bearing epitopes in a target antigen, a native protein sequence, *e.g.*, a tumor-associated antigen, or sequences from an infectious organism, or a donor tissue for transplantation, is screened using a means for computing, such as an intellectual calculation or a computer, to determine the presence of a supermotif or motif within the sequence. The information obtained from the analysis of native peptide can be used directly to evaluate the status of the native peptide or may be utilized subsequently to generate the peptide epitope.

Computer programs that allow the rapid screening of protein sequences for the occurrence of the subject supermotifs or motifs are encompassed by the present invention; as are programs that permit the generation of analog peptides. These programs are implemented to analyze any identified amino acid sequence or operate on an unknown sequence and simultaneously determine the sequence and identify motif-bearing epitopes thereof; analogs can be simultaneously determined as well. Generally, the identified sequences will be from a pathogenic organism or a tumor-associated peptide. For example, the target molecules considered herein include, without limitation, the gag, pol, env, nef, rev, tat, vif, vpr, and vpu proteins of HIV.

In cases where the sequence of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide, be conserved in a designated percentage, of the sequences evaluated for a specific protein antigen.

Because HIV rapidly mutates thereby resulting in the generation of virus strains that have divergent amino acid sequences, an alternative method of selecting epitopes for inclusion in a vaccine composition is employed herein. In order to target a broad population that may be infected with a number of different strains, it is preferable to include in vaccine compositions epitopes that are representative of HIV antigen sequences from different HIV strains. For example, by selecting 5 epitopes from the same region, each of which is 20% conserved among HIV strains, the combination of the epitopes achieves 100% coverage of that region. As appreciated y those in the art, lower or higher degress of conservancy, such as the 15% conservancy used for identification of

the epitopes set out in Tables VII-XX, can be employed as appropriate for a given antigenic target.

It is important that the selection criteria utilized for prediction of peptide binding are as accurate as possible, to correlate most efficiently with actual binding. Prediction of peptides that bind, for example, to HLA-A*0201, on the basis of the presence of the appropriate primary anchors, is positive at about a 30% rate (*see, e.g.*, Ruppert, J. *et al. Cell* 74:929, 1993). However, by extensively analyzing peptide-HLA binding data disclosed herein, data in related patent applications, and data in the art, the present inventors have developed a number of allele-specific polynomial algorithms that dramatically increase the predictive value over identification on the basis of the presence of primary anchor residues alone. These algorithms take into account not only the presence or absence of primary anchors, but also consider the positive or deleterious presence of secondary anchor residues (to account for the impact of different amino acids at different positions). The algorithms are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2i} \times a_{3i} \ldots \times a_{ni}$$

where a_{ji} is a coefficient that represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. An important assumption of this method is that the effects at each position are essentially independent of each other. This assumption is justified by studies that demonstrated that peptides are bound to HLA molecules and recognized by T cells in essentially an extended conformation. Derivation of specific algorithm coefficients has been described, for example, in Gulukota, K. *et al.*, *J. Mol. Biol.* 267:1258, 1997.

Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (*see, e.g.*, Milik *et al.*, *Nature Biotechnology* 16:753, 1998; Altuvia *et al.*, *Hum. Immunol.* 58:1, 1997; Altuvia *et al*, *J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al.*, *Bioinformatics* 14:121-130, 1998; Parker *et al.*, *J. Immunol.* 152:163, 1993; Meister *et al.*, *Vaccine* 13:581, 1995; Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994; Sturniolo *et al.*, *Nature Biotechnol.* 17:555 1999).

For example, it has been shown that in sets of A*0201 motif-bearing peptides containing at least one preferred secondary anchor residue while avoiding the presence of

any deleterious secondary anchor residues, 69% of the peptides will bind A*0201 with an IC_{50} less than 500 nM (Ruppert, J. *et al. Cell* 74:929, 1993). These algorithms are also flexible in that cut-off scores may be adjusted to select sets of peptides with greater or lower predicted binding properties, as desired.

In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS' program (Devereux, *et* al. *Nucl. Acids Res.* 12:387-395, 1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs of the invention in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

In accordance with the procedures described above, HIV peptide epitopes and analogs thereof that are able to bind HLA supertype groups or allele-specific HLA molecules have been identified (Tables VII-XX).

IV.H. Preparation of Peptide Epitopes

Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or from natural sources such as native tumors or pathogenic organisms. Peptide epitopes may be synthesized individually or as polyepitopic peptides. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to native fragments or particles.

The peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in accordance with the invention are either free of modifications such as glycosylation, side chain oxidation, or phosphorylation; or they contain these modifications, subject to the condition that modifications do not destroy the biological activity of the peptides as described herein.

When possible, it may be desirable to optimize HLA class I binding peptide epitopes of the invention to a length of about 8 to about 13 amino acid residues, preferably 9 to 10. HLA class II binding peptide epitopes may be optimized to a length of about 6 to about 30 amino acids in length, preferably to between about 13 and about 20 residues. Preferably, the peptide epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules.

In alternative embodiments, epitopes of the invention can be linked as a polyepitopic peptide, or as a minigene that encodes a polyepitopic peptide.

In another embodiment, it is preferred to identify native peptide regions that contain a high concentration of class I and/or class II epitopes. Such a sequence is generally selected on the basis that it contains the greatest number of epitopes per amino acid length. It is to be appreciated that epitopes can be present in a nested or overlapping manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope; upon intracellular processing, each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. This larger, preferably multi-epitopic, peptide can be generated synthetically, recombinantly, or via cleavage from the native source.

The peptides of the invention can be prepared in a wide variety of ways. For the preferred relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (*See*, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984). Further, individual peptide epitopes can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant polypeptides which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

The nucleotide coding sequence for peptide epitopes of the preferred lengths contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al., J. Am. Chem. Soc.* 103:3185 (1981). Peptide analogs can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode the native peptide sequence; exemplary nucleic acid substitutions are those that encode an amino acid defined by the motifs/supermotifs herein. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

IV.I. Assays to Detect T-Cell Responses

Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to the appropriate HLA proteins. These assays may involve evaluating the binding of a peptide of the invention to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* lacking peptide therein) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can give rise to CTL populations capable of reacting with selected target cells associated with

a disease. Corresponding assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

Conventional assays utilized to detect T cell responses include proliferation assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant non-human mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides and that have been transfected with the appropriate human class I gene, may be used to test for the capacity of the peptide to induce *in vitro* primary CTL responses.

Peripheral blood mononuclear cells (PBMCs) may be used as the responder cell source of CTL precursors. The appropriate antigen-presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that kill radio-labeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed forms of the antigen from which the peptide sequence was derived.

More recently, a method has been devised which allows direct quantification of antigen-specific T cells by staining with Fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other relatively recent technical developments include staining for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998).

HTL activation may also be assessed using such techniques known to those in the art such as T cell proliferation and secretion of lymphokines, *e.g.* IL-2 (*see, e.g.* Alexander *et al.*, Immunity 1:751-761, 1994).

Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse models including mice

with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed. Additional transgenic mouse models with other HLA alleles may be generated as necessary. Mice may be immunized with peptides emulsified in Incomplete Freund's Adjuvant and the resulting T cells tested for their capacity to recognize peptide-pulsed target cells and target cells transfected with appropriate genes. CTL responses may be analyzed using cytotoxicity assays described above. Similarly, HTL responses may be analyzed using such assays as T cell proliferation or secretion of lymphokines.

Exemplary immunogenic peptide epitopes are set out in Table XXIII.

IV.J. Use of Peptide Epitopes as Diagnostic Agents and for Evaluating Immune Responses

HLA class I and class II binding peptides as described herein are used, in one embodiment of the invention, as reagents to evaluate an immune response. The immune response to be evaluated may be induced by using as an immunogen any agent that may result in the production of antigen-specific CTLs or HTLs that recognize and bind to the peptide epitope(s) to be employed as the reagent. The peptide reagent need not be used as the immunogen. Assay systems that may be used for such an analysis include relatively recent technical developments such as tetramers, staining for intracellular lymphokines and interferon release assays, or ELISPOT assays.

For example, a peptide of the invention can be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs (*see, e.g.*, Ogg *et al.*, *Science* 279:2103-2106, 1998; and Altman *et al.*, *Science* 174:94-96, 1996) and determine the frequency of the antigen-specific CTL population in a sample of peripheral blood mononuclear cells.

A tetramer reagent using a peptide of the invention can typically be generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and β_2-microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the heavy chain at a site that was previously engineered into the protein. Tetramer formation is then induced by the addition of streptavidin. By means of fluorescently labeled streptavidin, the

tetramer can be used to stain antigen-specific cells. The cells may then be identified, for example, by flow cytometry. Such an analysis may be used for diagnostic or prognostic purposes.

Peptides of the invention are also used as reagents to evaluate immune recall responses. (see, *e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503-513, 1997 and Penna *et al.*, *J. Exp. Med.* 174:1565-1570, 1991.) For example, patient PBMC samples from individuals infected with HIV may be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells may be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.

The peptides are also used as reagents to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed using, for example, either of the methods described above. The patient is HLA typed, and peptide epitope reagents that recognize the allele-specific molecules present in that patient are selected for the analysis. The immunogenicity of the vaccine is indicated by the presence of HIV epitope-specific CTLs and/or HTLs in the PBMC sample.

The peptides of the invention are also used to make antibodies, using techniques well known in the art (see, *e.g.* *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual Harlow,* Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989), which may be useful as reagents to diagnose HIV infection. Such antibodies include those that recognize a peptide in the context of an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

IV.K. Vaccine Compositions

Vaccines and methods of preparing vaccines that contain an immunogenically effective amount of one or more peptides as described herein are further embodiments of the invention. Once appropriately immunogenic epitopes have been defined, they can be sorted and delivered by various means, herein referred to as "vaccine" compositions. Such vaccine compositions can include, for example, lipopeptides (*e.g.*,Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991: Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see*, *e.g.*,

Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions of the invention include nucleic acid-mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can also be administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the

immunogenic peptide, and thereby elicits a host CTL and/or HTL response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Furthermore, vaccines in accordance with the invention encompass compositions of one or more of the claimed peptides. A peptide can be present in a vaccine individually. Alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition can be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.*, acceptable) diluent such as water, or saline, preferably phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS).

Upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later infection, or at least partially resistant to developing an ongoing chronic infection, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some embodiments, it may be desirable to combine the class I peptide components with components that induce or facilitate neutralizing antibody and or helper T cell responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PanDR molecule, *e.g.*, PADRE™ (Epimmune, San Diego, CA; described, *e.g.*, in U.S. Patent Number 5,736,142).

A vaccine of the invention can also include antigen-presenting cells (APC), such as dendritic cells (DC), as a vehicle to present peptides of the invention. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*. For example, dendritic cells are transfected, *e.g.*, with a minigene in accordance with the invention, or are pulsed with peptides. The dendritic cell can then be administered to a patient to elicit immune responses *in vivo*.

Vaccine compositions, either DNA- or peptide-based, can also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

Antigenic peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat chronic infections, or tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated antigen) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cell (an infected cell or a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells.

The vaccine compositions of the invention can also be used in combination with other treatments used for HIV infection, including use in combination with therapy regimens including protease inhibitors and other immune adjuvants such as IL-2.

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polyepitopic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. Exemplary epitopes that may be utilized in a vaccine to treat or prevent HIV infection are set out in Tables XXXVII and XXXVIII. It is preferred that each of the following principles are balanced in order to make the selection. The multiple epitopes to be incorporated in a given vaccine composition can be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with HIV clearance. For HLA Class I this includes 3-4 epitopes that come from at least one antigen of HIV. For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one HIV antigen (*see e.g.*, Rosenberg *et al.*, *Science* 278:1447-1450).

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often useful to select analogs because the patient may have developed tolerance to the native epitope. When selecting epitopes for infectious disease-related antigens it is preferable to select either native or analoged epitopes.

5.) Of particular relevance are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A nested peptide sequence can comprise both HLA class I and HLA class II epitopes. When providing nested epitopes, a general objective is to provide the greatest number of epitopes per sequence. Thus, an aspect is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a multi-epitopic sequence, such as a sequence comprising nested epitopes, it is generally important to screen the sequence

in order to insure that it does not have pathological or other deleterious biological properties.

6.) If a polyepitopic protein is created, or when creating a minigene, an objective is to generate the smallest peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial polyepitopic peptide, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can, for example, be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

7.) In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

IV.K.1. Minigene Vaccines

A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention.

The use of multi-epitope minigenes is described below and in, *e.g.*, co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822,

1996; Whitton, J. L. *et al., J. Virol.* 67:348, 1993; Hanke, R. *et al., Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding nine dominant HLA-A*0201- and A11-restricted epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), a PADRE™ universal helper T cell (HTL) epitope, and an endoplasmic reticulum-translocating signal sequence was engineered.

The immunogenicity of a multi-epitopic minigene can be tested in transgenic mice to evaluate the magnitude of CTL induction responses against the epitopes tested. Further, the immunogenicity of DNA-encoded epitopes *in vivo* can be correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. Thus, these experiments can show that the minigene serves to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the encoded epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in the minigene sequence include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector

elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune

response by co-expression of immunosuppressive molecules (*e.g.* TGF-β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al., Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytolysis, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of

HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytolysis of peptide-loaded, ^{51}Cr-labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

IV.K.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising the peptides of the present invention, or analogs thereof, which have immunostimulatory activity may be modified to provide desired attributes, such as improved serum half life, or to enhance immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. The use of T helper epitopes in conjunction with CTL epitopes to enhance immunogenicity is illustrated, for example, in the co-pending applications U.S.S.N. 08/820,360, U.S.S.N. 08/197,484, and U.S.S.N. 08/464,234.

Although a CTL peptide can be directly linked to a T helper peptide, often CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer.

When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues. The CTL peptide epitope can be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in the majority of the population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. These are known as "loosely HLA-restricted" or "promiscuous" T helper sequences. Examples of amino acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: 51484), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: 51485), and *Streptococcus* 18kD protein at positions 116 (GAVDSILGGVATYGAA; SEQ ID NO: 51486). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see*, *e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferrably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, they can be modified to include D-amino acids to increase their resistance to proteases and thus extend their serum half life, or they can be conjugated to other molecules such as lipids, proteins, carbohydrates, and the like to increase their biological activity. For example, a T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

III.K.3. Combinations of CTL Peptides with T Cell Priming Agents

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ε-and α-amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic composition comprises palmitic acid attached to ε- and α- amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see*, *e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P_3CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

CTL and/or HTL peptides can also be modified by the addition of amino acids to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH_2 acylation, *e.g.*, by alkanoyl (C1-C20) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

IV.K.4. Vaccine Compositions Comprising DC Pulsed with CTL and/or HTL Peptides

An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes complexed with HLA molecules on their surfaces.

The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to one or more HIV antigens of interest. Optionally, a helper T cell (HTL) peptide such as a PADRE family molecule, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention, preferably comprising epitopes from multiple HIV antigens, is used to treat HIV infection.

IV.L. Administration of Vaccines for Therapeutic or Prophylactic Purposes

The peptides of the present invention and pharmaceutical and vaccine compositions of the invention are useful for administration to mammals, particularly humans, to treat and/or prevent HIV infection. Vaccine compositions containing the peptides of the invention are administered to a patient infected with HIV or to an individual susceptible to, or otherwise at risk for, HIV infection to elicit an immune response against HIV antigens and thus enhance the patient's own immune response capabilities.

As discussed herein, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The peptides (or DNA encoding them) can be administered individually or as fusions of one or more peptide sequences. The manner in which the peptide is contacted with the CTL or HTL is not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vivo* or *in vitro*. If the contacting occurs *in vivo*, the peptide itself can be administered to the patient, or other vehicles, *e.g.*, DNA vectors encoding one or more

peptides, viral vectors encoding the peptide(s), liposomes and the like, can be used, as described herein.

When the peptide is contacted *in vitro*, the vaccinating agent can comprise a population of cells, *e.g.*, peptide-pulsed dendritic cells, or HIV-specific CTLs, which have been induced by pulsing antigen-presenting cells *in vitro* with the peptide or by transfecting antigen-presenting cells with a minigene of the invention. Such a cell population is subsequently administered to a patient in a therapeutically effective dose.

In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective CTL and/or HTL response to the virus antigen and to cure or at least partially arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

The vaccine compositions of the invention can also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 µg and the higher value is about 10,000; 20,000; 30,000; or 50,000 µg. Dosage values for a human typically range from about 500 µg to about 50,000 µg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 µg to about 50,000 µg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

Where susceptible individuals are identified prior to infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

For pharmaceutical compositions, the immunogenic peptides of the invention, or DNA encoding them, are generally administered to an individual already infected with HIV. The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. HIV-infected patients can be treated with the immunogenic peptides separately or in conjunction with other treatments as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of HIV infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. The embodiment of the vaccine composition (*i.e.*, including, but not limited to embodiments such as peptide cocktails, polyepitopic polypeptides, minigenes, or HIV antigen-specific CTLs or pulsed dendritic cells) delivered to the patient may vary according to the stage of the disease or the patient's health status. For example, in some patients, a vaccine comprising HIV-specific CTL may be more efficacious in killing HIV-infected cells than alternative embodiments.

The peptide or other compositions used for the treatment or prophylaxis of HIV infection can be used, *e.g.*, in persons who have not manifested symptoms of disease but who act as a disease vector. In this context, it is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to effectively stimulate a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg. Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. Boosting doses may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood.

The peptides and compositions of the present invention may be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

Administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see*, *e.g.*, Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publising Co., Easton, Pennsylvania, 1985).

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic

compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

IV.M. Kits

The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired peptide compositions in a container, preferably in unit dosage form and instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

Summary

Epitopes in accordance with the present invention were successfully used to induce an immune response. Immune responses with these epitopes have been induced by administering the epitopes in various forms. The epitopes have been administered as peptides, as nucleic acids, and as viral vectors comprising nucleic acids that encode the epitope(s) of the invention. Upon administration of peptide-based epitope forms, immune responses have been induced by direct loading of an epitope onto an empty HLA molecule that is expressed on a cell, and via internalization of the epitope and processing via the HLA class I pathway; in either event, the HLA molecule expressing the epitope was then able to interact with and induce a CTL response. Peptides can be delivered directly or using such agents as liposomes. They can additionally be delivered using ballistic delivery, in which the peptides are typically in a crystalline form. When DNA is used to induce an immune response, it is administered either as naked DNA, generally in a dose range of approximately 1-5mg, or via the ballistic "gene gun" delivery, typically in a dose range of approximately 10-100 μg. The DNA can be delivered in a variety of conformations, *e.g.*, linear, circular *etc.* Various viral vectors have also successfully been used that comprise nucleic acids which encode epitopes in accordance with the invention.

Accordingly compositions in accordance with the invention exist in several forms. Embodiments of each of these composition forms in accordance with the invention have been successfully used to induce an immune response.

One composition in accordance with the invention comprises a plurality of peptides. This plurality or cocktail of peptides is generally admixed with one or more pharmaceutically acceptable excipients. The peptide cocktail can comprise multiple

copies of the same peptide or can comprise a mixture of peptides. The peptides can be analogs of naturally occurring epitopes. The peptides can comprise artificial amino acids and/or chemical modifications such as addition of a surface active molecule, *e.g.*, lipidation; acetylation, glycosylation, biotinylation, phosphorylation etc. The peptides can be CTL or HTL epitopes. In a preferred embodiment the peptide cocktail comprises a plurality of different CTL epitopes and at least one HTL epitope. The HTL epitope can be naturally or non-naturally (*e.g.*, PADRE®, Epimmune Inc., San Diego, CA). The number of distinct epitopes in an embodiment of the invention is generally a whole unit integer from one through one hundred fifty (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or 150).

An additional embodiment of a composition in accordance with the invention comprises a polypeptide multi-epitope construct, *i.e.*, a polyepitopic peptide. Polyepitopic peptides in accordance with the invention are prepared by use of technologies well-known in the art. By use of these known technologies, epitopes in accordance with the invention are connected one to another. The polyepitopic peptides can be linear or non-linear, *e.g.*, multivalent. These polyepitopic constructs can comprise artificial amino acids, spacing or spacer amino acids, flanking amino acids, or chemical modifications between adjacent epitope units. The polyepitopic construct can be a heteropolymer or a homopolymer. The polyepitopic constructs generally comprise epitopes in a quantity of any whole unit integer between 2-150 (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or 150). The polyepitopic construct can comprise CTL and/or HTL epitopes. One or more of the epitopes in the construct can be modified, *e.g.*, by addition of a surface active material, *e.g.* a lipid, or chemically modified, *e.g.*, acetylation, *etc.* Moreover, bonds in the multiepitopic construct can be other than peptide bonds, *e.g.*, covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds *etc.*

Alternatively, a composition in accordance with the invention comprises construct which comprises a series, sequence, stretch, *etc.*, of amino acids that have homology to (

i.e., corresponds to or is contiguous with) to a native sequence. This stretch of amino acids comprises at least one subsequence of amino acids that, if cleaved or isolated from the longer series of amino acids, functions as an HLA class I or HLA class II epitope in accordance with the invention. In this embodiment, the peptide sequence is modified, so as to become a construct as defined herein, by use of any number of techniques known or to be provided in the art. The polyepitopic constructs can contain homology to a native sequence in any whole unit integer increment from 70-100%, e.g., 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or, 100 percent.

A further embodiment of a composition in accordance with the invention is an antigen presenting cell that comprises one or more epitopes in accordance with the invention. The antigen presenting cell can be a "professional" antigen presenting cell, such as a dendritic cell. The antigen presenting cell can comprise the epitope of the invention by any means known or to be determined in the art. Such means include pulsing of dendritic cells with one or more individual epitopes or with one or more peptides that comprise multiple epitopes, by nucleic acid administration such as ballistic nucleic acid delivery or by other techniques in the art for administration of nucleic acids, including vector-based, *e.g.* viral vector, delivery of nucleic acids.

Further embodiments of compositions in accordance with the invention comprise nucleic acids that encode one or more peptides of the invention, or nucleic acids which encode a polyepitopic peptide in accordance with the invention. As appreciated by one of ordinary skill in the art, various nucleic acids compositions will encode the same peptide due to the redundancy of the genetic code. Each of these nucleic acid compositions falls within the scope of the present invention. This embodiment of the invention comprises DNA or RNA, and in certain embodiments a combination of DNA and RNA. It is to be appreciated that any composition comprising nucleic acids that will encode a peptide in accordance with the invention or any other peptide based composition in accordance with the invention, falls within the scope of this invention.

It is to be appreciated that peptide-based forms of the invention (as well as the nucleic acids that encode them) can comprise analogs of epitopes of the invention generated using priniciples already known, or to be known, in the art. Principles related to analoging are now known in the art, and are disclosed herein; moreover, analoging principles (heteroclitic analoging) are disclosed in co-pending application serial number

U.S.S.N. 09/226,775 filed 6 January 1999. Generally the compositions of the invention are isolated or purified.

The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

V. EXAMPLES

The following examples illustrate identification, selection, and use of immunogenic Class I and Class II peptide epitopes for inclusion in vaccine compositions.

Example 1. HLA Class I and Class II Binding Assays

The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al., J. Immunol.* 154:247 (1995); Sette, *et al., Mol. Immunol.* 31:813 (1994)). The cell lines used as sources of HLA molecules (Table XXIV) and the antibodies used for the extraction of the HLA molecules from the cell lysates (Table XXV) are also described in these publications.

Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.221-transfectants were used as sources of HLA class I molecules. These cells were cultured in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50μM 2-ME, 100μg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA).

Cell lysates were prepared as follows. Briefly, cells were lysed at a concentration of 10^8 cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at 15,000 x g for 30min.

HLA molecules were purified from lysates by affinity chromatography. Lysates were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein

A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then concentrated by centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM ^{125}I-radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301, which was performed at pH 4.5, and DRB1*1601 (DR2w21β_1) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (*see* Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN_3. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2β_1) assay makes separation of bound from unbound peaks more difficult under these conditions, all DRB1*1501 (DR2w2β_1) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and

integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

Radiolabeled peptides were iodinated using the chloramine-T method. Representative radiolabeled probe peptides utilized in each assay, and its assay specific IC_{50} nM, are summarized in Tables IV and V. Typically, in preliminary experiments, each MHC preparation was titered in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

Since under these conditions [label]<[HLA] and IC_{50}≥[HLA], the measured IC_{50} values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 μg/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC_{50} of a positive control for inhibition by the IC_{50} for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC_{50} nM values by dividing the IC_{50} nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation has proven to be the most accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

Because the antibody used for HLA-DR purification (LB3.1) is α-chain specific, β_1 molecules are not separated from β_3 (and/or β_4 and β_5) molecules. The β_1 specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2), and DRB1*0803 (DR8w3), where no β_3 is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2β_1), DRB5*0101 (DR2w2β_2), DRB1*1601 (DR2w21β_1), DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DRβ molecule specificity have been described previously (*see, e.g.*, Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998).

Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes as, for example, described in Example 2.

Example 2. Identification of HLA Supermotif- and Motif-Bearing CTL Candidate Epitopes

Vaccine compositions of the invention may include multiple epitopes that comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage was performed using the strategy described below.

Computer searches and algorthims for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in Examples 2 and 5 employed the protein sequence data from HIV-1 clade B virus strains that were available in the 1994 Los Alamos database.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs were performed as follows. All translated HIV protein sequences were analyzed using a text string search software program, *e.g.*, MotifSearch 1.4 (D. Brown, San Diego) to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally. Identified A2-, A3-, and DR-supermotif sequences were scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$\text{“}\Delta G\text{"} = a_{1i} \times a_{2i} \times a_{3i} \ldots\ldots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (*j*) at a given position (*i*) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue *j* occurs

at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i. For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

Complete protein sequences from nine HIV structural and regulatory proteins were aligned, then scanned, utilizing motif identification software, to identify conserved 9- and 10-mer sequences containing the HLA-A2-supermotif main anchor specificity. The analysis included all isolates in the 1994 Los Alamos database. The conservation criteria varied according to antigen: greater than 80% of clade B isolates for gag, pol, env; greater than 70% for nef, rev, tat, vif, vpr; great than 60% for vpu.)

A total of 233 conserved, HLA-A2 supermotif-positive sequences were identified. The peptides corresponding to the sequences were then synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule). Thirty peptides bound A*0201 with IC_{50} values ≤500 nM; of these 30, 5 bound with high binding affinities (IC_{50} values ≤50 nM) and 25 bound with intermediate binding affinities, in the 50-500 nM range (Table XXVII).

The thirty A*0201-binding peptides were subsequently tested for the capacity to bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). As

shown in Table XXVII, 20 of the 30 peptides were found to be A2-supertype cross-reactive binders, binding at least 3 of the 5 A2-supertype alleles tested.

Selection of HLA-A3 supermotif-bearing epitopes

The HIV protein sequences scanned above were also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. A total of 353 conserved 9- or 10-mer motif-containing sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the two most prevalent A3-supertype alleles. Sixty-six of the peptides were found to bind one of the two alleles with binding affinities of ≤500 nM (Table XXVIII). These peptides were then tested for binding cross-reactivity to the other common A3-supertype alleles (A*3101, A*3301, and A*6801). Twenty one of the peptides bound at least three of the five HLA-A3-supertype molecules tested (Table XXVIII). Table XXVIII also includes two 11-mer peptides that were not selected using the search criteria outlined above, but have been shown to be A3-supertype cross-reactive binders.

Selection of HLA-B7 supermotif bearing epitopes

When the same HIV target antigen protein sequences were also analyzed for the presence of conserved 9- or 10-mer peptides with the HLA-B7-supermotif, 54 sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-B*0702, the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Sixteen peptides bound B*0702 with IC_{50} of ≤500 nM (Table XXIX). These peptides were then tested for binding to other common B7-supertype molecules (B*3501, B*5101, B*5301, and B*5401). As shown in Table XXIX, eight of the sixteen peptides were capable of binding to three or more of the five B7-supertype alleles tested.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into vaccine constructs. An analysis of the protein sequence data from the HIV target antigens utilized above is also performed to identify HLA-A1- and A24-motif-containing conserved sequences.

Five conserved HIV-derived peptides that bind to A*0101 with an IC_{50} of 500 nM or less (Table XXX) have been identified. Eleven conserved HLA-A*2402-binding HIV-

derived peptides have also been identified, five of which bind with an IC_{50} of 100 nM or less (Table XXXI).

Example 3. Confirmation of Immunogenicity

*Evaluation of A*0201 immunogenicity*

It has been shown that CTL induced in A*0201/K^b transgenic mice exhibit specificity similar to CTL induced in the human system (*see, e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007-1015, 1991; Wentworth *et al.*, *Eur. J. Immunol.* 26:97-101, 1996). Accordingly, these mice were used to evaluate the immunogenicity of 19 of the 20 A2-supertype cross-reactive peptides identified in Example 2 above.

CTL induction in transgenic mice following peptide immmunization has been described (Vitiello *et al.*, *J. Exp. Med.* 173:1007-1015, 1991; Alexander *et al.*; *J. Immunol.* 159:4753-4761, 1997). In these studies, mice were injected subcutaneously at the base of the tail with each peptide (50 μg/mouse) emulsified in IFA in the presence of an excess of an IA^b-restricted helper peptide (140 μg/mouse) (HBV core 128-140, Sette *et al.*, *J. Immunol.* 153:5586-5592, 1994). Eleven days after injection, splenocytes were incubated in the presence of peptide-loaded syngenic LPS blasts. After six days, cultures were assayed for cytotoxic activity using peptide-pulsed targets. The data, summarized in Table XXXII, indicate that eight peptides were capable of inducing primary CTL responses in A*0201/K^b transgenic mice. (For these studies, a peptide was considered positive if it induced CTL (L.U. $30/10^6$ cells ≥2 in at least two transgenic animals (Wentworth *et al.*, *Eur. J. Immunol.* 26:97-101, 1996).

The cross-reactive candidate CTL epitopes were also tested for the ability to stimulate recall CTL reponses HIV-infected patients. Briefly, PBMC from patients infected with HIV were cultured in the presence of 10 μg/ml of synthetic peptide. After 7 and 14 days, the cultures were restimulated with peptide. The cultures were assayed for cytolytic activity on day 21 using target cells pulsed with the specific peptide in a ^{51}Cr release assay. These data are also summarized in Table XXXII. As shown, 15 of the 19 peptides analyzed were recognized in recall CTL responses using PBMC from HIV-infected patients.

The set of peptides screened for immunogenicity contained two redundant peptides, 1261.14 and 1261.04, which differ in length by a single amino acid. While both peptides exhibit supertype degenerate binding, only the short of the two peptides

exhibited immunogenicity. One supertype peptide not tested, 1211.09, has been reported to be recognized by CTL lines isolated from HIV-infected patients.
In summary, 16 A2-supertype cross-reactive peptides have been identified that are immungenic in humans; 53% of these peptides are also recognized in HLA-A2 transgenic mice. The sixteen peptides represent epitopes from five HIV antigens: env, gag, pol, vpr, and nef.

*Evaluation of A*03/A11 immunogenicity*

Twenty one of the A3-supertype cross-reactive peptides identified in Example 2 above were evaluated for immunogenicity (Table XXXIII). Peptides were screened using HLA-A11/K^b transgenic mice, using the protocol described above for HLA-A2 transgenic mice (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997) and using PBMC obtained from HIV-infected patients to test for the ability to stimulate CTL recall responses. Ten peptides that were capable of inducing CTL in HLA-A11 transgenic mice were identified.

Three peptides, 966.01, 940.03, and 1069.47, have been shown by collaborators to be immunogenic in HIV-infected patients. Peptides 966.01 and 1069.47 also induced CTL responses in transgenic mice, peptide 940.03 exhibited immunogenicity in patients only.

In summary, 11 of 23 A3-supertype cross-reactive binding peptides were found to be immunogenic in either HLA-A11 transgenic mice or HIV-infected patients. These peptides represent epitopes from three HIV antigens: pol, env, and nef.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified in Example 2 is used to evaluate immunogenicity using HLA-B7 transgenic mice and PBMC from in HIV-infected patients in a manner analagous to the evaluation of A2-and A3-supermotif-bearing peptides. Three of these peptides have been reported as being immunogenic in HIV-infected patients.

Example 4. Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also

allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analoged, or "fixed" to confer upon the peptide certain characteristics, *e.g.* greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analog peptides that exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

As shown in Example 2, twenty HIV-derived, A2-supertype-restricted epitopes were identified. Peptide engineering strategies are implemented to further increase the cross-reactivity of the candidate epitopes identified above which bind 3/5 of the A2 supertype alleles tested. On the basis of the data disclosed, *e.g.*, in related and co-pending U.S.S.N 09/226,775, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide can be tested for binding to one or all supertype members and then analogued to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

Similarly, analogs of HLA-A3 supermotif-bearing epitopes are also generated. For example, peptides binding to 3/5 of the A3-supertype molecules can be engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Typically, those peptides that demonstrate ≤ 500 nM binding capacity are then tested for A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, B7 supermotif-beariang peptide are also analoged. For example, peptides binding 3 or more B7-supertype alleles are modulated to achieve increased cross-reactive binding. B7 supermotif-bearing peptides can, for example, be engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

Analoging at Secondary Anchor Residues

Secondary anchor residues defined for HLA motifs and/or supermotifs are also used to engineer peptide with modified binding activity, typically increased cross-reactive binding and/or increased affinity. For example, the binding capacity of a B7 supermotif-bearing peptide representing a discreet single amino acid substitution at position 1 is analyzed. A peptide such as Peptide 1261.01 (Table XXIX), can, for example, be analogued to substitute L for F at position 1 and subsequently be evaluated for modulated binding activity, *e.g.*, increased binding affinity/ and or increased cross-reactivity. This procedure identifies analoged peptides with modified binding properties.

Engineered analogs with improved binding capacity or cross-reactivity are tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. The analoged peptides are typically additionally tested for the ability to stimulate a recall response using PBMC from HIV-infected patients.

Thus, by the use of even single amino acid substitutions, it is possible to increase the binding affinity and/or cross-reactivity of peptide ligands for HLA supertype molecules.

Example 5. Identification of HIV-derived sequences with HLA-DR binding motifs

Peptide epitopes bearing an HLA class II supermotif or motif are identified as outlined below using methodology similar to that described in Examples 1-3.

Selection of HLA-DR-supermotif-bearing epitopes.

To identify HIV-derived, HLA class II HTL epitopes, the protein sequences from the same HIV antigens used for the identification of HLA Class I supermotif/motif sequences were analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences were selected comprising a DR-supermotif, further comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates

sequences for the presence of secondary anchors. Using allele specific selection tables (see, *e.g.*, Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule. Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The HIV-derived peptides identified above were tested for their binding capacity for various common HLA-DR molecules. All peptides were initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least 2 of these 3 DR molecules were then tested for binding to DR2w2 β1, DR2w2 β2, DR6w19, and DR9 molecules in secondary assays. Finally, peptides binding at least 2 of the 4 secondary panel DR molecules, and thus cumulatively at least 4 of 7 different DR molecules, were screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least 7 of the 10 DR molecules comprising the primary, secondary, and tertiary screening assays were considered cross-reactive DR binders. The composition of these screening panels, and the phenotypic frequency of associated antigens, are shown in Table XXXIV.

Thirteen HIV-derived peptides were found to bind at least 7 of 10 common HLA-DR alleles. The sequence of these 13 peptides, and their binding capacity for each assay in the primary through tertiary panels, are shown in Table XXXV. This set of peptide epitopes is predominantly derived from pol, but also includes epitopes from gag and env.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is an important criterion in the selection of HTL epitopes. However, data generated previously indicated that DR3 only rarely cross-reacts with other DR alleles (Sidney *et al., J. Immunol.* 149:2634-2640, 1992; Geluk *et al.*, *J. Immunol.* 152:5742-5748, 1994; Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). This is not entirely surprising in that the DR3 peptide-binding motif appears to be distinct from the specificity of most other DR alleles. For maximum efficiency in developing vaccine candidates it would be desirable for DR3 motifs to be clustered in proximity with DR supermotif regions. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the distinct binding specifity of the

DR3 motif, peptides binding only to DR3 can also be ocnsidered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, the nine target HIV antigens were analyzed for conserved sequences carrying one of the two DR3 specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides were then synthesized and tested for the ability to bind DR3 with an affinity of 1μM or better, *i.e.*, less than 1 μM. ive peptides were found that met this binding criterion (Table XXXVI), and thereby qualify as HLA class II high affinity binders. Of these five, four represent epitopes from pol, and one is from vpu.

DR3 binding epitopes can also be included in vaccine compositions.

Example 6. Immunogenicity of HIV-derived HTL epitopes

Immunogenicity of HTL epitopes is typically evaluated in a manner analagous to the determination of immunogenicity of CTL epitopes using appropriate transgenic mice models and/or assessing the ability to stimulate recall responses using PBMC isolated from HIV-infected individuals.

The immunogenicity of 11 of the 13 HLA class II DR-supermotif binding epitopes identified in Example 5 was evaluated in a study testing PBMC isolated from HIV-infected individuals for recall proliferative responses. All eleven of these peptides were found to stimulate DR-restricted proliferative responses (Table XXXVII).

DR3-motif bearing peptides are typically evaluated in a similar manner. Such studies demonstrate the immunogenicity of class II epitopes derived from HIV proteins.

Example 7. Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

In order to analyze population coverage, gene frequencies of HLA alleles were determined. Gene frequencies for each HLA allele were calculated from antigen or allele frequencies utilizing the binomial distribution formulae gf=1-(SQRT(1-af)) (see, *e.g.*, Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies were calculated, and the cumulative antigen frequencies derived by the use of the inverse formula [$af=1-(1-Cgf)^2$].

Where frequency data was not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies was assumed. To obtain total potential supertype population coverage no linkage disequilibrium was assumed, and only alleles confirmed to belong to each of the supertypes were included (minimal estimates). Estimates of total potential coverage achieved by inter-loci combinations were made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., total=A+B*(1-A)). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34, A66, and A*7401, these alleles were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups (see Table XXI). Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%. An analagous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Summary of preferred HLA class I epitopes

In summary, on the basis of the data presented in the above examples, 47 immunogenic and/or cross-reactive binding preferred CTL peptide epitopes derived from HIV were identified (*see*, Table XXXVIII). Of these 47 eptiopes, 6 are derived from gag, 22 from pol, 10 from env, 3 from nef, and one epitope each from rev, vif, and vpr. This set of epitopes includes 16 HLA-A2 supermotif-bearing epitopes (two from gag, eight from pol, three from env, two from vpr,a nd one from nef), all of which are recognized in HIV-infected patients. The 10 HLA-A3 supermotif-bearing candidate epitopes include 6 pol-derived epitopes, two env-derived epitopes and one eptiope each from gag, vif, and

nef. With the exception of peptides 1273.08 and 1273.03, all of the epitopes are immunogenic in HLA transgenic mice. The two additional peptides are included to enhance antigen diversity.

The CTL epitope set also includes 8 B7-restricted peptides. Of these eight, 3 epitopes have been reported as immunogenic in patients. Five B7-supermotif-bearing peptides were included as candidates based on supertype binding. Immunogenicity studies in humans (*e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. Given these results, and in view of the limited immunogenicity data available for B7 supermotif-bearing peptides, the use of B7-supertype binding affinity is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

Similarly, A1- and A24-restricted peptides were included on the basis of both demonstrated immunogenicity of the candidate epitopes and on the basis of binding affinity. Five of the preferred epitopes have been reported to be recognized in recall CTL repsonses form HIV-infected patients. Because a high percentage of the peptides with binding affinities $\leq$ 100 nM are found to be immunogenic, four A24-restricted peptides were included as vaccine candidates. An additional five A24-restricted epitopes and four A1-restricted epitopes that bound their respective alleles with an IC_{50} of $\leq$ 500 nM were also included to provide a greater degree of population coverage.

With these 47 CTL epitopes, an average population coverage is predicted to be greater than 95% in each of five major ethnic populations. Using the game theory Monte Carlo simulation analysis, which is known in the art (see *e.g.*, Osborne, M.J. and Rubinstein, A. "A course in game theory" MIT Press, 1994), it is estimated that 90% of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize 7or more of the vaccine epitopes described herein (Figure 1)

Summary of preferred HLA class II epitopes

A list of preferred HIV-derived HTL epitopes for vaccine compositions is summarized in Table XXXIX. The set of HTL epitopes includes 13 DR supermotif-bearing peptides and 5 DR3 motif-bearing peptides. The majority of the epitopes are

derived from pol, 3 are from gag, 2 are from env and one is derived from vpu. The total estimated population coverage represented by this panel of HTL epitopes is estimated to be greater than 91% in each of five major ethnic groups (Table XL).

Example 8. CTL Recognition Of Endogenous Processed Antigens After Priming

This example determines that CTL induced by native or analoged peptide epitopes identified and selected as described in Examples 1-6 recognize endogenously synthesized, *i.e.*, native antigens.

Effector cells isolated from transgenic mice that are immunized with peptide epitopes as in Example 3, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with HIV expression vectors.

The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that is being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

Example 9. Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise an HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope selected from Table XXVI-XXIX, or an analog of that epitope. The HTL

epitope is, for example, selected from Table XXXII. The peptides may be lipidated, if desired.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991).

In vitro CTL activation: One week after priming, spleen cells (30x10^6 cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts (10x10^6 cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to 1.5x10^6) are incubated at 37°C in the presence of 200 µl of ^{51}Cr. After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1 µg/ml. For the assay, 10^4 ^{51}Cr-labeled target cells are added to different concentrations of effector cells (final volume of 200 µl) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = 100 x (experimental release - spontaneous release)/(maximum release - spontaneous release). To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour ^{51}Cr release assay. To obtain specific lytic units/10^6, the lytic units/10^6 obtained in the absence of peptide is subtracted from the lytic units/10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio

of 50:1 (i.e., $5x10^5$ effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., $5x10^4$ effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50{,}000)-(1/500{,}000)] \times 10^6 = 18$ LU.

The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in Example 3. Analyses similar to this may be performed to evaluate the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 10. Selection of CTL and HTL epitopes for inclusion in an HIV-specific vaccine.

This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or can be single and/or polyepitopic peptides.

The following principles are utilized when selecting an array of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

Epitopes are selected which, upon administration, mimic immune responses that correlate with virus clearance. For example, if it has been observed that patients who clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen, then 3-4 epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

When selecting an array of HIV epitopes, it is preferred that at least some of the epitopes are derived from early and late proteins. The early proteins of HIV are expressed when the virus is replicating, either following acute or dormant infection. Therefore, it is particularly preferred to use epitopes from early stage proteins to alleviate disease manifestations at the earliest stage possible.

Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less.

Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

When creating a polyepitopic compositions, *e.g.* a minigene, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes.

In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables XXVI-XXIX and Table XXXII. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

Example 11. Construction of Minigene Multi-Epitope DNA Plasmids

This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.

A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are identified, for example, in Tables XXVI-XXIX and XXXII. HLA class I supermotif or

motif-bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence os that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated Tm of each primer pair) for 30 sec, and 72°C for 1 min.

For the first PCR reaction, 5 μg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 μl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM $(NH_4)_2SO_4$, 20 mM Tris-chloride, pH 8.75, 2 mM $MgSO_4$, 0.1% Triton X-100, 100 μg/ml BSA), 0.25 mM each

dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 12. The plasmid construct and the degree to which it induces immunogenicity.

The degree to which a plasmid construct, for example a plasmid constructed in accordance with Example 11, is able to induce immunogenicity can be evaluated *in vitro* by testing for epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines "antigenicity" and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.*, Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by infected or transfected target cells, and then determining the concentration of peptide necessary to obtained equivalent levels of lysis or lymphokine release (*see, e.g.*, Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

Atlernatively, immunogenicity can be evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in copending U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994.

For example, to assess the capacity of a DNA minigene construct (*e.g.*, a pMin minigene construct generated as decribed in U.S.S.N. 09/311,784) containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 μg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ^{51}Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitope that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 μg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4+ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ^{3}H-thymidine incorporation proliferation assay, (*see, e.g.*, Alexander et al. Immunity 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in Example 11, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 μg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period

(ranging from 3-9 weeks), the mice are boosted IP with 10^7 pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 μg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN-γ ELISA.

It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes.

The use of prime boost protocols in humans is described in Example 20.

Example 13. Peptide Composition for Prophylactic Uses

Vaccine compositions of the present invention can be used to prevent HIV infection in persons who are at risk for such infection. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in Examples 9 and/or 10, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV infection.

For example, a peptide-based composition can be provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freunds Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 μg, generally 100-5,000 μg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

Alternatively, a composition typically comprising transfecting agents can be used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

Example 14. Polyepitopic Vaccine Compositions Derived from Native HIV Sequences

A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify "relatively short" regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The "relatively short" peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping, for example, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native HIV antigens thus avoiding the need

to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

Example 15. Polyepitopic Vaccine Compositions Directed To Multiple Diseases

The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

Example 16. Use of peptides to evaluate an immune response

Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be performed in a manner as that described by Ogg *et al., Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, HIV HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al., N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal

addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300 x g for 5 minutes and resuspended in 50 μl of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

Example 17. Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected with HIV, or who have been vaccinated with an HIV vaccine.

For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO

Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 μg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 μg/ml to each well and HBV core 128-140 epitope is added at 1 μg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4 x 10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 μl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al., Nature Med.* 2:1104,1108, 1996; Rehermann *et al., J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al. J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al. J. Virol.* 66:2670-2678, 1992).

Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 μM, and labeled with 100 μCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: 100 x [(experimental release-spontaneous release)/maximum release-spontaneous release)]. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

The class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 μg/ml synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μCi ^{3}H-thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^{3}H-thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^{3}H-thymidine incorporation in the presence of antigen divided by the ^{3}H-thymidine incorporation in the absence of antigen.

Example 18. Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μg of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

The vaccine is found to be both safe and efficacious.

Example 19. Phase II Trials In Patients Infected With HIV

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to HIV-infected patients. The main objectives of the trials are to determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in $CD4^+$ cells counts. Such a study is designed, for example, as follows:

The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic backgrounds. All of them are infected with HIV for over five years and are HCV, HBV and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.

The viral load and $CD4^+$ levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

Example 20. Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization is performed using an expression vector, such as that constructed in Example 11, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster is, for example, recombinant fowlpox virus administered at a dose of $5\text{-}10^7$ to $5x10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results indicates that a magnitude of sufficient response to achieve protective immunity against HIV is generated.

Example 21. Administration of Vaccine Compositions Using Dendritic Cells

Vaccines comprising peptide epitopes of the invention can be administered using APCs, or "professional" APCs such as DC. In this example, the peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction of the specific target cells that bear the proteins from which the epitopes in the vaccine are derived.

For example, a cocktail of epitope-bearing peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (*see, e.g., Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although 2-50 x 10^6

DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC containing DC generated after treatment with an agent such as Progenipoietin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10}. Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoietin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive 5×10^6 DC, then the patient will be injected with a total of 2.5×10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoietin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

Ex vivo activation of CTL/HTL responses

Alternatively, *ex vivo* CTL or HTL responses to HIV antigens can be induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cells.

Example 22. Alternative Method of Identifying Motif-Bearing Peptides

Another way of identifying motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can then be infected with a pathogenic organism or transfected with nucleic acids that express the antigen of interest, *e.g.* HIV regulatory or structural proteins. Thereafter, peptides produced by endogenous antigen processing of peptides produced consequent to infection (or as a result of transfection) will bind to HLA molecules within the cell and be transported and displayed on the cell surface.

The peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, *e.g.*, by mass spectral analysis (*e.g.*, Kubo *et al.*, *J. Immunol.* 152:3913, 1994). Because the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express any endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells can then be used as described, *i.e.*, they can be infected with a pathogenic organism or transfected with nucleic acid encoding an antigen of interest to isolate peptides corresponding to the pathogen or antigen of interest that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than infection or transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

The above examples are provided to illustrate the invention but not to limit its scope. For example, the human terminology for the Major Histocompatibility Complex, namely HLA, is used throughout this document. It is to be appreciated that these principles can be extended to other species as well. Thus, other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent application cited herein are hereby incorporated by reference for all purposes.

TABLE I

SUPERMOTIFS	POSITION 2 (Primary Anchor)	POSITION 3 (Primary Anchor)	POSITION C Terminus (Primary Anchor)
A1	**TIL***VMS*		**FWY**
A2	**LIVM***ATQ*		**IV***MATL*
A3	**VSMA***TLI*		**RK**
A24	**YF***WIVLMT*		**FI***YWLM*
B7	**P**		**VILF***MWYA*
B27	**RHK**		**FYL***WMIVA*
B44	**E***D*		**FWYLIMVA**
B58	**ATS**		**FWY***LIVMA*
B62	**QL***IVMP*		**FWY***MIVLA*
MOTIFS			
A1	**TSM**		**Y**
A1		**DE***AS*	**Y**
A2.1	**LM***VQIAT*		**V***LIMAT*
A3	**LMVISATF***CGD*		**KYR***HFA*
A11	**VTMLISAGN***CDF*		**K***RYH*
A24	**YFW***M*		**FLIW**
A*3101	**MVT***ALIS*		**R***K*
A*3301	**MVALF***IST*		**RK**
A*6801	**AVT***MSLI*		**RK**
B*0702	**P**		**LMF***WYAIV*
B*3501	**P**		**LMFWY***IVA*
B51	**P**		**LIVF***WYAM*
B*5301	**P**		**IMFWY***ALV*
B*5401	**P**		**ATIV***LMFWY*

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE Ia

SUPERMOTIFS	POSITION 2 (Primary Anchor)	POSITION 3 (Primary Anchor)	POSITION C Terminus (Primary Anchor)
A1	**TI***LVMS*		**FWY**
A2	*VQAT*		**V***LIMAT*
A3	**VSMA***TLI*		**RK**
A24	**YF***WIVLMT*		**FI***YWLM*
B7	**P**		**VILF***MWYA*
B27	**RHK**		**FYL***WMIVA*
B58	**ATS**		**FWY***LIVMA*
B62	**QL***IVMP*		**FWY***MIVLA*
MOTIFS			
A1	**TSM**		**Y**
A1		**DE***AS*	**Y**
A2.1	*VQAT**		**V***LIMAT*
A3.2	**LMVISATF***CGD*		**KYR***HFA*
A11	**VTMLISAGN***CDF*		**K***RHY*
A24	**YFW**		**FLIW**

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE II

SUPERMOTIFS		POSITION 1	2	3	4	5	6	7	8	C-terminus
A1			<u>1° Anchor</u> TIL*VMS*							<u>1° Anchor</u> FWY
A2			<u>1° Anchor</u> LIVM*ATQ*							<u>1° Anchor</u> LIVMAT
A3	preferred		<u>1° Anchor</u> VSMA*TLI*	YFW (4/5)			YFW (3/5)	YFW (4/5)	P (4/5)	<u>1°Anchor</u> RK
	deleterious	DE (3/5); P (5/5)		DE (4/5)						
A24			<u>1° Anchor</u> YF*WIVLM* *T*							<u>1° Anchor</u> FI*YWLM*
B7	preferred	FWY (5/5) LIVM (3/5)	<u>1°Anchor</u> P	FWY (4/5)					FWY (3/5)	<u>1°Anchor</u> VILF*MWYA*
	deleterious	DE (3/5); P(5/5); G(4/5); A(3/5); QN (3/5)				DE (3/5)	G (4/5)	QN (4/5)	DE (4/5)	
B27			<u>1° Anchor</u> RHK							<u>1° Anchor</u> FYL*WMIVA*
B44			<u>1° Anchor</u> *ED*							<u>1° Anchor</u> FWYLIMVA
B58			<u>1° Anchor</u> ATS							<u>1° Anchor</u> FWY*LIVMA*
B62			<u>1° Anchor</u> QL*IVMP*							<u>1° Anchor</u> FWY*MIVLA*

		POSITION								
		1	2	3	4	5	6	7	8	C-terminus

		POSITION								
		1	2	3	4	5	6	7	8	C-terminus
MOTIFS										
A1 9-mer	preferred	GFYW	1°Anchor STM	DEA	YFW		P	DEQN	YFW	1°Anchor Y
	deleterious	DE		RHKLIVM P	A	G	A			
A1 9-mer	preferred	GRHK	ASTCLIV M	1°Anchor DE*AS*	GSTC		ASTC	LIVM	DE	1°Anchor Y
	deleterious	A	RHKDEPY FW		DE	PQN	RHK	PG	GP	

		POSITION									
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A1 10-mer	peferred	YFW	1°Anchor STM	DEAQN	A	YFWQN		PASTC	GDE	P	1°Anchor Y
	deleterious	GP		RHKGLIV M	DE	RHK	QNA	RHKYFW	RHK	A	
A1 10-mer	preferred	YFW	STCLIVM	1°Anchor DE*AS*	A	YFW		PG	G	YFW	1°Anchor Y
	deleterious	RHK	RHKDEPY FW			P	G		PRHK	QN	
A2.1 9-mer	preferred	YFW	1°Anchor LM*IVQAT*	YFW	STC	YFW		A	P	1°Anchor V*LIMAT*	
	deleterious	DEP		DERKH			RKH	DERKH			
A2.1 10-mer	preferred	AYFW	1°Anchor LM*IVQAT*	LVIM	G		G		FYWL VIM		1°Anchor V*LIMAT*
	deleterious	DEP		DE	RKHA	P		RKH	DERK H	RKH	

		POSITION									
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A3	preferred	RHK	1°Anchor LMVISAT F*CGD*	YFW	PRHKYFW	A	YFW		P	1°Anchor KYR*HFA*	
	deleterious	DEP		DE							
A11	preferred	A	1°Anchor VTLMISA GN*CDF*	YFW	YFW	A	YFW	YFW	P	1°Anchor K*RYH*	
	deleterious	DEP						A	G		
A24 9-mer	preferred	YFWRHK	1°Anchor YFW*M*		STC			YFW	YFW	1°Anchor FLIW	
	deleterious	DEG		DE	G	QNP	DERHK	G	AQN		
A24 10-mer	preferred		1°Anchor YFW*M*		P	YFWP		P			1°Anchor FLIW
	deleterious			GDE	QN	RHK	DE	A	QN	DEA	

		POSITION									
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A3101	preferred	RHK	<u>1°Anchor</u> MVT*ALIS*	YFW	P		YFW	YFW	AP	<u>1°Anchor</u> R*K*	
	deleterious	DEP		DE		ADE	DE	DE	DE		
A3301	preferred		<u>1°Anchor</u> MVALF*IS* *T*	YFW				AYFW		<u>1°Anchor</u> RK	
	deleterious	GP		DE							
A6801	preferred	YFWSTC	<u>1°Anchor</u> AVT*MSLI*			YFWLIV M		YFW	P	<u>1°Anchor</u> RK	
	deleterious	GP		DEG		RHK			A		
B0702	preferred	RHKFWY	<u>1°Anchor</u> P	RHK		RHK	RHK	RHK	PA	<u>1°Anchor</u> LMF*WYAIV*	
	deleterious	DEQNP		DEP	DE	DE	GDE	QN	DE		
B3501	preferred	FWYLIVM	<u>1°Anchor</u> P	FWY				FWY		<u>1°Anchor</u> LMFWY*IVA*	
	deleterious	AGP				G	G				

		POSITION									
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
B51	preferred	LIVMFWY	1°Anchor P	FWY	STC	FWY		G	FWY	1°Anchor LIVF*WYAM*	
	deleterious	AGPDERHKSTC				DE	G	DEQN	GDE		
B5301	preferred	LIVMFWY	1°Anchor P	FWY	STC	FWY		LIVMFWY	FWY	1°Anchor IMFWY*ALV*	
	deleterious	AGPQN					G	RHKQN	DE		
B5401	preferred	FWY	1°Anchor P	FWYLIVM		LIVM		ALIVM	FWYAP	1°Anchor ATIV*LMFWY*	
	deleterious	GPQNDE		GDESTC		RHKDE	DE	QNDGE	DE		

Italicized residues indicate less preferred or "tolerated" residues.
The information in Table II is specific for 9-mers unless otherwise specified.

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TABLE III

POSITION

MOTIFS		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4	preferred	FMY*LIVW*	M	T		I	VST*CPALIM*	MH		MH
	deleterious				W			R		WDE
DR1	preferred	MF*LIVWY*			PAMQ		VMAT*SPLIC*	M		AVM
	deleterious		C	CH	FD	CWD		GDE	D	
DR7	preferred	MF*LIVWY*	M	W	A		IVMSA*CTPL*	M		IV
	deleterious		C		G			GRD	N	G
DR Supermotif		MF*LIVWY*					VMSTA*CPLI*			
DR3 MOTIFS		1° anchor 1	2	3	1° anchor 4	5	1° anchor 6			
motif a	preferred	LIVMFY			D					
motif b	preferred	LIVMFAY			DNQEST		KRH			

Italicized residues indicate less preferred or "tolerated" residues.

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Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	25
A*0201	941.01	FLPSDYFPSV	5.0
A*0202	941.01	FLPSDYFPSV	4.3
A*0203	941.01	FLPSDYFPSV	10
A*0205	941.01	FLPSDYFPSV	4.3
A*0206	941.01	FLPSDYFPSV	3.7
A*0207	941.01	FLPSDYFPSV	23
A*6802	1141.02	FTQAGYPAL	40
A*0301	941.12	KVFPYALINK	11
A*1101	940.06	AVDLYHFLK	6.0
A*3101	941.12	KVFPYALINK	18
A*3301	1083.02	STLPETYVVRR	29
A*6801	941.12	KVFPYALINK	8.0
A*2402	979.02	AYIDNYNKF	12
B*0702	1075.23	APRTLVYLL	5.5
B*3501	1021.05	FPFKYAAAF	7.2
B51	1021.05	FPFKYAAAF	5.5
B*5301	1021.05	FPFKYAAAF	9.3
B*5401	1021.05	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2β1	507.02	GRTQDENPVVHFFKNIV TPRTPPP	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2β2	553.01	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

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Table VI

HLA-supertype	Allele-specific HLA-supertype members	
	Verified[a]	Predicted[b]
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6801	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	B*1801, B*1802, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4901, B*5001
B58	B*5701, B*5702, B*5801, B*5802, B*1516, B*1517	
B62	B*1501, B*1502, B*1513, B*5201	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1510

a. Verified alleles includes alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.

b. Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specificity.

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	KLWVTVYY	44	8	11	17		1
ENV	NLWVTVYY	44	8	35	56		2
ENV	DTEVIINVW	75	8	19	30		3
ENV	VTENFNMW	102	8	34	53		4
ENV	RIGPGQTF	357	8	11	17		5
ENV	GIGPGQTF	360	8	01	33		6
ENV	SIGSGQAF	360	8	01	33		7
ENV	KLREIRQF	405	8	01	25		8
ENV	STNGTETF	537	8	01	17		9
ENV	AVGIGAVF	595	8	11	17		10
ENV	HLLKLTVW	650	8	13	20		11
ENV	HLLQLTVW	650	8	34	53		12
ENV	HMLQLTVW	650	8	10	16		13
ENV	RVLAVERY	665	8	33	52		14
ENV	NVPWNSSW	693	8	13	20		15
ENV	EIWDNMTW	716	8	13	20		16
ENV	DLLALDKW	754	8	21	33		17
ENV	ELLELDKW	754	8	20	31		18
ENV	DITNWLWY	769	8	10	16		19
ENV	WLWYIKIF	773	8	50	78		20
ENV	LIGLRIIF	787	8	16	25		21
ENV	LIGLRIVF	787	8	29	45		22
ENV	SIRLVNGF	842	8	13	20		23
ENV	SIRLVSGF	842	8	13	20		24
ENV	DLRNLCLF	856	8	17	27		25
ENV	DLRSLCLF	856	8	38	59		26
ENV	RSLCLFSY	858	8	35	55		27
ENV	ELLGRRGW	881	8	31	37		28
ENV	TVYYGVPVW	48	9	55	86		29
ENV	NVTENFNMW	101	9	34	53		30
ENV	DSSNSTGNY	218	9	01	20		31
ENV	ILKCNDKKF	271	9	12	19		32
ENV	RIGPGQTFY	357	9	11	17		33
ENV	GIGPGQTFY	360	9	01	33		34
ENV	SIGSGQAFY	360	9	01	33		35
ENV	DLEITTHSF	428	9	21	33		36
ENV	HSFNCGGEF	434	9	36	56		37
ENV	HSFNCRGEF	434	9	16	25		38
ENV	RIKQIINMW	488	9	30	47		39
ENV	RIKQIVNMW	488	9	12	19		40
ENV	GSENGTETF	538	9	02	18		41
ENV	GIGAVFLGF	598	9	11	18		42
ENV	MLGAMFLGF	599	9	04	36		43
ENV	TIGAMFLGF	599	9	03	27		44
ENV	LICTTAVPW	688	9	19	30		45
ENV	LICTTNVPW	688	9	17	27		46
ENV	LICTTTVPW	688	9	12	19		47
ENV	ALDKWASLW	757	9	11	17		48

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	GLIGLRIVF	786	9	29	45		51
ENV	IVNRVRQGY	799	9	38	59		52
ENV	RSIRLVNGF	841	9	12	19		53
ENV	RSIRLVSGF	841	9	13	20		54
ENV	VSGFLALAW	846	9	16	25		55
ENV	FSYHRLRDF	863	9	18	28		56
ENV	SLKGLRLGW	889	9	11	39		57
ENV	SLRGLQRGW	889	9	05	18		58
ENV	RLGWEGLKY	894	9	09	29		59
ENV	VTVYYGVPVW	47	10	55	86		60
ENV	QMHEDIISLW	116	10	29	45		61
ENV	ITQACPKVSF	245	10	29	45		62
ENV	VSFEPIPIHY	253	10	28	44		63
ENV	PIHYCAPAGF	260	10	27	42		64
ENV	PIHYCTPAGF	260	10	10	16		65
ENV	AILKCNDKKF	270	10	12	19		66
ENV	NTSPRSRVAY	376	10	01	33		67
ENV	HSFNCGGEFF	434	10	35	55		68
ENV	HSFNCRGEFF	434	10	16	25		69
ENV	NTETNKTETF	537	10	01	17		70
ENV	NTTGNTTETF	537	10	01	17		71
ENV	KLICTTAVPW	687	10	19	30		72
ENV	KLICTTNVPW	687	10	17	27		73
ENV	KLICTTTVPW	687	10	12	19		74
ENV	TTNVPWNSS	691	10	11	17		75
ENV	SIVNRVRQGY	798	10	36	56		76
ENV	LVSGFLALAW	845	10	16	25		77
ENV	DLRNLCLFSY	856	10	16	25		78
ENV	DLRSLCLFSY	856	10	35	55		79
ENV	IVELLGRRGW	879	10	22	34		80
ENV	SSLKGLRLGW	886	10	10	16		81
ENV	WVTVYYGVPV	46	11	55	86		82
ENV	PVWKEATTTL	54	11	22	34		83
ENV	TLFCASDAKA	64	11	40	63		84
ENV	VITQACPKVSF	244	11	14	22		85
ENV	KVSFEPIPIHY	252	11	28	44		86
ENV	GTAGNSSRAA	375	11	01	33		87
ENV	TTHSFNCGGE	432	11	16	25		88
ENV	TTHSFNCRGE	432	11	12	19		89
ENV	VMHSFNCGGE	432	11	13	20		90
ENV	HSFNCGGEFFY	434	11	35	55		91
ENV	HSFNCRGEFFY	434	11	16	25		92
ENV	NMWQEVGKA	494	11	15	23		93
ENV	DMRDNWRSEL	552	11	37	58		94
ENV	AVGIGAVFLGF	595	11	11	17		95
ENV	YLKDQQLLGI	672	11	27	42		96
ENV	YLRDQQLLGI	672	11	18	28		97
ENV	CTTNVPWNSS	690	11	11	17		98
ENV	WMEWEREIDN	723	11	10	16		99
ENV	LLALDKWASL	755	11	11	17		100

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	LLELDKWASL	755	11	18	28		101
ENV	ALDKWASLW	757	11	10	16		102
ENV	ELDKWASLWN	757	11	16	25		103
ENV	ISNWLWYIKIF	770	11	11	17		104
ENV	ITKWLWYIKIF	770	11	12	19		105
ENV	ITNWLWYIKIF	770	11	14	22		106
ENV	LSIVNRVRQGY	797	11	34	53		107
ENV	RVRQGYSPLSF	802	11	47	73		108
ENV	RLVSGFLALA	844	11	16	25		109
ENV	CLFSYHRLRDF	861	11	18	28		110
ENV	RIVELLGRRG	878	11	22	34		111
ENV	GLRLGWEGLK	892	11	09	29		112
ENV	RLGWEGLKYL	894	11	07	23		113
GAG	ASRELERF	38	8	46	72		114
GAG	SSQVSQNY	145	8	15	31		115
GAG	KVIEEKAF	178	8	24	38		116
GAG	KVVEEKAF	178	8	28	44		117
GAG	TLQEQIAW	263	8	12	19		118
GAG	TLQEQIGW	263	8	27	42		119
GAG	PIPVGDIY	279	8	11	17		120
GAG	PIPVGEIY	279	8	35	55		121
GAG	ASQEVKNW	333	8	11	17		122
GAG	ATQDVKNW	333	8	15	23		123
GAG	ATQEVKNW	333	8	18	28		124
GAG	IMMQKSNF	408	8	11	17		125
GAG	IMMQRGNF	408	8	27	42		126
GAG	CTERQANF	459	8	55	87		127
GAG	ETHDKDLY	537	8	01	25		128
GAG	LTSLKSLF	549	8	13	20		129
GAG	LTSLRSLF	549	8	12	19		130
GAG	LSGGKLDAW	8	9	16	25		131
GAG	GSEELRSLY	73	9	12	19		132
GAG	NSSQVSQNY	144	9	14	31		133
GAG	ISPRTLNAW	168	9	36	56		134
GAG	LSPRTLNAW	168	9	17	27		135
GAG	FSPEVIPMF	185	9	54	84		136
GAG	TINEEAAEW	225	9	53	83		137
GAG	STLQEQIAW	262	9	12	19		138
GAG	STLQEQIGW	262	9	27	42		139
GAG	PVGDIYKRW	281	9	18	28		140
GAG	PVGEIYKRW	281	9	40	63		141
GAG	GLNKIVRMY	293	9	60	94	0.0017	142
GAG	NIMMQRGNF	407	9	10	17		143
GAG	TIMMQRGNF	407	9	13	22		144
GAG	SSKGRPGNF	476	9	11	18		145
GAG	PTAPPAESF	495	9	20	31		146
GAG	PTAPPEESF	495	9	15	23		147
GAG	PTAPPAESF	507	9	02	67		148
GAG	PTAPPPESF	507	9	01	33		149
GAG	PLASLKSLF	548	9	15	23		150

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
GAG	PLTSLKSLF	548	9	12	19		151
GAG	PLTSLRSLF	548	9	12	19		152
GAG	VLSGGKLDAW	7	10	15	23		153
GAG	RLRPGGKKKY	20	10	34	53		154
GAG	SLFNTVATLY	79	10	15	23		155
GAG	SLYNTVATLY	79	10	22	34		156
GAG	AISPRTLNAW	167	10	29	45		157
GAG	ALSPRTLNAW	167	10	10	16		158
GAG	WVKVIEEKAF	176	10	24	38		159
GAG	WVKVVEEKAF	176	10	28	44		160
GAG	DTINEEAAEW	224	10	31	48		161
GAG	ETINEEAAEW	224	10	22	34		162
GAG	TSTLQEQIAW	261	10	12	19		163
GAG	TSTLQEQIGW	261	10	27	42		164
GAG	DIKQGPKEPF	308	10	19	30		165
GAG	DIRQGPKEPF	308	10	41	64		166
GAG	ATIMMQRGNF	406	10	11	28		167
GAG	PSHKGRPGNF	475	10	23	36		168
GAG	PSNKGRPGNF	475	10	14	22		169
GAG	PSSKGRPGNF	475	10	11	17		170
GAG	SVLSGGKLDA	6	11	15	23		171
GAG	IVWASRELERF	35	11	19	30		172
GAG	LVWASRELER	35	11	25	39		173
GAG	RSLYNTVATL	78	11	15	24		174
GAG	TTSTLQEQIA	260	11	11	17		175
GAG	TTSTLQEQIG	260	11	27	43		176
GAG	PIPVGEIYKRW	279	11	34	53		177
GAG	ILGLNKIVRMY	291	11	57	89		178
GAG	ASAQQDLKGG	392	11	01	50		179
GAG	ATAQQDLKGG	392	11	01	50		180
GAG	PTAPPAESFGF	495	11	10	16		181
GAG	PTAPPEESFRF	495	11	14	22		182
GAG	PTAPPAESFRF	507	11	02	67		183
GAG	PTAPPPESFRF	507	11	01	33		184
NEF	ATNADCAW	71	8	12	22		185
NEF	PMTYKGAF	105	8	12	19		186
NEF	DILDLWVY	185	8	20	31		187
NEF	EILDLWVY	185	8	33	52		188
NEF	WVYHTQGF	191	8	13	20		189
NEF	WVYHTQGY	191	8	21	33		190
NEF	GIRYPLTF	213	8	13	20		191
NEF	GTRFPLTF	213	8	13	20		192
NEF	PLTFGWCF	219	8	43	67		193
NEF	WSKSSIVGW	5	9	20	31		194
NEF	QVPLRPMTF	100	9	10	16		195
NEF	QVPLRPMTY	100	9	46	72	0.0008	196
NEF	WVYHTQGFF	191	9	13	20		197
NEF	WVYHTQGYF	191	9	21	33		198
NEF	HTQGFFPDW	194	9	14	22		199
NEF	HTQGYFPDW	194	9	25	39		200

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
NEF	NTQGYFPDW	194	9	12	19		201
NEF	YTPGPGIRY	207	9	17	27		202
NEF	YTPGPGTRF	207	9	13	20		203
NEF	DLWVYHTQGF	188	10	13	20		204
NEF	DLWVYHTQGY	188	10	21	33		205
NEF	GIRYPLTFGW	213	10	13	20		206
NEF	GTRFPLTFGW	213	10	12	19		207
NEF	HMARELHPEY	320	10	10	16		208
NEF	NTAATNADCA	68	11	12	19		209
NEF	PLRPMTYKGA	102	11	12	19		210
NEF	DLWVYHTQGF	188	11	13	20		211
NEF	DLWVYHTQGY	188	11	21	33		212
NEF	HMARELHPEY	320	11	10	16		213
POL	DINLPGKW	122	8	13	20		214
POL	EINLPGKW	122	8	12	19		215
POL	MIGGIGGF	133	8	62	97		216
POL	QIGCTLNF	179	8	41	64		217
POL	QLGCTLNF	179	8	16	25		218
POL	KIGPENPY	238	8	51	80		219
POL	RIGPENPY	238	8	11	17		220
POL	VLDVGDAY	297	8	60	94		221
POL	SVPLDKDF	306	8	18	28		222
POL	MTKILEPF	353	8	44	69		223
POL	QLPEKDSW	434	8	13	20		224
POL	VLPEKDSW	434	8	13	20		225
POL	KLVGKLNW	448	8	62	97		226
POL	ATESIVIW	568	8	19	30		227
POL	ETWWTDYW	591	8	10	16		228
POL	PIVGAETF	625	8	28	44		229
POL	IVGAETFY	626	8	28	44		230
POL	KTELQAIY	668	8	12	19		231
POL	NIVTDSQY	686	8	62	97		232
POL	LIKKEKVY	717	8	35	55		233
POL	AVHVASGY	828	8	59	92		234
POL	ETGQETAY	844	8	59	92		235
POL	ILKLAGRW	853	8	34	53		236
POL	LLKLAGRW	853	8	25	39		237
POL	HTDNGSNF	866	8	51	80		238
POL	TTVKAACW	876	8	15	23		239
POL	AVKAACWW	877	8	32	50		240
POL	TVKAACWW	877	8	24	38		241
POL	QIIKIQNF	968	8	12	19		242
POL	QITKIQNF	968	8	35	55		243
POL	KIQNFRVY	971	8	52	81		244
POL	PTRRELQVW	30	9	13	20		245
POL	FSFPQITLW	85	9	14	22		246
POL	KMIGGIGGF	132	9	62	97		247
POL	ELNKRTQDF	268	9	57	89		248
POL	TVLDVGDAY	296	9	57	89	0.0180	249
POL	VLDVGDAYF	297	9	60	94		250

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	FSVPLDKDF	305	9	18	28		251
POL	PLDKDFRKY	308	9	19	30		252
POL	ETPGIRYQY	327	9	52	81	0.0052	253
POL	SMTKILEPF	352	9	43	67		254
POL	ELREHLLKW	393	9	17	27		255
POL	ELRQHLLRW	393	9	15	23		256
POL	IVLPEKDSW	433	9	13	20		257
POL	KLNWASQIY	452	9	60	94	0.0070	258
POL	VIWGKTPKF	573	9	47	73		259
POL	KLPIQKETW	582	9	20	31		260
POL	RLPIQKETW	582	9	26	41		261
POL	WTDYWQATW	594	9	14	22		262
POL	WTEYWQATW	594	9	24	38		263
POL	ATWIPEWEF	600	9	52	81		264
POL	NTPPLVKLW	610	9	57	89		265
POL	PIVGAETFY	625	9	28	44	0.0007	266
POL	ETKLGKAGY	641	9	35	55	0.0010	267
POL	QLIKKEKVY	716	9	28	44	0.0007	268
POL	SSGIRKVLF	745	9	26	41		269
POL	QVDCSPGIW	805	9	57	89		270
POL	ETGQETAYF	844	9	57	89		271
POL	FILKLAGRW	852	9	32	50		272
POL	FLLKLAGRW	852	9	25	39		273
POL	STTVKAACW	875	9	15	23		274
POL	TTVKAACWW	876	9	15	23		275
POL	KTAVQMAVF	925	9	57	89		276
POL	QMAVFIHNF	929	9	60	94		277
POL	KIQNFRVYY	971	9	52	81	0.0056	278
POL	LTQIGCTLNF	177	10	41	64		279
POL	LTQLGCTLNF	177	10	15	23		280
POL	GMDGPKVKQ	201	10	51	80		281
POL	ISKIGPENPY	236	10	42	66	0.0130	282
POL	ISRIGPENPY	236	10	11	17		283
POL	AIKKKDSTKW	251	10	57	89		284
POL	STKWRKLVDF	257	10	58	91		285
POL	ELNKRTQDFW	268	10	57	89		286
POL	VTVLDVGDAY	295	10	56	88	0.2800	287
POL	TVLDVGDAYF	296	10	57	89		288
POL	SSMTKILEPF	351	10	33	52		289
POL	VIYQYMDDLY	368	10	51	80	0.2500	290
POL	PIQLPEKDSW	432	10	13	20		291
POL	PIVLPEKDSW	432	10	13	20		292
POL	ILKEPVHGVY	498	10	40	63	0.0017	293
POL	EIQKQGQDQW	520	10	13	20		294
POL	EIQKQGQGQW	520	10	15	23		295
POL	WTYQIYQEPF	529	10	42	66		296
POL	KIATESIVIW	566	10	14	22		297
POL	IVIWGKTPKF	572	10	47	73		298
POL	PIQKETWEAW	584	10	15	23		299
POL	PIQKETWETW	584	10	27	42		300

Table VII

HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	ETWETWWTD	588	10	10	16		301
POL	ETWETWWTE	588	10	10	16		302
POL	NTPPLVKLWY	610	10	57	89	0.0041	303
POL	EVNIVTDSQY	684	10	59	92	0.0530	304
POL	VSAGIRKVLF	744	10	15	23		305
POL	VSSGIRKVLF	744	10	26	41		306
POL	LVAVHVASGY	826	10	53	83	0.0390	307
POL	THITDNGSNF	864	10	14	22		308
POL	VHITDNGSNF	864	10	24	38		309
POL	TSAAVKAACW	874	10	27	42		310
POL	TSTTVKAACW	874	10	14	22		311
POL	STTVKAACW	875	10	15	23		312
POL	GIKQEFGIPY	886	10	22	34	0.0010	313
POL	GIQQEFGIPY	886	10	11	17		314
POL	HKIQNFRVY	969	10	12	19		315
POL	ITKIQNFRVY	969	10	36	57	0.0010	316
POL	NSPTRRELQV	28	11	12	19		317
POL	VSFSFPQITLW	78	11	07	15		318
POL	GTTLNFPQITF	79	11	01	17		319
POL	PSLSFPQITLW	79	11	02	33		320
POL	GTLNCPQITL	80	11	01	33		321
POL	PTFNFPQITLW	80	11	01	33		322
POL	SSFSFPQITLW	82	11	03	30		323
POL	VLEDINLPGKW	119	11	13	20		324
POL	VLEEINLPGKW	119	11	12	19		325
POL	GIGGFIKVRQY	136	11	53	83		326
POL	LLTQIGCTLNF	176	11	21	33		327
POL	MLTQIGCTLNF	176	11	17	27		328
POL	MLTQLGCTLN	176	11	10	16		329
POL	KISKIGPENPY	235	11	41	64		330
POL	KISRIGPENPY	235	11	11	17		331
POL	DSTKWRKLVD	256	11	58	91		332
POL	SVTVLDVGDA	294	11	56	88		333
POL	VTVLDVGDAY	295	11	56	88		334
POL	SVPLDKDFRK	306	11	18	28		335
POL	SINNETPGIRY	323	11	32	50		336
POL	STNNETPGIRY	323	11	11	17		337
POL	QSSMTKILEPF	350	11	33	52		338
POL	IVIYQYMDDLY	367	11	42	66		339
POL	ELREHLLKWG	393	11	14	22		340
POL	ELRQHLLRWG	393	11	12	19		341
POL	WMGYELHPDK	418	11	60	94		342
POL	DIQKLVGKLN	445	11	62	97		343
POL	EILKEPVHGVY	497	11	40	63		344
POL	ILKEPVHGVYY	498	11	38	59		345
POL	SIVIWGKTPKF	571	11	41	64		346
POL	PIQKETWEAW	584	11	15	23		347
POL	PIQKETWETW	584	11	27	42		348
POL	ETWETWWTD	588	11	10	16		349
POL	FVNTPPLVKL	608	11	54	86		350

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	LIKKEKVYLA	717	11	20	31		351
POL	LIKKEKVYLSW	717	11	13	20		352
POL	LVSAGIRKVLF	743	11	15	23		353
POL	LVSSGIRKVLF	743	11	26	41		354
POL	HSNWRAMAS	768	11	32	50		355
POL	ILVAVHVASGY	825	11	53	83		356
POL	KVIHTDNGSNF	863	11	21	33		357
POL	FTSAAVKAAC	873	11	27	42		358
POL	FTSTTVKAAC	873	11	14	22		359
POL	TSAAVKAACW	874	11	27	42		360
POL	TSTTVKAACW	874	11	14	22		361
POL	HLKTAVQMAV	923	11	57	89		362
POL	AVQMAVFIHN	927	11	60	94		363
POL	QIIKIQNFRVY	968	11	12	19		364
POL	QITKIQNFRVY	968	11	35	55		365
POL	IIKIQNFRVYY	969	11	12	19		366
POL	ITKIQNFRVYY	969	11	36	57	0.0110	367
POL	PIWKGPAKLL	985	11	35	55		368
POL	PLWKGPAKLL	985	11	18	28		369
REV	ILYQSNPY	23	8	27	42		370
REV	AVRIIKILY	17	9	13	20		371
REV	KILYQSNPY	22	9	26	41		372
REV	IIKILYQSNPY	20	11	18	28		373
TAT	PVDPNLEPW	3	9	20	31		374
TAT	PVDPRLEPW	3	9	14	22		375
TAT	FLNKGLGISY	41	10	14	22		376
VIF	SLVKHHMY	23	8	44	69		377
VIF	RLVITTYW	65	8	12	19		378
VIF	QLIHLYYF	110	8	14	22		379
VIF	QLIHMHYF	110	8	14	22		380
VIF	HLYYFDCF	113	8	16	25		381
VIF	HMHYFDCF	113	8	15	23		382
VIF	IVSPRCEY	133	8	14	22		383
VIF	KSLVKHHMY	22	9	18	28		384
VIF	NSLVKHHMY	22	9	24	38		385
VIF	GLHTGERDW	73	9	22	34		386
VIF	GLQTGERDW	73	9	12	19		387
VIF	SIEWRLRRY	89	9	11	17		388
VIF	QVDRMKIRTW	12	10	12	19		389
VIF	QVDRMRINTW	12	10	10	16		390
VIF	QVDRMRIRTW	12	10	31	48		391
VIF	HLGHGVSIEW	83	10	25	39		392
VIF	HLGQGVSIEW	83	10	26	41		393
VIF	VSIEWRLRRY	88	10	11	17		394
VIF	LIHLYYFDCF	111	10	16	25		395
VIF	LIHMHYFDCF	111	10	15	23		396
VIF	SVKKLTEDRW	174	10	13	20		397
VIF	GVSIEWRLRR	87	11	10	16		398
VIF	GLADQLIHMH	106	11	11	17		399
VIF	QLIHLYYFDCF	110	11	13	20		400

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
VIF	QLIHMHYFDCF	110	11	14	22		401
VIF	PSVKKLTEDR	173	11	13	20		402
VPR	KSEAVRHF	27	8	15	23		403
VPR	WLHGLGQY	38	8	11	17		404
VPR	RILQQLLF	62	8	45	70		405
VPR	AVRHFPRIW	30	9	14	22		406
VPR	AVRHFPRPW	30	9	34	53		407
VPR	ELKNEAVRHF	25	10	17	27		408
VPR	ELKSEAVRHF	25	10	15	23		409
VPR	WLHGLGQHY	38	10	20	31		410
VPR	HIYETYGDTW	45	10	17	27		411
VPR	HIYNTYGDTW	45	10	14	22		412
VPR	YIYETYGDTW	45	10	14	22		413
VPR	IIRILQQLLF	60	10	41	64		414
VPR	ILQQLLFIHF	63	10	35	55		415
VPR	AIIRILQQLLF	59	11	38	59		416
VPR	RILQQLLFIHF	62	11	34	53		417
VPU	LIIAIVVW	26	8	10	16		418
VPU	IVVWTIVF	30	8	15	23		419
VPU	WTIVFIEY	34	8	12	19		420
VPU	EMGHHAPW	89	8	11	17		421
VPU	AIVVWTIVF	29	9	14	22		422
VPU	VVWTIVFIEY	31	10	12	19		423
VPU	GVEMGHHAP	91	10	01	50		424
VPU	KVDYRIVIVAF	7	11	01	33		425
VPU	IVVWTIVFIEY	30	11	12	19		426
VPU	RIKEIRDDSDY	64	11	01	50		427
VPU	RIREIRDDSDY	64	11	01	50		428

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LILGLVII	21	8	09	15						429
ENV	GLVIICSA	28	8	10	16						430
ENV	GMLMICSA	28	8	12	19						431
ENV	QLYATVYA	34	8	01	50						432
ENV	WVTVYYGV	46	8	58	91						433
ENV	TVYYGVPV	48	8	55	86						434
ENV	GVPVWKEA	52	8	34	53						435
ENV	PVWKEATT	54	8	22	34						436
ENV	ATTTLFCA	59	8	24	38						437
ENV	TLFCASDA	64	8	54	84						438
ENV	EVHNVWAT	77	8	36	56						439
ENV	ATHACVPT	83	8	56	88						440
ENV	NVTENFNM	101	8	34	53						441
ENV	NMWKNDMV	107	8	12	19						442
ENV	NMWKNNMV	107	8	34	53						443
ENV	EQMHEDII	115	8	24	38						444
ENV	DQSLKPCV	126	8	50	78						445
ENV	SLKPCVKL	128	8	55	86						446
ENV	KLTPLCVT	134	8	53	83						447
ENV	LTPLCVTL	135	8	54	84						448
ENV	VTSTGNSA	161	8	01	20						449
ENV	ALFYKLDV	202	8	10	16						450
ENV	ALFYRLDV	202	8	12	19						451
ENV	NISPKNNT	217	8	01	33						452
ENV	LINCNTSA	237	8	17	27						453
ENV	NTSAITQA	241	8	14	22						454
ENV	NTSVITQA	241	8	13	20						455
ENV	ITQACPKV	245	8	37	58						456
ENV	PIPIIYCA	258	8	40	63						457
ENV	PIPIIYCT	258	8	18	28						458
ENV	PIIYCAPA	260	8	37	58						459
ENV	PIIYCTPA	260	8	18	28						460
ENV	CAPAGFAI	264	8	29	45						461
ENV	CTPAGFAI	264	8	10	16						462
ENV	GTGPCKNV	281	8	17	27						463
ENV	NVSTVQCT	287	8	51	80						464
ENV	TVQCTHGI	290	8	51	80						465
ENV	CTHGIKPV	294	8	33	52						466
ENV	CTHGIRPV	294	8	26	41						467
ENV	GIKPVVST	297	8	33	52						468
ENV	GIRPVVST	297	8	26	41						469
ENV	PVVSTQLL	300	8	60	94						470
ENV	VVSTQLLL	301	8	60	94						471
ENV	QLLLNGSL	305	8	57	89						472
ENV	LLLNGSLA	306	8	55	86						473
ENV	SLAEEEVV	311	8	14	22						474
ENV	LAEEEVVI	312	8	13	20						475
ENV	IIRSENLT	319	8	10	16						476
ENV	CTRPNNNT	345	8	29	45						477
ENV	NTRKSIRI	351	8	10	16						478

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NTSPRSRV	376	8	01	33						479
ENV	TAGNSSRA	376	8	01	33						480
ENV	IIGDIRQA	377	8	30	49						481
ENV	MQNGTNIT	458	8	01	17						482
ENV	IITEGNITL	478	8	01	50						483
ENV	NITLPCRI	482	8	11	17						484
ENV	TITLPCRI	482	8	14	22						485
ENV	RIKQIINM	488	8	30	47						486
ENV	RIKQIVNM	488	8	12	19						487
ENV	IINMWQEV	492	8	17	27						488
ENV	WQEVGKAM	496	8	18	28						489
ENV	WQRVGQAM	496	8	11	17						490
ENV	EVGKAMYA	498	8	18	28						491
ENV	RVGQAMYA	498	8	10	16						492
ENV	KAMYAPPI	502	8	23	36						493
ENV	QAMYAPPI	502	8	14	22						494
ENV	RAMYAPPI	502	8	12	19						495
ENV	QIRCSSNI	512	8	11	17						496
ENV	NITGLILT	519	8	11	17						497
ENV	NITGLLLT	519	8	35	55						498
ENV	ELYKYKVV	560	8	56	89						499
ENV	KVVKIEPL	565	8	25	39						500
ENV	KIEPLGVA	568	8	23	37						501
ENV	PTKAKRRV	576	8	22	34						502
ENV	VVEREKRA	588	8	32	50						503
ENV	VVQREKRA	588	8	17	27						504
ENV	VQREKRAV	589	8	17	27						505
ENV	RAVGIGAV	594	8	12	19						506
ENV	GALFLGFL	601	8	12	19						507
ENV	GAMFLGFL	601	8	13	20						508
ENV	GAVFLGFL	601	8	22	34						509
ENV	FLGFLGAA	604	8	48	75						510
ENV	FLGAAGST	608	8	55	86						511
ENV	AAGSTMGA	611	8	58	91						512
ENV	STMGAASI	614	8	39	61						513
ENV	TMGAASIT	615	8	39	61						514
ENV	GAASITLT	617	8	39	61						515
ENV	AASITLTV	618	8	36	56						516
ENV	SITLTVQA	620	8	32	50						517
ENV	LTVQARQL	623	8	38	59						518
ENV	TVQARQLL	624	8	36	56						519
ENV	RQLLSGIV	628	8	49	77						520
ENV	IVQQQNNL	634	8	26	41						521
ENV	IVQQQSNL	634	8	32	50						522
ENV	VQQQNNLL	635	8	26	41						523
ENV	VQQQSNLL	635	8	32	50						524
ENV	QQNNLLRA	637	8	26	41						525
ENV	QQSNLLRA	637	8	26	41						526
ENV	NLLRAIEA	640	8	51	80						527
ENV	AIEAQQHL	644	8	49	77						528

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	AQQHLLKL	647	8	13	20						529
ENV	AQQHLLQL	647	8	35	55						530
ENV	AQQHMLQL	647	8	10	16						531
ENV	QQHLLKLT	648	8	13	20						532
ENV	QQHLLQLT	648	8	34	53						533
ENV	QQHMLQLT	648	8	10	16						534
ENV	LQLTVWGI	652	8	44	69						535
ENV	TVWGIKQL	655	8	59	92						536
ENV	KQLQARVL	660	8	41	64						537
ENV	QLQARVLA	661	8	41	64						538
ENV	LQARVLAV	662	8	33	52						539
ENV	VLAVERYL	666	8	34	53						540
ENV	YLKDQQLL	672	8	31	48	0.0001					541
ENV	YLRDQQLL	672	8	18	28						542
ENV	KLICTTAV	687	8	19	30						543
ENV	KLICTTNV	687	8	17	27						544
ENV	KLICTTTV	687	8	12	19						545
ENV	WMEWEREI	723	8	12	19						546
ENV	LLALDKWA	755	8	19	30						547
ENV	LLELDKWA	755	8	21	33						548
ENV	ALDKWASL	757	8	11	17						549
ENV	ELDKWASL	757	8	18	28						550
ENV	SLWNWFDI	763	8	17	27						551
ENV	ITKWLWYI	770	8	16	25						552
ENV	ITNWLWYI	770	8	19	30						553
ENV	YIKIFIMI	776	8	43	67						554
ENV	FIMIVGGL	780	8	44	69						555
ENV	IMIVGGLI	781	8	35	56						556
ENV	IVGGLIGL	783	8	42	66						557
ENV	IVGGLVGL	783	8	10	16						558
ENV	GLIGLRII	786	8	15	23						559
ENV	GLIGLRIV	786	8	32	50						560
ENV	GLRIIFAV	789	8	18	28						561
ENV	GLRIVFAV	789	8	29	45						562
ENV	IIFAVLSI	792	8	15	23						563
ENV	IVFAVLSI	792	8	20	31						564
ENV	VLSIVNRV	796	8	38	59						565
ENV	PLSFQTLL	809	8	10	16						566
ENV	PLSFQTLT	809	8	13	20						567
ENV	GLDRPGGT	823	8	01	33						568
ENV	RLVNGFLA	844	8	13	20						569
ENV	RLVSGFLA	844	8	20	31						570
ENV	LVNGFLAL	845	8	14	22						571
ENV	LVSGFLAL	845	8	19	30						572
ENV	LALAWDDL	850	8	25	39						573
ENV	CLFSYHRL	861	8	42	66						574
ENV	RLRDLLLI	867	8	13	20	0.0001					575
ENV	IAARTVEL	874	8	12	19						576
ENV	AARTVELL	876	8	11	17						577
ENV	ELLGHSSL	881	8	09	15						578

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LQYWSQEL	907	8	16	25						579
ENV	GQELKNSA	911	8	12	19						580
ENV	SQELKNSA	911	8	12	19						581
ENV	SAVSLLNA	917	8	11	17						582
ENV	AVSLLNAT	918	8	11	17						583
ENV	SLLNATAI	920	8	14	22						584
ENV	LLNATAIA	921	8	15	23						585
ENV	DTIAIAVA	923	8	10	16						586
ENV	NATAIAVA	923	8	14	22						587
ENV	AIAVAEGT	926	8	32	50						588
ENV	VAEGTDRI	929	8	19	30						589
ENV	VAEGTDRV	929	8	16	25						590
ENV	GTDRVIEV	932	8	11	17						591
ENV	ILHIPRRI	947	8	13	20						592
ENV	PTRIRQGL	951	8	12	19						593
ENV	RQGLERAL	955	8	35	55						594
ENV	VTVYYGVPV	47	9	55	86	0.0003					595
ENV	GVPVWKEAT	52	9	22	34	0.0002					596
ENV	PVWKEATTT	54	9	22	34	0.0002					597
ENV	EATTTLFCA	58	9	24	38	0.0002					598
ENV	TTLFCASDA	61	9	52	81	0.0002					599
ENV	DAKAYDTEV	70	9	17	27	0.0002					600
ENV	DTEVHNVWA	75	9	18	28	0.0001					601
ENV	NVWATHACV	80	9	49	77	0.0002					602
ENV	WATHACVPT	82	9	56	88	0.0002					603
ENV	PTDPNPQEI	89	9	25	39						604
ENV	PTDPNPQEV	89	9	21	33	0.0002					605
ENV	MVEQMHEDI	113	9	23	36	0.0002					606
ENV	QMHEDIISL	116	9	29	45	0.0023					607
ENV	IISLWDQSL	121	9	38	59	0.0180					608
ENV	VISLWDQSL	121	9	10	16						609
ENV	SLKPCVKLT	128	9	55	86	0.0001					610
ENV	CVKLTPLCV	132	9	55	86	0.0002					611
ENV	KLTPLCVTL	134	9	52	81	0.1600					612
ENV	PLCVTLNCT	137	9	22	34	0.0005					613
ENV	EIKNCSFNI	181	9	13	20						614
ENV	ALFYRLDVV	202	9	11	17						615
ENV	VQNNNNSNT	218	9	01	20						616
ENV	RLINCNTSA	236	9	17	27						617
ENV	LINCNTSAI	237	9	15	23						618
ENV	AITQACPKV	244	9	13	20						619
ENV	VITQACPKV	244	9	15	23						620
ENV	KVSFEPIPI	252	9	30	47						621
ENV	CAPAGFAIL	264	9	29	45	0.0001					622
ENV	STVQCTHGI	289	9	51	80	0.0001					623
ENV	CTHGIKPVV	294	9	32	50						624
ENV	CTHGIRPVV	294	9	26	41	0.0001					625
ENV	PVVSTQLLL	300	9	60	94	0.0001					626
ENV	TQLLLNGSL	304	9	57	89						627
ENV	QLLLNGSLA	305	9	55	86	0.0001					628

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	SLAEEEVVI	311	9	13	20	0.0020					629
ENV	NAKTIIVQL	329	9	14	22						630
ENV	ATGDIIGDI	369	9	12	19						631
ENV	DIIGDIRQA	372	9	12	19						632
ENV	EIIGDIRQA	372	9	09	15						633
ENV	GTAGNSSRA	375	9	01	33						634
ENV	NTSPRSRVA	376	9	01	33						635
ENV	TAGNSSRAA	376	9	01	33						636
ENV	DIRQAHCNI	380	9	15	23						637
ENV	DIRQAHCNV	380	9	10	16						638
ENV	TLPCRIKQI	484	9	26	41						639
ENV	QIINMWQEV	491	9	17	27	0.0026					640
ENV	NMWQEVGKA	494	9	15	23	0.0022					641
ENV	GQAMYAPPI	501	9	14	22						642
ENV	GQIRCSSNI	511	9	11	17						643
ENV	QIRCSSNIT	512	9	11	17	0.0001					644
ENV	NTETNKTET	537	9	01	17						645
ENV	NTTGNTTET	537	9	01	17						646
ENV	VVKIEPLGV	566	9	23	36						647
ENV	PLGVAPTKA	571	9	23	36	0.0001					648
ENV	PTKAKRRVV	576	9	22	34	0.0001					649
ENV	RVVEREKRA	587	9	32	50						650
ENV	RVVQREKRA	587	9	17	27	0.0001					651
ENV	VVEREKRAV	588	9	25	39						652
ENV	VVQREKRAV	588	9	16	25						653
ENV	AVGIGAVFL	595	9	11	17						654
ENV	ALFLGFLGA	602	9	11	17	0.0950					655
ENV	AMFLGFLGA	602	9	12	19						656
ENV	AVFLGFLGA	602	9	19	30						657
ENV	FLGAAGSTM	608	9	55	86	0.0190					658
ENV	GAAGSTMGA	610	9	55	86	0.0009					659
ENV	AAGSTMGAA	611	9	45	70	0.0001					660
ENV	STMGAASIT	614	9	39	61						661
ENV	TMGAASITL	615	9	39	61						662
ENV	GAASITLTV	617	9	36	56						663
ENV	TLTVQARQL	622	9	37	58						664
ENV	LTVQARQLL	623	9	36	56						665
ENV	QARQLLSGI	626	9	38	59						666
ENV	GIVQQQNNL	633	9	26	41	0.0001					667
ENV	GIVQQQSNL	633	9	32	50						668
ENV	IVQQQNNLL	634	9	26	41	0.0001					669
ENV	IVQQQSNLL	634	9	32	50						670
ENV	QQQNNLLRA	636	9	25	39						671
ENV	QQQSNLLRA	636	9	26	41						672
ENV	QQNNLLRAI	637	9	26	41						673
ENV	QQSNLLRAI	637	9	26	41						674
ENV	RAIEAQQHL	643	9	45	70						675
ENV	AIEAQQHLL	644	9	48	75						676
ENV	EAQQHLLKL	646	9	12	19						677
ENV	EAQQHLLQL	646	9	35	56						678

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	AQQHLLKLT	647	9	13	20						679
ENV	AQQHLLQLT	647	9	34	53						680
ENV	AQQHMLQLT	647	9	10	16						681
ENV	QQHLLKLTV	648	9	13	20						682
ENV	QQHLLQLTV	648	9	34	53						683
ENV	LLKLTVWGI	651	9	13	20						684
ENV	LLQLTVWGI	651	9	34	53	0.5100	0.0200	0.2300	0.1500	0.0620	685
ENV	MLQLTVWGI	651	9	10	16	0.2500					686
ENV	LTVWGIKQL	654	9	59	92	0.0001					687
ENV	GIKQLQARV	658	9	40	63	0.0001					688
ENV	KQLQARVLA	660	9	41	64						689
ENV	QLQARVLAV	661	9	33	52	0.0085					690
ENV	RVLAVERYL	665	9	33	52	0.0009					691
ENV	GIWGCSGKL	680	9	48	75	0.0011					692
ENV	QQEKNEQDL	747	9	16	25						693
ENV	QQEKNEQEL	747	9	18	28						694
ENV	DLLALDKWA	754	9	15	23						695
ENV	ELLELDKWA	754	9	18	28	0.0002					696
ENV	LALDKWASL	756	9	11	17						697
ENV	SLWNWFDIT	763	9	13	20						698
ENV	DITNWLWYI	769	9	10	16						699
ENV	WLWYIKIFI	773	9	49	77	0.0360					700
ENV	YIKIFIMIV	776	9	39	61	0.0001					701
ENV	FIMIVGGLI	780	9	35	55						702
ENV	MIVGGLIGL	782	9	36	56						703
ENV	LIGLRIIFA	787	9	16	25						704
ENV	LIGLRIVFA	787	9	21	33						705
ENV	GLRIIFAVL	789	9	17	27						706
ENV	GLRIVFAVL	789	9	28	44	0.0009					707
ENV	RIIFAVLSI	791	9	14	22						708
ENV	RIVFAVLSI	791	9	19	30	0.0002					709
ENV	IIFAVLSIV	792	9	15	23						710
ENV	IVFAVLSIV	792	9	18	28	0.0012					711
ENV	AVLSIVNRV	795	9	31	48	0.0130					712
ENV	RVRQGYSPL	802	9	55	86	0.0005					713
ENV	SIRLVNGFL	842	9	11	17						714
ENV	SIRLVSGFL	842	9	13	20						715
ENV	RLVNGFLAL	844	9	12	19						716
ENV	RLVSGFLAL	844	9	19	30						717
ENV	LVSGFLALA	845	9	16	25						718
ENV	FLALAWDDL	849	9	25	39						719
ENV	LAWDDLRSL	852	9	20	31						720
ENV	LIAARTVEL	873	9	12	19						721
ENV	IAARTVELL	874	9	11	17						722
ENV	LLGRRGWEA	882	9	10	16						723
ENV	GLRLGWEGL	892	9	10	32						724
ENV	LLQYWSQEL	906	9	16	25	0.0270					725
ENV	GQELKNSAI	911	9	12	19						726
ENV	SQELKNSAV	911	9	10	16						727
ENV	ELKNSAINL	913	9	10	16						728

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	ELKNSAISL	913	9	10	16						729
ENV	ELKNSAVSL	913	9	12	19						730
ENV	SAVSLLNAT	917	9	11	17	0.0001					731
ENV	AVSLLNATA	918	9	11	17						732
ENV	SLLNATAIA	920	9	14	22						733
ENV	LLNATAIAV	921	9	15	23						734
ENV	IAIAVAEGT	925	9	10	16						735
ENV	TAIAVAEGT	925	9	22	34						736
ENV	AVAEGTDRI	928	9	16	25						737
ENV	AVAEGTDRV	928	9	14	22	0.0008					738
ENV	VAEGTDRII	929	9	18	28						739
ENV	VAEGTDRVI	929	9	16	25	0.0001					740
ENV	AILHIPRRI	946	9	12	19						741
ENV	RIRQGLERA	953	9	34	53	0.0003					742
ENV	RQGLERALL	955	9	34	53						743
ENV	ILGLVHCSA	26	10	10	16						744
ENV	LLGMLMICSA	26	10	10	16						745
ENV	QLYATVYAGV	34	10	01	50						746
ENV	KLWVTVYYGV	44	10	11	17	0.0150					747
ENV	NLWVTVYYGV	44	10	34	54	0.0160					748
ENV	WVTVYYGVPV	46	10	55	86	0.0009					749
ENV	GVPVWKEATT	52	10	22	34	0.0001					750
ENV	PVWKEATTTL	54	10	22	34	0.0001					751
ENV	KTTLFCASDA	60	10	12	19						752
ENV	TTTLFCASDA	60	10	24	38	0.0001					753
ENV	TLFCASDAKA	64	10	46	72	0.0006					754
ENV	CASDAKAYDT	67	10	19	30	0.0001					755
ENV	KAYDTEVHNV	72	10	17	27	0.0013					756
ENV	DTEVHNVWAT	75	10	18	28	0.0001					757
ENV	EVHNVWATHA	77	10	35	55	0.0001					758
ENV	PTDPNPQEVV	89	10	13	20						759
ENV	NMVEQMHEDI	112	10	20	31	0.0001					760
ENV	MVEQMHEDII	113	10	23	36	0.0001					761
ENV	EQMHEDIISL	115	10	22	34						762
ENV	DIISLWDQSL	120	10	38	59	0.0001					763
ENV	DVISLWDQSL	120	10	10	16						764
ENV	DQSLKPCVKL	126	10	47	73						765
ENV	CVKLTPLCVT	132	10	53	83	0.0001					766
ENV	STSNSSNSST	159	10	01	50						767
ENV	VTSTGNSAGT	161	10	01	20						768
ENV	EIKNCSFNIT	181	10	12	19						769
ENV	SVQNNNNSNT	217	10	01	33						770
ENV	RLINCNTSAI	236	10	15	24						771
ENV	LINCNTSAIT	237	10	14	22						772
ENV	SAITQACPKV	243	10	13	20						773
ENV	SVITQACPKV	243	10	15	23						774
ENV	PIPIHYCAPA	258	10	36	56	0.0002					775
ENV	PIPIHYCTPA	258	10	18	28						776
ENV	GTGPCKNVST	281	10	12	19						777
ENV	CTNVSTVQCT	285	10	13	20						778

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	VQCTHGIKPV	292	10	32	50						779
ENV	VQCTHGIRPV	292	10	25	39						780
ENV	GIKPVVSTQL	297	10	33	52						781
ENV	GIRPVVSTQL	297	10	26	41	0.0002					782
ENV	STQLLLNGSL	303	10	57	89	0.0001					783
ENV	TQLLLNGSLA	304	10	55	86						784
ENV	RIGPGQTFYA	357	10	10	16						785
ENV	GIGPGQTFYA	360	10	01	33						786
ENV	SIGSGQAFYV	360	10	01	33						787
ENV	YATGDIIGDI	368	10	11	17						788
ENV	GTAGNSSRAA	375	10	01	33						789
ENV	MQNGTNITST	458	10	01	17						790
ENV	NANITIPCRI	478	10	01	50						791
ENV	ITLPCRIKQI	483	10	25	39						792
ENV	TLPCRIKQII	484	10	15	23						793
ENV	TLPCRIKQIV	484	10	10	16						794
ENV	KQIINMWQEV	490	10	17	27						795
ENV	NMWQEVGKAM	494	10	15	23	0.0004					796
ENV	WQEVGKAMYA	496	10	18	28						797
ENV	WQRVGQAMYA	496	10	10	16						798
ENV	GQIRCSSNIT	511	10	11	17						799
ENV	EIFRPGGGDM	544	10	17	27	0.0001					800
ENV	ETFRPGGGDM	544	10	21	33						801
ENV	DMRDNWRSEL	552	10	37	58	0.0001					802
ENV	ELYKYKVVEI	560	10	13	21						803
ENV	ELYKYKVVKI	560	10	29	46						804
ENV	KVVKIEPLGV	565	10	23	36						805
ENV	VVKIEPLGVA	566	10	23	36						806
ENV	KIEPLGVAPT	568	10	23	37						807
ENV	VAPTKAKRRV	574	10	17	27	0.0001					808
ENV	STRTHREKRA	586	10	01	50						809
ENV	RVVEREKRAV	587	10	25	39						810
ENV	RVVQREKRAV	587	10	16	25						811
ENV	RAVGIGAVFL	594	10	11	17						812
ENV	GIGAVFLGFL	598	10	11	18						813
ENV	MLGAMFLGFL	599	10	04	36						814
ENV	TIGAMFLGFL	599	10	03	27						815
ENV	GALFLGFLGA	601	10	11	17	0.0003					816
ENV	GAMFLGFLGA	601	10	12	19						817
ENV	GAVFLGFLGA	601	10	19	30						818
ENV	ALFLGFLGAA	602	10	11	17	0.5000					819
ENV	AMFLGFLGAA	602	10	12	19						820
ENV	AVFLGFLGAA	602	10	19	30						821
ENV	GAAGSTMGAA	610	10	42	66	0.0004					822
ENV	STMGAASITL	614	10	39	61						823
ENV	TMGAASITLT	615	10	39	61						824
ENV	AASITLTVQA	618	10	28	44						825
ENV	ITLTVQARQL	621	10	27	42						826
ENV	TLTVQARQLL	622	10	35	55						827
ENV	VQARQLLSGI	625	10	36	56						828

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	QARQLLSGIV	626	10	38	59						829
ENV	GIVQQQNNLL	633	10	26	41	0.0002					830
ENV	GIVQQQSNLL	633	10	32	50						831
ENV	VQQQNNLLRA	635	10	25	39						832
ENV	VQQQSNLLRA	635	10	26	41						833
ENV	QQQNNLLRAI	636	10	25	39						834
ENV	QQQSNLLRAI	636	10	26	41						835
ENV	RAIEAQQHLL	643	10	44	69						836
ENV	EAQQHLLKLT	646	10	12	19						837
ENV	EAQQHLLQLT	646	10	34	54						838
ENV	AQQHLLKLTV	647	10	13	20						839
ENV	AQQHLLQLTV	647	10	34	53						840
ENV	HLLKLTVWGI	650	10	13	20						841
ENV	HLLQLTVWGI	650	10	34	53						842
ENV	KLTVWGIKQL	653	10	13	20						843
ENV	QLTVWGIKQL	653	10	44	69	0.0015					844
ENV	TVWGIKQLQA	655	10	49	77	0.0150					845
ENV	GIKQLQARVL	658	10	40	63	0.0002					846
ENV	KQLQARVLAV	660	10	33	52						847
ENV	YLKDQQLLGI	672	10	27	42						848
ENV	YLRDQQLLGI	672	10	18	28						849
ENV	GIWGCSGKLI	680	10	48	75	0.0004					850
ENV	MTWMEWEREI	721	10	12	19						851
ENV	NQQEKNEQDL	746	10	13	20						852
ENV	NQQEKNEQEL	746	10	15	23						853
ENV	QQEKNEQDLL	747	10	16	25						854
ENV	QQEKNEQELL	747	10	18	28						855
ENV	LLALDKWASL	755	10	11	17						856
ENV	LLELDKWASL	755	10	18	28	0.0024					857
ENV	WASLWNWFDI	761	10	17	27						858
ENV	ITKWLWYIKI	770	10	15	23						859
ENV	ITNWLWYIKI	770	10	14	22	0.0002					860
ENV	WLWYIKIFIM	773	10	43	67	0.0001					861
ENV	KIFIMIVGGL	778	10	38	59	0.0003					862
ENV	IMIVGGLIGL	781	10	34	54						863
ENV	IVGGLIGLRI	783	10	42	66						864
ENV	GLIGLRIIFA	786	10	15	23						865
ENV	GLIGLRIVFA	786	10	21	33						866
ENV	LIGLRIIFAV	787	10	16	25						867
ENV	LIGLRIVFAV	787	10	21	33						868
ENV	RIIFAVLSIV	791	10	14	22						869
ENV	RIVFAVLSIV	791	10	17	27	0.0007					870
ENV	FAVLSIVNRV	794	10	31	48	0.0002					871
ENV	SIRLVSGFLA	842	10	12	19						872
ENV	RLVSGFLALA	844	10	16	25						873
ENV	ALAWDDLRSL	851	10	19	30						874
ENV	NLCLFSYHRL	859	10	11	17						875
ENV	SLCLFSYHRL	859	10	31	48						876
ENV	LIAARTVELL	873	10	11	17						877
ENV	ELLGRRGWEA	881	10	10	16						878

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LLGRRGWEAL	882	10	09	15						879
ENV	RLGWEGLKYL	894	10	09	29						880
ENV	NLLQYWSQEL	905	10	16	25	0.0059					881
ENV	ELKNSAVSLL	913	10	10	16						882
ENV	SAVSLLNATA	917	10	11	17						883
ENV	AVSLLNATAI	918	10	11	17						884
ENV	SLLNATAIAV	920	10	14	22	0.0650	0.0074	0.0390	0.0600	0.0390	885
ENV	LLNATAIAVA	921	10	14	22	0.0740					886
ENV	ATAIAVAEGT	924	10	14	22						887
ENV	IAVAEGTDRI	927	10	16	25						888
ENV	IAVAEGTDRV	927	10	14	22	0.0001					889
ENV	AVAEGTDRII	928	10	15	23						890
ENV	AVAEGTDRVI	928	10	14	22	0.0004					891
ENV	RAILHIPRRI	945	10	12	19						892
ENV	HIPRRIRQGL	949	10	13	21						893
ENV	NIPRRIRQGL	949	10	11	17						894
ENV	RIRQGLERAL	953	10	34	53	0.0001					895
ENV	LILGLVIICSA	21	11	09	15						896
ENV	KQLYATVYSGV	34	11	01	50						897
ENV	GVPVWKEATTT	52	11	22	34						898
ENV	ATTTLFCASDA	59	11	23	36						899
ENV	TTLFCASDAKA	61	11	44	69						900
ENV	NVWATHACVPT	80	11	48	75						901
ENV	CVPTDPNPQEI	87	11	25	39						902
ENV	CVPTDPNPQEV	87	11	21	33						903
ENV	PTDPNPQEVVL	89	11	12	19						904
ENV	NMWKNNMVEQM	107	11	30	47						905
ENV	NMVEQMHEDII	112	11	20	31						906
ENV	SLWDQSLKPCV	123	11	47	75						907
ENV	DQSLKPCVKLT	126	11	47	73						908
ENV	SLKPCVKLTPL	128	11	54	84						909
ENV	CVKLTPLCVTL	132	11	52	81						910
ENV	LTPLCVTLNCT	135	11	22	34						911
ENV	EIKNCSFNITT	181	11	11	17						912
ENV	RLINCNTSAIT	236	11	14	22						913
ENV	QACPKVSFEPI	248	11	30	47						914
ENV	PIHYCAPAGFA	260	11	27	42						915
ENV	PIHYCTPAGFA	260	11	10	16						916
ENV	GTGPCKNVSTV	281	11	12	19						917
ENV	NVSTVQCTHGI	287	11	51	80						918
ENV	TVQCTHGIKPV	290	11	28	44						919
ENV	TVQCTHGIRPV	290	11	22	34						920
ENV	VQCTHGIKPVV	292	11	31	48						921
ENV	VQCTHGIRPVV	292	11	25	39						922
ENV	CTHGIKPVVST	294	11	32	50						923
ENV	CTHGIRPVVST	294	11	26	41						924
ENV	GIKPVVSTQLL	297	11	33	52						925
ENV	GIRPVVSTQLL	297	11	26	41						926
ENV	STQLLLNGSLA	303	11	55	86						927
ENV	LLNGSLAEEEV	307	11	16	25						928

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	EINCTRPNNNT	342	11	10	16						929
ENV	RIGPGQTFYAT	357	11	10	16						930
ENV	GIGPGQTFYAT	360	11	01	33						931
ENV	SIGSGQAFYVT	360	11	01	33						932
ENV	EMHTNYTSNDT	458	11	01	17						933
ENV	NITLPCRIKQI	482	11	11	17						934
ENV	TITLPCRIKQI	482	11	13	20						935
ENV	ITLPCRIKQII	483	11	15	23						936
ENV	IINMWQEVGKA	492	11	12	19						937
ENV	EVGKAMYAPPI	498	11	18	28						938
ENV	RVGQAMYAPPI	498	11	10	16						939
ENV	QIRCSSNITGL	512	11	11	17						940
ENV	KVVKIEPLGVA	565	11	23	36						941
ENV	GVAPTKAKRRV	573	11	17	27						942
ENV	VAPTKAKRRVV	574	11	17	27						943
ENV	NIITPIIREKRA	586	11	01	50						944
ENV	STRTHREKRAV	586	11	01	50						945
ENV	VVEREKRAVGI	588	11	11	17						946
ENV	GALFLGFLGAA	601	11	11	17						947
ENV	GAMFLGFLGAA	601	11	12	19						948
ENV	GAVFLGFLGAA	601	11	19	30						949
ENV	FLGFLGAAGST	604	11	48	75						950
ENV	FLGAAGSTMGA	608	11	55	86						951
ENV	AAGSTMGAASI	611	11	34	53						952
ENV	STMGAASITLT	614	11	39	61						953
ENV	TMGAASITLTV	615	11	36	56						954
ENV	GAASITLTVQA	617	11	28	44						955
ENV	SITLTVQARQL	620	11	27	42						956
ENV	ITLTVQARQLL	621	11	27	42						957
ENV	TVQARQLLSGI	624	11	36	56						958
ENV	VQARQLLSGIV	625	11	36	56						959
ENV	IVQQQHNLLRA	634	11	25	39						960
ENV	IVQQQSNLLRA	634	11	26	41						961
ENV	VQQQNNLLRAI	635	11	25	39						962
ENV	VQQQSNLLRAI	635	11	26	41						963
ENV	QQNNLLRAIEA	637	11	26	41						964
ENV	QQSNLLRAIEA	637	11	23	36						965
ENV	LLRAIEAQQHL	641	11	45	70						966
ENV	AIEAQQHLLKL	644	11	12	19						967
ENV	AIEAQQHLLQL	644	11	35	55						968
ENV	EAQQHLLKLTV	646	11	12	19						969
ENV	EAQQHLLQLTV	646	11	34	54						970
ENV	LQLTVWGIKQL	652	11	44	69						971
ENV	LTVWGIKQLQA	654	11	49	77						972
ENV	GIKQLQARVLA	658	11	40	63						973
ENV	QARVLAVERYL	663	11	33	52						974
ENV	AVERYLKDQQL	668	11	23	36						975
ENV	AVERYLRDQQL	668	11	11	17						976
ENV	LLGIWGCSGKL	678	11	46	72						977
ENV	NMTWMEWEREI	720	11	12	19						978

Table VIII
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NQQEKNEQDLL	746	11	13	20						979
ENV	NQQEKNEQELL	746	11	15	23						980
ENV	QQEKNEQDLLA	747	11	16	25						981
ENV	EQDLLALDKWA	752	11	12	19						982
ENV	EQELLELDKWA	752	11	11	17						983
ENV	ELLELDKWASL	754	11	15	23						984
ENV	WASLWNWFDIT	761	11	13	20						985
ENV	WLWYIKIFIMI	773	11	43	67						986
ENV	KIFIMIVGGLI	778	11	31	48						987
ENV	FIMIVGGLIGL	780	11	34	53						988
ENV	MIVGGLIGLRI	782	11	36	56						989
ENV	IVGGLIGLRII	783	11	12	19						990
ENV	IVGGLIGLRIV	783	11	30	47						991
ENV	GLIGLRIIFAV	786	11	15	23						992
ENV	GLIGLRIVFAV	786	11	21	33						993
ENV	LIGLRIIFAVL	787	11	15	23						994
ENV	LIGLRIVFAVL	787	11	20	31						995
ENV	GLRIIFAVLSI	789	11	14	22						996
ENV	GLRIVFAVLSI	789	11	19	30						997
ENV	RQGYSPLSFQT	804	11	45	70						998
ENV	SIRLVSGFLAL	842	11	11	17						999
ENV	LALAWDDLRSL	850	11	19	30						1000
ENV	LAWDDLRSLCL	852	11	20	31						1001
ENV	CLFSYHRLRDL	861	11	20	31						1002
ENV	ELLGRRGWEAL	881	11	09	15						1003
ENV	SQELKNSAVSL	911	11	10	16						1004
ENV	SAVSLLNATAI	917	11	11	17						1005
ENV	AVSLLNATAIA	918	11	11	17						1006
ENV	SLLNATAIAVA	920	11	13	20	0.2700					1007
ENV	NATAIAVAEGT	923	11	13	20						1008
ENV	AIAVAEGTDRI	926	11	16	25						1009
ENV	AIAVAEGTDRV	926	11	14	22						1010
ENV	IAVAEGTDRII	927	11	15	23						1011
ENV	IAVAEGTDRVI	927	11	14	22						1012
ENV	PTRIRQGLERA	951	11	11	17						1013
ENV	RIRQGLERALL	953	11	33	52						1014
GAG	SVLSGGEL	6	8	11	17						1015
GAG	SVLSGGKL	6	8	28	44						1016
GAG	KLDAWEKI	12	8	18	28						1017
GAG	KLDKWEKI	12	8	10	16						1018
GAG	DAWEKIRL	14	8	17	27						1019
GAG	KLKHIVWA	31	8	13	20						1020
GAG	RLKHLVWA	31	8	17	27						1021
GAG	IVWASREL	35	8	21	33						1022
GAG	LVWASREL	35	8	36	56						1023
GAG	FALNPGLL	46	8	22	34						1024
GAG	FAVNPGLL	46	8	16	25						1025
GAG	QLQPALQT	65	8	17	27						1026
GAG	QLQPSLQT	65	8	15	23						1027
GAG	LQTGSEEL	70	8	17	27						1028

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	GTEELRSL	73	8	12	19						1029
GAG	ELRSLYNT	76	8	17	27						1030
GAG	SLFNTVAT	79	8	16	25						1031
GAG	SLYNTVAT	79	8	22	34						1032
GAG	TVATLYCV	83	8	41	64						1033
GAG	DVKDTKEA	95	8	11	17						1034
GAG	EVKDTKEA	95	8	22	34						1035
GAG	AQQAAADT	119	8	10	16						1036
GAG	AQQAAAAT	132	8	01	33						1037
GAG	KVSQNYPI	148	8	15	27						1038
GAG	QVSQNYPI	148	8	27	48						1039
GAG	VQNAQGQM	156	8	21	33						1040
GAG	VQNLQGQM	156	8	29	45						1041
GAG	GQMVHQAI	161	8	28	44						1042
GAG	HQAISPRT	165	8	29	45						1043
GAG	HQALSPRT	165	8	11	17						1044
GAG	QAISPRTL	166	8	29	45						1045
GAG	QALSPRTL	166	8	11	17						1046
GAG	TLNAWVKV	172	8	61	95						1047
GAG	KAFSPEVI	183	8	50	78						1048
GAG	EVIPMFSA	188	8	46	72						1049
GAG	EVIPMFTA	188	8	14	22						1050
GAG	VIPMFSAL	189	8	46	72						1051
GAG	VIPMFTAL	189	8	14	22						1052
GAG	FTALSEGA	193	8	15	23						1053
GAG	SALSEGAT	194	8	44	69						1054
GAG	TALSEGAT	194	8	15	23						1055
GAG	ATPQDLNM	200	8	12	19						1056
GAG	ATPQDLNT	200	8	42	66						1057
GAG	PQDLNMML	202	8	12	19						1058
GAG	PQDLNTML	202	8	43	67						1059
GAG	DLNMMLNI	204	8	12	19						1060
GAG	DLNTMLNT	204	8	44	69						1061
GAG	NIVGGHQA	210	8	12	19						1062
GAG	NTVGGHQA	210	8	47	73						1063
GAG	IVGGHQAA	211	8	12	19						1064
GAG	TVGGHQAA	211	8	47	73						1065
GAG	HQAAMQML	215	8	61	95						1066
GAG	AMQMLKDT	218	8	33	52						1067
GAG	AMQMLKET	218	8	26	41						1068
GAG	MQMLKDTI	219	8	33	52						1069
GAG	MQMLKETI	219	8	26	41						1070
GAG	DTINEEAA	224	8	33	52						1071
GAG	ETINEEAA	224	8	22	34						1072
GAG	EAAEWDRL	229	8	39	61						1073
GAG	EAAEWDRV	229	8	15	23						1074
GAG	PVHAGPIA	238	8	19	30						1075
GAG	DIAGTTST	256	8	55	86						1076
GAG	IAGTTSTL	257	8	48	75						1077
GAG	STLQEQIA	262	8	12	19						1078

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	LQEQIAWM	264	8	14	22						1079
GAG	LQEQIGWM	264	8	29	45						1080
GAG	WMTNNPPI	270	8	20	31						1081
GAG	WMTSNPPI	270	8	16	25						1082
GAG	DIYKRWII	284	8	17	27						1083
GAG	EIYKRWII	284	8	39	61						1084
GAG	IILGLNKI	290	8	57	89						1085
GAG	ILGLNKIV	291	8	58	91						1086
GAG	GLNKIVRM	293	8	60	94						1087
GAG	IVRMYSPT	297	8	15	23						1088
GAG	IVRMYSPV	297	8	42	66						1089
GAG	RMYSPTSI	299	8	14	22						1090
GAG	RMYSPVSI	299	8	40	63						1091
GAG	YVDRFFKT	320	8	28	44						1092
GAG	YVDRFYKT	320	8	28	44						1093
GAG	KTLRAEQA	326	8	54	84						1094
GAG	TLRAEQAT	327	8	35	55						1095
GAG	SQEVKNWM	334	8	11	17						1096
GAG	TQDVKNWM	334	8	15	23						1097
GAG	TQEVKNWM	334	8	18	28						1098
GAG	WMTDTLLV	340	8	22	34						1099
GAG	WMTETLLV	340	8	37	58						1100
GAG	DTLLVQNA	343	8	22	34						1101
GAG	ETLLVQNA	343	8	37	58						1102
GAG	NANPDCKT	349	8	45	70						1103
GAG	ILKALGPA	357	8	16	25						1104
GAG	KALGPAAT	359	8	16	25						1105
GAG	ALGPAATL	360	8	16	25						1106
GAG	ALGPGATL	360	8	18	28						1107
GAG	PAATLEEM	363	8	16	25						1108
GAG	AATLEEMM	364	8	16	25						1109
GAG	GASLEEMM	364	8	10	16						1110
GAG	GATLEEMM	364	8	29	45						1111
GAG	ATLEEMMT	365	8	46	72						1112
GAG	SLEEMMTA	366	8	11	17						1113
GAG	TLEEMMTA	366	8	46	72						1114
GAG	MMTACQGV	370	8	60	94						1115
GAG	KARVLAEA	383	8	57	89						1116
GAG	LAEAMSQA	387	8	17	27						1117
GAG	LAEAMSQV	387	8	36	57						1118
GAG	SQVTNSAT	394	8	10	16						1119
GAG	IIAKNCRA	433	8	18	28						1120
GAG	IIARNCRA	433	8	13	20						1121
GAG	HLARNCRA	433	8	21	33						1122
GAG	QANFLGKI	466	8	57	89						1123
GAG	GTRPGNYV	480	8	02	100						1124
GAG	LQNRPEPT	487	8	10	16						1125
GAG	LQSRPEPT	487	8	28	44						1126
GAG	ELYPLASL	543	8	14	22						1127
GAG	ELYPLTSL	543	8	11	17						1128

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	PLASLKSL	548	8	15	23						1129
GAG	PLTSLKSL	548	8	12	19						1130
GAG	PLTSLRSL	548	8	12	19						1131
GAG	SLFGNDPL	554	8	12	19						1132
GAG	SLFGSDPL	554	8	11	17						1133
GAG	VLSGGKLDA	7	9	15	23						1134
GAG	HIVWASREL	34	9	21	33						1135
GAG	HLVWASREL	34	9	36	56						1136
GAG	ALNPGLLET	47	9	19	30						1137
GAG	AVNPGLLET	47	9	14	22						1138
GAG	ETSEGCRQI	54	9	16	25						1139
GAG	ILGQLQPSL	62	9	11	17						1140
GAG	GQLQPSLQT	64	9	11	17						1141
GAG	LQPALQTGT	66	9	14	22						1142
GAG	SLQTGSEEL	69	9	14	22						1143
GAG	ELRSLYNTV	76	9	15	23						1144
GAG	SLFNTVATL	79	9	16	25	0.0037					1145
GAG	SLYNTVATL	79	9	22	34	0.0053	0.0012	0.2000	0.0001	0.0004	1146
GAG	NTVATLYCV	82	9	41	64						1147
GAG	TLYCVHQKI	86	9	12	19						1148
GAG	TLYCVHQRI	86	9	15	23						1149
GAG	HQRIEVKDT	91	9	10	16						1150
GAG	DVKDTKEAL	95	9	11	17						1151
GAG	EVKDTKEAL	95	9	20	31						1152
GAG	DTKEALDKI	98	9	32	50						1153
GAG	DTKEALEKI	98	9	10	16						1154
GAG	EQNKSKKKA	109	9	17	27						1155
GAG	KAQQAAADT	118	9	10	16						1156
GAG	SQVSQNYPI	146	9	22	44						1157
GAG	KVSQNYPIV	148	9	15	27						1158
GAG	QVSQNYPIV	148	9	27	48	0.0001					1159
GAG	IVQNAQGQM	155	9	21	33						1160
GAG	IVQNLQGQM	155	9	29	45						1161
GAG	VQNAQGQMV	156	9	14	22						1162
GAG	VQNLQGQMV	156	9	29	45						1163
GAG	AQGQMVHQA	159	9	12	19						1164
GAG	LQGQMVHQA	159	9	21	33						1165
GAG	HQAISPRTL	165	9	29	45						1166
GAG	HQALSPRTL	165	9	11	17						1167
GAG	AISPRTLNA	167	9	29	45						1168
GAG	ALSPRTLNA	167	9	10	16						1169
GAG	RTLNAWVKV	171	9	61	95	0.0012					1170
GAG	TLNAWVKVI	172	9	30	47	0.0032					1171
GAG	TLNAWVKVV	172	9	31	48	0.0005					1172
GAG	WVKVIEEKA	176	9	25	39						1173
GAG	WVKVVEEKA	176	9	28	44						1174
GAG	EVIPMFSAL	188	9	46	72	0.0001					1175
GAG	EVIPMFTAL	188	9	14	22						1176
GAG	FTALSEGAT	193	9	15	23						1177
GAG	GATPQDLNM	199	9	12	19						1178

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	GATPQDLNT	199	9	42	66						1179
GAG	ATPQDLNMM	200	9	12	19						1180
GAG	ATPQDLNTM	200	9	42	66						1181
GAG	DLNMMLNIV	204	9	12	19						1182
GAG	DLNTMLNTV	204	9	42	66	0.0001					1183
GAG	NIVGGHQAA	210	9	12	19						1184
GAG	NTVGGHQAA	210	9	47	73						1185
GAG	IVGGHQAAM	211	9	12	19						1186
GAG	TVGGHQAAM	211	9	47	73						1187
GAG	AAMQMLKDT	217	9	33	52						1188
GAG	AAMQMLKET	217	9	26	41						1189
GAG	AMQMLKDTI	218	9	33	52						1190
GAG	AMQMLKETI	218	9	26	41						1191
GAG	DIAGTTSTL	256	9	48	75	0.0001					1192
GAG	TTSTLQEQI	260	9	45	71						1193
GAG	TLQEQIAWM	263	9	12	19						1194
GAG	TLQEQIGWM	263	9	27	42						1195
GAG	LQEQIAWMT	264	9	14	22						1196
GAG	LQEQIGWMT	264	9	29	45						1197
GAG	MTNNPPIPV	271	9	20	31	0.0300	0.0006	0.3000	0.0023	3.3000	1198
GAG	MTSNPPIPV	271	9	16	25						1199
GAG	DIYKRWIIL	284	9	17	27						1200
GAG	EIYKRWIIL	284	9	37	58	0.0001					1201
GAG	WIILGLNKI	289	9	57	89	0.0091					1202
GAG	IILGLNKIV	290	9	57	89	0.0003					1203
GAG	KIVRMYSPT	296	9	15	23						1204
GAG	KIVRMYSPV	296	9	41	64						1205
GAG	RMYSPTSIL	299	9	14	22	0.0007					1206
GAG	RMYSPVSIL	299	9	40	63						1207
GAG	YVDRFFKTL	320	9	27	42						1208
GAG	YVDRFYKTL	320	9	28	44	0.0010					1209
GAG	KTLRAEQAT	326	9	34	53						1210
GAG	RAEQASQEV	329	9	12	19						1211
GAG	RAEQATQDV	329	9	15	23						1212
GAG	RAEQATQEV	329	9	27	42						1213
GAG	ATQDVKNWM	333	9	15	23						1214
GAG	ATQEVKNWM	333	9	18	28						1215
GAG	SQEVKNWMT	334	9	11	17						1216
GAG	TQDVKNWMT	334	9	15	23						1217
GAG	TQEVKNWMT	334	9	18	28						1218
GAG	DVKNWMTDT	336	9	12	19						1219
GAG	DVKNWMTET	336	9	12	19						1220
GAG	EVKNWMTET	336	9	25	39						1221
GAG	NANPDCKSI	349	9	11	17						1222
GAG	NANPDCKTI	349	9	45	70						1223
GAG	TILKALGPA	356	9	16	25						1224
GAG	ILKALGPAA	357	9	16	25	0.0001					1225
GAG	ILRALGPGA	357	9	18	28						1226
GAG	KALGPAATL	359	9	16	25	0.0001					1227
GAG	PAATLEEMM	363	9	16	25						1228

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	AATLEEMMT	364	9	16	25						1229
GAG	GASLEEMMT	364	9	10	16						1230
GAG	GATLEEMMT	364	9	28	44						1231
GAG	ATLEEMMTA	365	9	46	72						1232
GAG	EMMTACQGV	369	9	59	92	0.0006					1233
GAG	GVGGPGHKA	376	9	37	58						1234
GAG	GVGGPSHKA	376	9	23	36						1235
GAG	KARVLAEAM	383	9	57	89						1236
GAG	VLAEAMSQA	386	9	16	25						1237
GAG	VLAEAMSQV	386	9	33	52	0.1100					1238
GAG	LAEAMSQVT	387	9	23	37						1239
GAG	AMSQVTNSA	390	9	11	17						1240
GAG	CTERQANFL	459	9	55	87						1241
GAG	RQANFLGKI	465	9	56	88						1242
GAG	FLQNRPEPT	486	9	10	16						1243
GAG	FLQSRPEPT	486	9	28	44	0.0110	0.0004	0.3100	0.0002	0.0130	1244
GAG	LQNRPEPTA	487	9	10	16						1245
GAG	LQSRPEPTA	487	9	28	44						1246
GAG	PAEPTAPPA	492	9	01	50						1247
GAG	KQEPIDKEL	531	9	12	19						1248
GAG	PIDKELYPL	534	9	12	19						1249
GAG	KQEPIDKEL	535	9	01	25						1250
GAG	KQETIDKDL	535	9	01	25						1251
GAG	PIDKELYPL	538	9	01	25						1252
GAG	TIDKDLYPL	538	9	01	25						1253
GAG	RASVLSGGEL	4	10	11	17						1254
GAG	RASVLSGGKL	4	10	28	44						1255
GAG	SVLSGGKLDA	6	10	15	23						1256
GAG	KLDAWEKIRL	12	10	16	25						1257
GAG	KLDKWEKIRL	12	10	10	16						1258
GAG	WASRELERFA	37	10	44	69						1259
GAG	FALNPGLLET	46	10	18	28						1260
GAG	FAVNPGLLET	46	10	14	22						1261
GAG	ETSEGCRQIL	54	10	14	22						1262
GAG	QILGQLQPSL	61	10	11	17						1263
GAG	QLQPALQTGT	65	10	14	22						1264
GAG	QTGSEELRSL	71	10	12	19						1265
GAG	ELRSLYNTVA	76	10	15	23						1266
GAG	ATLYCVHQKI	85	10	12	19						1267
GAG	ATLYCVHQRI	85	10	15	23						1268
GAG	RIEVKDTKEA	93	10	13	20						1269
GAG	GAAAATDSNI	123	10	01	50						1270
GAG	AAGTGNSSQV	130	10	01	50						1271
GAG	SQVSQNYPIV	146	10	22	44						1272
GAG	SQNYPIVQNA	150	10	22	34						1273
GAG	SQNYPIVQNL	150	10	30	47						1274
GAG	PIVQNAQGQM	154	10	21	33						1275
GAG	PIVQNLQGQM	154	10	29	45						1276
GAG	IVQNAQGQMV	155	10	14	22						1277
GAG	IVQNLQGQMV	155	10	29	45						1278

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	NAQGQMVHQA	158	10	12	19						1279
GAG	NLQGQMVHQA	158	10	21	33						1280
GAG	LQGQMVHQAI	159	10	15	23						1281
GAG	MVHQAISPRT	163	10	27	42						1282
GAG	QAISPRTLNA	166	10	29	45						1283
GAG	QALSPRTLNA	166	10	10	16						1284
GAG	RTLNAWVKVI	171	10	30	47						1285
GAG	RTLNAWVKVV	171	10	31	48	0.0003					1286
GAG	KAFSPEVIPM	183	10	50	78						1287
GAG	PMFSALSEGA	191	10	45	70						1288
GAG	PMFTALSEGA	191	10	15	23						1289
GAG	GATPQDLNMM	199	10	12	19						1290
GAG	GATPQDLNTM	199	10	42	66						1291
GAG	ATPQDLNMML	200	10	12	19						1292
GAG	ATPQDLNTML	200	10	42	66						1293
GAG	PQDLNMMLNI	202	10	11	17						1294
GAG	PQDLNTMLNT	202	10	43	67						1295
GAG	MLNIVGGHQA	208	10	12	19						1296
GAG	MLNTVGGHQA	208	10	47	73	0.0022					1297
GAG	NIVGGHQAAM	210	10	12	19						1298
GAG	NTVGGHQAAM	210	10	47	73						1299
GAG	QAAMQMLKDT	216	10	33	52						1300
GAG	QAAMQMLKET	216	10	26	41						1301
GAG	AAMQMLKDTI	217	10	33	52						1302
GAG	AAMQMLKETI	217	10	26	41						1303
GAG	MLKDTINEEA	221	10	32	50						1304
GAG	MLKETINEEA	221	10	22	34						1305
GAG	AAEWDRLHPV	230	10	34	53						1306
GAG	AAEWDRVHPV	230	10	14	22						1307
GAG	RLHPVHAGPI	235	10	22	34						1308
GAG	RVHPVHAGPI	235	10	14	22						1309
GAG	HAGPIAPGQM	240	10	18	28						1310
GAG	HAGPIPPGQM	240	10	17	27						1311
GAG	QMREPRGSDI	248	10	44	69						1312
GAG	GTTSTLQEQI	259	10	45	70						1313
GAG	TTSTLQEQIA	260	10	11	17						1314
GAG	STLQEQIAWM	262	10	12	19						1315
GAG	STLQEQIGWM	262	10	27	42						1316
GAG	TLQEQIAWMT	263	10	12	19						1317
GAG	TLQEQIGWMT	263	10	27	42						1318
GAG	WMTNNPPIPV	270	10	20	31	0.0510	0.0014	0.5900	0.0002	0.0180	1319
GAG	WMTSNPPIPV	270	10	16	25						1320
GAG	GANSIPVGDI	276	10	01	50						1321
GAG	PVGDIYKRWI	281	10	17	27						1322
GAG	PVGEIYKRWI	281	10	40	63						1323
GAG	WIILGLNKIV	289	10	57	89	0.0009					1324
GAG	ILGLNKIVRM	291	10	57	89	0.0010					1325
GAG	IVRMYSPTSI	297	10	14	22						1326
GAG	IVRMYSPVSI	297	10	40	63						1327
GAG	QASQEVKNWM	332	10	11	17						1328

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	QATQDVKNWM	332	10	15	23						1329
GAG	QATQEVKNWM	332	10	18	28						1330
GAG	ATQDVKNWMT	333	10	15	23						1331
GAG	ATQEVKNWMT	333	10	18	28						1332
GAG	DVKNWMTDTL	336	10	12	19						1333
GAG	DVKNWMTETL	336	10	11	17						1334
GAG	EVKNWMTETL	336	10	25	39						1335
GAG	MTDTLLVQNA	341	10	22	34						1336
GAG	MTETLLVQNA	341	10	36	56						1337
GAG	VQNANPDCKT	347	10	45	70						1338
GAG	NANPDCKSIL	349	10	11	17						1339
GAG	NANPDCKTIL	349	10	45	70						1340
GAG	KTILKALGPA	355	10	16	25						1341
GAG	TILKALGPAA	356	10	16	25						1342
GAG	TILRALGPGA	356	10	13	20						1343
GAG	ILKALGPAAT	357	10	16	25						1344
GAG	PAATLEEMMT	363	10	16	25						1345
GAG	AATLEEMMTA	364	10	16	25						1346
GAG	GASLEEMMTA	364	10	10	16						1347
GAG	QATLEEMMTA	364	10	28	44						1348
GAG	RVLAEAMSQA	385	10	16	25						1349
GAG	RVLAEAMSQV	385	10	33	52	0.0058					1350
GAG	VLAEAMSQVT	386	10	20	31						1351
GAG	EAMSQVTNSA	389	10	11	17						1352
GAG	AMSQVTNSAT	390	10	10	16						1353
GAG	QMKDCTERQA	455	10	49	77						1354
GAG	FLQNRPEPTA	486	10	10	16						1355
GAG	FLQSRPEPTA	486	10	28	44	0.0013					1356
GAG	PAESFRFEET	511	10	02	67						1357
GAG	TTPSQKQEPI	522	10	09	45						1358
GAG	ETIDKDLYPL	537	10	01	25						1359
GAG	PIDKELYPLT	538	10	01	25						1360
GAG	RTENSLYPPL	538	10	01	25						1361
GAG	TIDKDLYPLA	538	10	01	25						1362
GAG	WASRELERFAL	37	11	22	34						1363
GAG	WASRELERFAV	37	11	17	27						1364
GAG	ELERFALNPGL	42	11	14	22						1365
GAG	ELERFAVNPGL	42	11	15	23						1366
GAG	LLETSEGCRQI	52	11	16	25						1367
GAG	RQILGQLQPSL	60	11	11	17						1368
GAG	LQTGSEELRSL	70	11	11	17						1369
GAG	ELRSLYNTVAT	76	11	13	20						1370
GAG	VATLYCVHQKI	84	11	12	19						1371
GAG	VATLYCVHQRI	84	11	15	23						1372
GAG	RIEVKDTKEAL	93	11	12	19						1373
GAG	PIVQNAQGQMV	154	11	14	22						1374
GAG	PIVQNLQGQMV	154	11	29	45						1375
GAG	NLQGQMVHQAI	158	11	15	23						1376
GAG	QMVHQAISPRT	162	11	27	42						1377
GAG	MVHQAISPRTL	163	11	27	42						1378

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	HQAISPRTLNA	165	11	29	45						1379
GAG	HQALSPRTLNA	165	11	10	16						1380
GAG	AISPRTLNAWV	167	11	29	45						1381
GAG	ALSPRTLNAWV	167	11	10	16						1382
GAG	NAWVKVIEEKA	174	11	25	39						1383
GAG	NAWVKVVEEKA	174	11	27	42						1384
GAG	VIEEKAFSPEV	179	11	20	31						1385
GAG	VVEEKAFSPEV	179	11	28	44						1386
GAG	PMFSALSEGAT	191	11	44	69						1387
GAG	PMFTALSEGAT	191	11	15	23						1388
GAG	ALSEGATPQDL	195	11	58	91						1389
GAG	GATPQDLNMML	199	11	12	19						1390
GAG	GATPQDLNTML	199	11	42	66						1391
GAG	PQDLNMMLNIV	202	11	11	17						1392
GAG	PQDLNTMLNTV	202	11	41	64						1393
GAG	MMLNIVGGHQA	207	11	12	19						1394
GAG	TMLNTVGGHQA	207	11	43	67						1395
GAG	MLNIVGGHQAA	208	11	12	19						1396
GAG	MLNTVGGHQAA	208	11	47	73						1397
GAG	IVGGHQAAMQM	211	11	11	17						1398
GAG	TVGGHQAAMQM	211	11	47	73						1399
GAG	HQAAMQMLKDT	215	11	33	52						1400
GAG	HQAAMQMLKET	215	11	26	41						1401
GAG	QAAMQMLKDTI	216	11	33	52						1402
GAG	QAAMQMLKETI	216	11	26	41						1403
GAG	QMLKDTINEEA	220	11	32	50						1404
GAG	QMLKETINEEA	220	11	22	34						1405
GAG	MLKDTINEEAA	221	11	32	50						1406
GAG	MLKETINEEAA	221	11	22	34						1407
GAG	EAAEWDRLHPV	229	11	34	53						1408
GAG	EAAEWDRVHPV	229	11	14	22						1409
GAG	RLHPVHAGPIA	235	11	15	23						1410
GAG	GQMREPRGSDI	247	11	44	69						1411
GAG	QMREPRGSDIA	248	11	44	69						1412
GAG	GTTSTLQEQIA	259	11	11	17						1413
GAG	STLQEQIAWMT	262	11	12	19						1414
GAG	STLQEQIGWMT	262	11	27	42						1415
GAG	QIGWMTNNPPI	267	11	18	29						1416
GAG	QIGWMTSNPPI	267	11	10	16						1417
GAG	PVGDIYKRWII	281	11	17	27						1418
GAG	PVGEIYKRWII	281	11	39	61						1419
GAG	DIYKRWIILGL	284	11	17	27						1420
GAG	EIYKRWIILGL	284	11	37	58						1421
GAG	IILGLNKIVRM	290	11	56	88						1422
GAG	KIVRMYSPTSI	296	11	14	22						1423
GAG	KIVRMYSPVSI	296	11	39	61						1424
GAG	IVRMYSPTSIL	297	11	14	22						1425
GAG	IVRMYSPVSIL	297	11	40	63						1426
GAG	RMYSPTSILDI	299	11	13	20						1427
GAG	RMYSPVSILDI	299	11	38	59						1428

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	YVDRFFKTLRA	320	11	27	42						1429
GAG	YVDRFYKTLRA	320	11	28	44						1430
GAG	TLRAEQASQEV	327	11	12	19						1431
GAG	TLRAEQATQDV	327	11	11	17						1432
GAG	TLRAEQATQEV	327	11	24	38						1433
GAG	EQASQEVKNWM	331	11	11	17						1434
GAG	EQATQDVKNWM	331	11	15	23						1435
GAG	EQATQEVKNWM	331	11	18	28						1436
GAG	QASQEVKNWMT	332	11	11	17						1437
GAG	QATQDVKNWMT	332	11	15	23						1438
GAG	QATQEVKNWMT	332	11	18	28						1439
GAG	SQEVKNWMTET	334	11	11	17						1440
GAG	TQDVKNWMTDT	334	11	11	17						1441
GAG	TQEVKNWMTET	334	11	14	22						1442
GAG	DVKNWMTDTLL	336	11	12	19						1443
GAG	DVKNWMTETLL	336	11	11	17						1444
GAG	EVKNWMTETLL	336	11	25	39						1445
GAG	WMTDTLLVQNA	340	11	22	34						1446
GAG	WMTETLLVQNA	340	11	35	55						1447
GAG	LVQNANPDCKT	346	11	45	70						1448
GAG	VQNANPDCKSI	347	11	10	16						1449
GAG	VQNANPDCKTI	347	11	45	70						1450
GAG	KTILKALGPAA	355	11	16	25						1451
GAG	KTILRALGPGA	355	11	13	20						1452
GAG	TILKALGPAAT	356	11	16	25						1453
GAG	ILKALGPAATL	357	11	16	25						1454
GAG	ALGPAATLEEM	360	11	16	25						1455
GAG	ALGPGATLEEM	360	11	17	27						1456
GAG	PAATLEEMMTA	363	11	16	25						1457
GAG	CQGVGGPGHKA	374	11	36	56						1458
GAG	CQGVGGPSHKA	374	11	23	36						1459
GAG	GVGGPGHKARV	376	11	36	56						1460
GAG	GVGGPSHKARV	376	11	19	30						1461
GAG	RVLAEAMSQVT	385	11	20	31						1462
GAG	EAMSQVTNSAT	389	11	10	16						1463
GAG	SAQQDLKGGYT	393	11	01	50						1464
GAG	TAQQDLKGGYT	393	11	01	50						1465
GAG	HQMKDCTERQA	454	11	49	77						1466
GAG	PAEPTAPPAEI	492	11	01	50						1467
GAG	PAESFRFEETT	511	11	02	67						1468
GAG	SQKQEPIDKEL	529	11	09	15						1469
GAG	ETIDKDLYPLA	537	11	01	25						1470
GAG	RTENSLYPPLT	538	11	01	25						1471
GAG	SLKSLFGNDPL	551	11	12	19						1472
NEF	RAQAEPAA	32	8	01	17						1473
NEF	AQAEPAAA	33	8	01	17						1474
NEF	PAADGVGA	41	8	15	23						1475
NEF	PAAEGVGA	41	8	21	33						1476
NEF	AADGVGAV	42	8	11	18						1477
NEF	AAEGVGAA	42	8	10	16						1478

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
NEF	AAEGVGAV	42	8	17	28						1479
NEF	DLEKHGAI	57	8	14	22						1480
NEF	GAITSSNT	62	8	32	50						1481
NEF	GALTSSNT	62	8	10	16						1482
NEF	AITSSNTA	63	8	27	42						1483
NEF	ITSSNTAA	64	8	15	23						1484
NEF	AATNADCA	70	8	12	22						1485
NEF	EAQEEEEV	82	8	16	25						1486
NEF	PVRPQVPL	95	8	48	75						1487
NEF	PQVPLRPM	99	8	56	88						1488
NEF	QVPLRPMT	100	8	57	89	0.0001					1489
NEF	ALDLSHFL	111	8	11	17						1490
NEF	AVDLSHFL	111	8	15	23						1491
NEF	FLKEKGGL	117	8	56	88						1492
NEF	SQKRQDIL	177	8	12	19						1493
NEF	QTEPAAVGV	32	9	01	17						1494
NEF	RAEPAADGV	32	9	01	17						1495
NEF	RAQAEPAAA	32	9	01	17						1496
NEF	RTEPAAVGV	32	9	01	17						1497
NEF	QAEPAAEGV	33	9	01	17						1498
NEF	QAPTAAKGV	33	9	01	17						1499
NEF	QAEPAAAGV	34	9	01	33						1500
NEF	PAADGVGAV	41	9	11	17						1501
NEF	PAAEGVGAV	41	9	12	19						1502
NEF	GVGAASQDL	45	9	11	17						1503
NEF	GVGAVSQDL	45	9	21	33						1504
NEF	GVGAVSRDL	45	9	17	27	0.0001					1505
NEF	DLEKHGAIT	57	9	14	22						1506
NEF	GAITSSNTA	62	9	27	42						1507
NEF	AITSSNTAA	63	9	14	22						1508
NEF	ITSSNTAAT	64	9	13	20						1509
NEF	TAATNADCA	69	9	12	19						1510
NEF	ATNADCAWL	71	9	12	22						1511
NEF	NADCAWLEA	73	9	17	27						1512
NEF	PQVPLRPMT	99	9	56	88						1513
NEF	PLRPMTYKA	102	9	21	33						1514
NEF	MTYKGAFDL	106	9	12	19						1515
NEF	GAFDLSFFL	110	9	10	16						1516
NEF	RQDILDLWV	182	9	20	31						1517
NEF	RQEILDLWV	182	9	35	55						1518
NEF	ILDLWVYHT	186	9	34	53						1519
NEF	ILDLWVYNT	186	9	19	30						1520
NEF	LTFGWCFKL	221	9	39	61	0.1400	0.1300	0.0022	0.0180	7.2000	1521
NEF	LVPVDPREV	229	9	11	17						1522
NEF	KQAEPAAEGV	32	10	01	17						1523
NEF	RQAPTAAKGV	32	10	01	17						1524
NEF	AQAEPAAAGV	33	10	01	17						1525
NEF	GAITSSNTAA	62	10	14	22						1526
NEF	AITSSNTAAT	63	10	13	20						1527
NEF	NTAATNADCA	68	10	12	19						1528

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
NEF	AATNADCAWL	70	10	12	22						1529
NEF	WLEAQEEEEV	79	10	15	24						1530
NEF	EVGFPVRPQV	91	10	40	63						1531
NEF	PLRPMTYKAA	102	10	20	31						1532
NEF	PLRPMTYKGA	102	10	25	39						1533
NEF	PMTYKGAFDL	105	10	12	19						1534
NEF	LIYSKKRQEI	174	10	18	28						1535
NEF	SQKRQDILDL	177	10	12	19						1536
NEF	DILDLWVYHT	185	10	12	19						1537
NEF	EILDLWVYHT	185	10	22	34						1538
NEF	EILDLWVYNT	185	10	11	17						1539
NEF	WQNYTPGPGI	204	10	18	29						1540
NEF	WQNYTPGPGT	204	10	21	33						1541
NEF	WQNYTPGPGV	204	10	11	17						1542
NEF	PLTFGWCFKL	219	10	39	61	0.0350	0.0058	0.0021	0.0010	0.8400	1543
NEF	LTFGWCFKLV	221	10	35	55	0.0170	0.0880	0.0540	0.0640	6.5000	1544
NEF	KLVPVDPREV	228	10	11	17						1545
NEF	LLHPICQHGM	257	10	10	16						1546
NEF	LLHPMSQHGM	257	10	12	19						1547
NEF	QTEPAAVGVGA	32	11	01	17						1548
NEF	RAEPAADGVGA	32	11	01	17						1549
NEF	RAQAEPAAAGV	32	11	01	17						1550
NEF	RTEPAAVGVGA	32	11	01	17						1551
NEF	QAEPAAEGVGA	33	11	01	17						1552
NEF	QAPTAAKGVGA	33	11	01	17						1553
NEF	QAEPAAAGVGA	34	11	01	33						1554
NEF	AVSRDLEKHGA	48	11	11	17						1555
NEF	GAITSSNTAAT	62	11	13	20						1556
NEF	ITSSNTAATNA	64	11	12	19						1557
NEF	TAATNADCAWL	69	11	12	19						1558
NEF	ATNADCAWLEA	71	11	12	22						1559
NEF	AQEEEEVGFPV	83	11	17	27						1560
NEF	PVRPQVPLRPM	95	11	47	73						1561
NEF	QVPLRPMTYKA	100	11	20	31						1562
NEF	FLKEKGGLDGL	117	11	26	41						1563
NEF	FLKEKGGLEGL	117	11	29	45						1564
NEF	GLIYSKKRQEI	173	11	18	28						1565
NEF	LIYSKKRQEIL	174	11	18	28						1566
NEF	YTPGPGIRYPL	207	11	16	25						1567
NEF	YTPGPGTRFPL	207	11	13	20						1568
NEF	PLTFGWCFKLV	219	11	35	55						1569
NEF	CLLHPMSQHGM	256	11	10	16						1570
POL	LAFPQGEA	6	8	12	19						1571
POL	LAFPQGKA	6	8	12	19						1572
POL	LAFQQGEA	6	8	16	25						1573
POL	QTRANSPT	21	8	28	45						1574
POL	PTRRELQV	30	8	14	22						1575
POL	QTRANSPT	35	8	01	33						1576
POL	PTSRELQV	36	8	01	33						1577
POL	GADRQGIV	70	8	01	20						1578

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	GTLNCPQI	80	8	01	33						1579
POL	PTFNFPQI	80	8	01	33						1580
POL	ITLWQRPL	90	8	47	73						1581
POL	TLWQRPLV	91	8	49	77						1582
POL	WQRPLVTI	93	8	21	33						1583
POL	WQRPLVTV	93	8	19	30						1584
POL	TIKIGGQL	99	8	17	27						1585
POL	TVKIGGQL	99	8	11	17						1586
POL	GQLIEALL	104	8	10	16						1587
POL	GQLKEALL	104	8	34	53						1588
POL	LIEALLDT	106	8	10	16						1589
POL	EALLDTGA	108	8	61	95						1590
POL	DTGADDTV	112	8	63	98						1591
POL	TVLEDINL	118	8	13	20						1592
POL	TVLEEINL	118	8	15	23						1593
POL	GIGGFIKV	136	8	64	100						1594
POL	KVRQYDQI	142	8	41	64						1595
POL	RQYDQILI	144	8	20	31						1596
POL	RQYDQIPI	144	8	13	20						1597
POL	EICGHKAI	152	8	19	30						1598
POL	EICGKKAI	152	8	24	38						1599
POL	KAIGTVLV	157	8	48	75						1600
POL	GTVLVGPT	160	8	60	94						1601
POL	VLVGPTPV	162	8	53	83						1602
POL	NIIGRNLL	170	8	26	41						1603
POL	NIIGRNML	170	8	31	48						1604
POL	IIGRNLLT	171	8	26	41						1605
POL	IIGRNMLT	171	8	30	47						1606
POL	LLTQIGCT	176	8	21	33						1607
POL	MLTQIGCT	176	8	18	28						1608
POL	MLTQLGCT	176	8	10	16						1609
POL	LTQIGCTL	177	8	42	66						1610
POL	LTQLGCTL	177	8	15	23						1611
POL	PISPIETV	187	8	57	89						1612
POL	PVKLKPGM	195	8	56	88						1613
POL	KVKQWPLT	207	8	49	77						1614
POL	LTEEKIKA	213	8	56	88						1615
POL	KIKALTEI	217	8	28	44						1616
POL	KIKALVEI	217	8	15	23						1617
POL	KALTEICT	219	8	12	19						1618
POL	KALVEICT	219	8	15	24						1619
POL	LVEICTEM	221	8	15	24						1620
POL	EMEKEGKI	229	8	42	66						1621
POL	AIKKKDST	251	8	59	92						1622
POL	STKWRKLV	257	8	59	92						1623
POL	KLVDFREL	262	8	63	98						1624
POL	RTQDFWEV	272	8	55	86						1625
POL	QLGIPHPA	280	8	56	89						1626
POL	GIPHPAGL	282	8	56	89						1627
POL	GLKKKKSV	288	8	52	81						1628

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	TVLDVGDA	296	8	58	91						1629
POL	DAYFSVPL	302	8	55	86						1630
POL	TAFTIPSI	317	8	37	58						1631
POL	TAFTIPST	317	8	13	20						1632
POL	GIRYQYNV	330	8	52	81						1633
POL	PAIFQSSM	346	8	42	66						1634
POL	AIFQSSMT	347	8	39	61						1635
POL	FQSSMTKI	349	8	38	59						1636
POL	KQNPDIVI	362	8	14	22						1637
POL	DIVIYQYM	366	8	18	28						1638
POL	EIVIYQYM	366	8	24	38						1639
POL	DLYVGSDL	375	8	63	98						1640
POL	YVGSDLEI	377	8	58	91						1641
POL	HLLKWGFT	397	8	22	34						1642
POL	HLLRWGFT	397	8	25	39						1643
POL	LLKWGFTT	398	8	23	36						1644
POL	LLRWGFTT	398	8	24	38						1645
POL	HQKEPPFL	410	8	62	97						1646
POL	FLWMGYEL	416	8	64	100						1647
POL	ELHPDKWT	422	8	60	94						1648
POL	WTVQPIQL	428	8	28	44						1649
POL	WTVQPIVL	428	8	13	20						1650
POL	TVNDIQKL	442	8	62	97						1651
POL	IQKLVGKL	446	8	62	97						1652
POL	LVGKLNWA	449	8	61	95						1653
POL	KLNWASQI	452	8	61	95						1654
POL	QIYAGIKV	458	8	27	43						1655
POL	QIYPGIKV	458	8	27	43						1656
POL	KVKQLCKL	464	8	29	45						1657
POL	KVRQLCKL	464	8	19	30						1658
POL	KLLRGAKA	470	8	25	40						1659
POL	KLLRGTKA	470	8	24	38						1660
POL	LLRGAKAL	471	8	30	47						1661
POL	LLRGTKAL	471	8	24	38						1662
POL	GAKALTDI	474	8	25	39						1663
POL	GTKALTEV	474	8	19	30						1664
POL	ALTDIVPL	477	8	21	33						1665
POL	ALTEVIPL	477	8	16	25						1666
POL	LTDIVPLT	478	8	23	36						1667
POL	LTEVIPLT	478	8	16	25						1668
POL	IVPLTEEA	481	8	13	20						1669
POL	VIPLTEEA	481	8	11	17						1670
POL	PLTEEAEL	483	8	30	47						1671
POL	ELAENREI	491	8	57	89						1672
POL	LAENREIL	492	8	57	89						1673
POL	KQGQDQWT	523	8	15	23						1674
POL	KQGQGQWT	523	8	25	39						1675
POL	YQEPFKNL	534	8	43	67						1676
POL	NLKTGKYA	540	8	58	92						1677
POL	KTGKYAKM	542	8	19	30						1678

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	KTGKYARM	542	8	13	21						1679
POL	RTAHTNDV	550	8	11	17						1680
POL	HTNDVKQL	553	8	49	77						1681
POL	DVKQLTEA	556	8	33	52						1682
POL	LTEAVQKI	560	8	34	53						1683
POL	EAVQKIAT	562	8	11	17						1684
POL	KIATESIV	566	8	14	22						1685
POL	IATESIVI	567	8	14	22						1686
POL	SIVIWGKT	571	8	42	66						1687
POL	KLPIQKET	582	8	20	31						1688
POL	RLPIQKET	582	8	26	41						1689
POL	IQKETWEA	585	8	15	23						1690
POL	IQKETWET	585	8	27	42						1691
POL	ETWEAWWT	588	8	11	17						1692
POL	ETWETWWT	588	8	22	34						1693
POL	WTDYWQAT	594	8	15	23						1694
POL	WTEYWQAT	594	8	24	38						1695
POL	WIPEWEFV	602	8	52	84						1696
POL	FVNTPPLV	608	8	54	86						1697
POL	NTPPLVKL	610	8	57	89						1698
POL	LVKLWYQL	614	8	58	91						1699
POL	KLWYQLET	616	8	12	19						1700
POL	YQLEKDPI	619	8	14	22						1701
POL	YQLEKEPI	619	8	31	48						1702
POL	YQLETEPI	619	8	11	17						1703
POL	QLEKEPIV	620	8	16	25						1704
POL	ETFYVDGA	630	8	55	86						1705
POL	AANRETKL	637	8	30	47						1706
POL	KLGKAGYV	643	8	36	56						1707
POL	RQKVVSLT	655	8	19	30						1708
POL	KVVSLTET	657	8	11	17						1709
POL	VVSLTDTT	658	8	10	16						1710
POL	VVSLTETT	658	8	11	17						1711
POL	TTNQKTEL	664	8	55	86						1712
POL	NQKTELHA	666	8	12	19						1713
POL	NQKTELQA	666	8	42	66						1714
POL	ELQAIHLA	670	8	16	25						1715
POL	ELQAIYLA	670	8	12	19						1716
POL	LQAIHLAL	671	8	16	25						1717
POL	LQAIYLAL	671	8	12	19						1718
POL	LALQDSGL	676	8	27	42						1719
POL	LQDSGLEV	678	8	27	42						1720
POL	LQDSGSEV	678	8	25	39						1721
POL	GLEVNIVT	682	8	26	41						1722
POL	IVTDSQYA	687	8	61	95						1723
POL	VTDSQYAL	688	8	59	92						1724
POL	SQYALGII	691	8	59	92						1725
POL	YALGIIQA	693	8	58	91						1726
POL	NQIIEQLI	711	8	24	38						1727
POL	SQIIEQLI	711	8	20	31						1728

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	QLIKKEKV	716	8	28	44						1729
POL	WVPAHKGI	727	8	63	98						1730
POL	GIGGNEQV	733	8	59	92						1731
POL	QVDKLVSA	739	8	16	25						1732
POL	SAGIRKVL	745	8	15	23						1733
POL	GIRKVLFL	747	8	51	80						1734
POL	KVLFLDGI	750	8	50	78						1735
POL	FLDGIDKA	753	8	55	86						1736
POL	AMASDFNL	773	8	45	70						1737
POL	PIVAKEIV	782	8	26	41						1738
POL	PVVAKEIV	782	8	28	44						1739
POL	IVAKEIVA	783	8	26	41						1740
POL	VVAKEIVA	783	8	31	48						1741
POL	CQLKGEAM	795	8	53	83						1742
POL	QVDCSPGI	805	8	57	89						1743
POL	GIWQLDCT	811	8	59	92						1744
POL	WQLDCTHL	813	8	61	95						1745
POL	CTHLEGKI	817	8	35	55						1746
POL	CTHLEGKV	817	8	26	41						1747
POL	HLEGKIIL	819	8	31	48						1748
POL	HLEGKVIL	819	8	23	36						1749
POL	HLVAVHV	824	8	30	47						1750
POL	VILVAVHV	824	8	24	38						1751
POL	ILVAVHVA	825	8	54	84						1752
POL	VASGYIEA	831	8	52	81						1753
POL	PAETGQET	842	8	58	91						1754
POL	GQETAYFI	846	8	31	48						1755
POL	GQETAYFL	846	8	26	41						1756
POL	TAYFILKL	849	8	32	50						1757
POL	TAYFLLKL	849	8	27	42						1758
POL	KLAGRWPV	855	8	59	92						1759
POL	FTSAAVKA	873	8	28	44						1760
POL	FTSTTVKA	873	8	14	22						1761
POL	AACWWAGI	880	8	32	50						1762
POL	GIKQEFGI	886	8	22	34						1763
POL	GIQQEFGI	886	8	11	17						1764
POL	SQGVVESM	899	8	53	83						1765
POL	DQAEHLKT	919	8	46	72						1766
POL	EQAEHLKT	919	8	13	20						1767
POL	QAEHLKTA	920	8	59	92						1768
POL	HLKTAVQM	923	8	57	89						1769
POL	KTAVQMAV	925	8	57	89						1770
POL	AVQMAVFI	927	8	60	94						1771
POL	RIIDIIAT	951	8	29	45						1772
POL	RIVDIIAT	951	8	12	19						1773
POL	IIASDIQT	955	8	15	23						1774
POL	IIATDIQT	955	8	41	64						1775
POL	LQKQIIKI	965	8	13	20						1776
POL	LQKQITKI	965	8	36	56						1777
POL	LLWKGEGA	993	8	62	97						1778

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	VIQDNSDI	1003	8	37	58						1779
POL	VIQDNSEI	1003	8	12	19						1780
POL	KVVPRRKA	1011	8	52	81						1781
POL	KVVPRRKV	1011	8	11	17						1782
POL	QMAGDDCV	1027	8	44	69						1783
POL	MAGDDCVA	1028	8	44	69						1784
POL	NLAFPQGEA	5	9	10	16						1785
POL	NLAFQQGEA	5	9	16	25						1786
POL	EQTRANSPT	20	9	26	41						1787
POL	SQTRANSPT	34	9	01	33						1788
POL	QTRANSPTT	35	9	01	33						1789
POL	EAGADRQGT	64	9	10	16						1790
POL	GQRQGTVSL	69	9	01	17						1791
POL	GTTLNFPQI	79	9	01	17						1792
POL	AISLSLPQI	80	9	01	33						1793
POL	GTLNCPQIT	80	9	01	33						1794
POL	PTFNFPQIT	80	9	01	33						1795
POL	QITLWQRPL	89	9	47	73						1796
POL	ITLWQRPLV	90	9	47	73						1797
POL	TLWQRPLVT	91	9	39	61	0.0185	0.0002	0.0040	0.0002	0.0140	1798
POL	VTIKIGGQL	98	9	17	27						1799
POL	VTVKIGGQL	98	9	11	17						1800
POL	KIGGQLKEA	101	9	23	36						1801
POL	QLIEALLDT	105	9	10	16						1802
POL	QLKEALLDT	105	9	34	53						1803
POL	LLDTGADDT	110	9	63	98						1804
POL	DTGADDTVL	112	9	61	95						1805
POL	DTVLEDINL	117	9	13	20						1806
POL	DTVLEEINL	117	9	14	22						1807
POL	MIGGIGGFI	133	9	62	97	0.0025					1808
POL	KVRQYDQIL	142	9	21	33	0.0001					1809
POL	LIEICGHKA	150	9	10	16						1810
POL	LIEICGKKA	150	9	13	20						1811
POL	TVLVGPTPV	161	9	53	83	0.0047					1812
POL	LVGPTPVNI	163	9	54	84	0.0110	0.0280	0.5200	0.0013	0.5900	1813
POL	PVNIIGRNL	168	9	26	41	0.0001					1814
POL	PVNIIGRNM	168	9	24	38						1815
POL	NIIGRNLLT	170	9	26	41						1816
POL	NIIGRNMLT	170	9	30	47						1817
POL	NLLTQIGCT	175	9	21	33						1818
POL	NMLTQIGCT	175	9	18	28						1819
POL	NMLTQLGCT	175	9	10	16						1820
POL	LLTQIGCTL	176	9	21	33	0.0002					1821
POL	MLTQIGCTL	176	9	18	28						1822
POL	MLTQLGCTL	176	9	10	16						1823
POL	TLNFPISPI	183	9	61	97	0.0660	0.0029	9.3000	0.0019	0.7000	1824
POL	PIETVPVKL	190	9	53	83	0.0001					1825
POL	PLTEEKIKA	212	9	54	84						1826
POL	LTEEKIKAL	213	9	56	88						1827
POL	ALVEICTEM	220	9	15	23	0.0230	0.0230	0.0710	0.0140	0.0140	1828

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	FAIKKKDST	250	9	59	92						1829
POL	TQDFWEVQL	273	9	55	86						1830
POL	VQLGIPHPA	279	9	54	84						1831
POL	GLKKKKSVT	288	9	49	77						1832
POL	VTVLDVGDA	295	9	57	89						1833
POL	DVGDAYFSV	299	9	54	84	0.0005					1834
POL	YTAFTIPSI	316	9	37	58	0.1900	0.7100	1.1000	0.5300	2.4000	1835
POL	YTAFTIPST	316	9	13	20						1836
POL	TIPSINNET	320	9	37	58						1837
POL	TIPSTNNET	320	9	14	22						1838
POL	SINNETPGI	323	9	32	50						1839
POL	STNNETPGI	323	9	11	17						1840
POL	GIRYQYNVL	330	9	52	81	0.0001					1841
POL	PQGWKGSPA	339	9	59	92						1842
POL	PAIFQSSMT	346	9	39	61						1843
POL	FQSSMTKIL	349	9	38	59						1844
POL	VIYQYMDDL	368	9	51	80	0.0004					1845
POL	YQYMDDLYV	370	9	61	95						1846
POL	DLEIGQHRA	381	9	28	44						1847
POL	DLEIGQHRT	381	9	21	33						1848
POL	EIGQHRAKI	383	9	26	41						1849
POL	EIGQHRTKI	383	9	21	33						1850
POL	KIEELREHL	390	9	19	30						1851
POL	KIEELRQHL	390	9	17	27	0.0001					1852
POL	HLLKWGFTT	397	9	22	34						1853
POL	HLLRWGFTT	397	9	24	38						1854
POL	ELHPDKWTV	422	9	60	94	0.0001					1855
POL	QLPEKDSWT	434	9	13	20						1856
POL	VLPEKDSWT	434	9	13	20						1857
POL	WTVNDIQKL	441	9	62	97	0.0001					1858
POL	TVNDIQKLV	442	9	61	95	0.0001					1859
POL	DIQKLVGKL	445	9	62	97	0.0001					1860
POL	KLVGKLNWA	448	9	61	95	0.0840	0.3400	1.7000	0.0930	0.0130	1861
POL	WASQIYAGI	455	9	27	42	0.0020					1862
POL	WASQIYPGI	455	9	29	45						1863
POL	SQIYAGIKV	457	9	27	42						1864
POL	SQIYPGIKV	457	9	27	42						1865
POL	YAGIKVKQL	460	9	18	28						1866
POL	KVKQLCKLL	464	9	28	44						1867
POL	KVRQLCKLL	464	9	19	30						1868
POL	QLCKLLRGA	467	9	25	39						1869
POL	QLCKLLRGT	467	9	21	33						1870
POL	KLLRGAKAL	470	9	25	40						1871
POL	KLLRGTKAL	470	9	24	38	0.0069					1872
POL	LLRGAKALT	471	9	30	47						1873
POL	LLRGTKALT	471	9	24	38						1874
POL	GAKALTDIV	474	9	24	38						1875
POL	GTKALTEVI	474	9	11	17						1876
POL	KALTDIVPL	476	9	21	33						1877
POL	KALTEVIPL	476	9	16	25						1878

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	ALTDIVPLT	477	9	21	33						1879
POL	ALTEVIPLT	477	9	16	25						1880
POL	DIVPLTEEA	480	9	13	20						1881
POL	EVIPLTEEA	480	9	11	17						1882
POL	LTEEAELEL	484	9	37	58						1883
POL	ELAENREIL	491	9	57	89	0.0001					1884
POL	ILKEPVHGV	498	9	41	64	0.0055					1885
POL	GQDQWTYQI	525	9	13	20						1886
POL	GQGQWTYQI	525	9	25	39						1887
POL	YAKMRTAHT	546	9	10	16						1888
POL	YARMRGAHT	546	9	13	20						1889
POL	HTNDVKQLT	553	9	43	67						1890
POL	DVKQLTEAV	556	9	33	52	0.0001					1891
POL	QLTEAVQKI	559	9	34	53	0.0007					1892
POL	LTEAVQKIA	560	9	26	41						1893
POL	VQKIATESI	564	9	14	22						1894
POL	KIATESIVI	566	9	14	22						1895
POL	KTPKFKLPI	577	9	17	27						1896
POL	KTPKFRLPI	577	9	29	45						1897
POL	PIQKETWEA	584	9	15	23						1898
POL	PIQKETWET	584	9	27	42						1899
POL	PLVKLWYQL	613	9	54	84	0.0002					1900
POL	YQLEKEPIV	619	9	16	25						1901
POL	IVGAETFYV	626	9	28	44	0.0099					1902
POL	ETFYVDGAA	630	9	51	80						1903
POL	GAANRETKL	636	9	30	47						1904
POL	KLGKAGYVT	643	9	36	56	0.0002					1905
POL	VTDRGRQKV	650	9	30	47						1906
POL	KVVSLTETT	657	9	11	17						1907
POL	LTDTTNQKT	661	9	19	30						1908
POL	LTETTNQKT	661	9	25	39						1909
POL	DTTNQKTEL	663	9	26	41						1910
POL	ETTNQKTEL	663	9	29	45						1911
POL	NQKTELHAI	666	9	12	19						1912
POL	NQKTELQAI	666	9	42	66						1913
POL	KTELQAHIL	668	9	15	23						1914
POL	KTELQAIYL	668	9	12	19						1915
POL	ELQAHILAL	670	9	16	25	0.0001					1916
POL	ELQAIYLAL	670	9	12	19						1917
POL	HLALQDSGL	675	9	15	23	0.0005					1918
POL	ALQDSGLEV	677	9	27	42	0.0083					1919
POL	ALQDSGSEV	677	9	25	39						1920
POL	NIVTDSQYA	686	9	61	95						1921
POL	IVTDSQYAL	687	9	59	92	0.0024					1922
POL	LVNQHEQL	709	9	19	30						1923
POL	LVSQHEQL	709	9	19	30						1924
POL	EQLIKKEKV	715	9	28	44						1925
POL	LIKKEKVYL	717	9	35	55	0.0001					1926
POL	KVYLAWVPA	722	9	20	32						1927
POL	KVYLSWVPA	722	9	23	37						1928

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	EQVDKLVSA	738	9	16	25						1929
POL	LVSAGIRKV	743	9	15	23	0.0001					1930
POL	LVSSGIRKV	743	9	26	41						1931
POL	RAMASDFNL	772	9	41	64	0.0230	0.0370	0.0004	0.0710	0.0130	1932
POL	PIVAKEIVA	782	9	25	39						1933
POL	PVVAKEIVA	782	9	28	44						1934
POL	VASCDKCQL	789	9	43	67						1935
POL	GQVDCSPGI	804	9	57	89						1936
POL	CTHLEGKII	817	9	35	55						1937
POL	CTHLEGKVI	817	9	26	41						1938
POL	HLEGKIILV	819	9	31	48	0.0010					1939
POL	HLEGKVILV	819	9	23	36	0.0006					1940
POL	KIILVAVHV	823	9	30	47	0.0002					1941
POL	KVILVAVHV	823	9	23	36	0.0001					1942
POL	IILVAVHVA	824	9	30	47						1943
POL	VILVAVHVA	824	9	23	36						1944
POL	AVHVASGYI	828	9	53	83						1945
POL	HVASGYIEA	830	9	52	81						1946
POL	YIEAEVIPA	835	9	53	83						1947
POL	EAEVIPAET	837	9	62	98						1948
POL	PAETGQETA	842	9	58	91						1949
POL	GQETAYFIL	846	9	31	48						1950
POL	GQETAYFLL	846	9	26	41						1951
POL	ETAYFILKL	848	9	31	48						1952
POL	ETAYFLLKL	848	9	27	42						1953
POL	TAYFILKLA	849	9	32	50						1954
POL	TAYFLLKLA	849	9	27	42						1955
POL	LAGRWPVKT	856	9	14	22						1956
POL	LAGRWPVKV	856	9	30	47						1957
POL	HTDNGSNFT	866	9	49	77						1958
POL	FTSAAVKAA	873	9	27	42						1959
POL	FTSTTVKAA	873	9	14	22						1960
POL	AVKAACWWA	877	9	32	50						1961
POL	TVKAACWWA	877	9	23	36						1962
POL	KAACWWAGI	879	9	31	49	0.0180	0.0040	0.1200	0.0230	0.0150	1963
POL	VVESMNKEL	902	9	48	75						1964
POL	SMNKELKKI	905	9	53	83						1965
POL	ELKKIIGQV	909	9	57	89	0.0001					1966
POL	IIGQVRDQA	913	9	44	69						1967
POL	IIGQVREQA	913	9	13	20						1968
POL	QVRDQAEHL	916	9	48	75	0.0001					1969
POL	QVREQAEHL	916	9	13	20						1970
POL	DQAEHLKTA	919	9	46	72						1971
POL	EQAEHLKTA	919	9	13	20						1972
POL	QAEHLKTAV	920	9	59	92						1973
POL	HLKTAVQMA	923	9	57	89	0.0033					1974
POL	TAVQMAVFI	926	9	59	92						1975
POL	SAGERIIDI	947	9	41	64						1976
POL	SAGERIVDI	947	9	14	22						1977
POL	IIDIIASDI	952	9	12	19						1978

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	IIDIIATDI	952	9	29	45						1979
POL	IVDIIATDI	952	9	12	19						1980
POL	DIIASDIQT	954	9	15	23						1981
POL	DIIATDIQT	954	9	40	63						1982
POL	ATDIQTKEL	957	9	35	55						1983
POL	QTKELQKQI	961	9	46	72						1984
POL	ELQKQIIKI	964	9	13	21						1985
POL	ELQKQITKI	964	9	34	54						1986
POL	IIKIQNFRV	969	9	12	19						1987
POL	ITKIQNFRV	969	9	36	57						1988
POL	PIWKGPAKL	985	9	36	56						1989
POL	PLWKGPAKL	985	9	19	30						1990
POL	KLLWKGEGA	992	9	60	94	0.0002					1991
POL	LLWKGEGAV	993	9	62	97	0.0230					1992
POL	VVIQDNSDI	1002	9	37	58	0.0001					1993
POL	VVIQDNSEI	1002	9	12	19						1994
POL	IQDNSDIKV	1004	9	38	59						1995
POL	IQDNSEIKV	1004	9	12	19						1996
POL	VVPRRKAKI	1012	9	51	80						1997
POL	VVPRRKVKI	1012	9	11	17						1998
POL	IIKDYGKQM	1020	9	11	17						1999
POL	IIRDYGKQM	1020	9	50	78						2000
POL	KQMAGDDCV	1026	9	44	69						2001
POL	QMAGDDCVA	1027	9	44	69	0.0001					2002
POL	KAREFSSEQT	12	10	10	16						2003
POL	RANSPTRREL	26	10	16	25						2004
POL	RANSPTSREL	26	10	10	16						2005
POL	STNSPTSREL	32	10	01	33						2006
POL	SQTRANSPTT	34	10	01	33						2007
POL	RANSPSSREL	35	10	01	33						2008
POL	RANSPTTREL	37	10	01	50						2009
POL	GAISLSLPQI	79	10	01	17						2010
POL	GTTLNFPQIT	79	10	01	17						2011
POL	AISLSLPQIT	80	10	01	33						2012
POL	GTLNCPQITL	80	10	01	33						2013
POL	PTFNFPQITL	80	10	01	33						2014
POL	PQITLWQRPL	88	10	47	73						2015
POL	QITLWQRPLV	89	10	47	73						2016
POL	ITLWQRPLVT	90	10	37	58						2017
POL	TLWQRPLVTI	91	10	21	33						2018
POL	TLWQRPLVTV	91	10	18	28						2019
POL	WQRPLVTIKI	93	10	14	22						2020
POL	WQRPLVTVKI	93	10	12	19						2021
POL	LVTIKIGGQL	97	10	13	20						2022
POL	KIGGQLKEAL	101	10	23	36	0.0002					2023
POL	GQLIEALLDT	104	10	10	16						2024
POL	GQLKEALLDT	104	10	34	53						2025
POL	LIEALLDTGA	106	10	10	16						2026
POL	ALLDTGADDT	109	10	61	95						2027
POL	LLDTGADDTV	110	10	63	98	0.0005					2028

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	GADDTVLEDI	114	10	15	23						2029
POL	GADDTVLEEI	114	10	18	28						2030
POL	GADDTVLEEM	114	10	11	17						2031
POL	NLPGKWKPKM	124	10	35	55						2032
POL	KMIGGIGGFI	132	10	62	97	0.0290	0.0790	2.1000	0.0048	0.0120	2033
POL	FIKVRQYDQI	140	10	41	64						2034
POL	KVRQYDQILI	142	10	20	31						2035
POL	KVRQYDQIPI	142	10	13	20						2036
POL	RQYDQILIEI	144	10	20	31						2037
POL	RQYDQIPIEI	144	10	12	19						2038
POL	ILIEICGKKA	149	10	13	20						2039
POL	LIEICGHKAI	150	10	10	16						2040
POL	LIEICGKKAI	150	10	13	20						2041
POL	EICGHKAIGT	152	10	19	30						2042
POL	EICGKKAIGT	152	10	24	38						2043
POL	AIGTVLVGPT	158	10	52	81						2044
POL	GTVLVGPTPV	160	10	53	83						2045
POL	VLVGPTPVNI	162	10	53	83	0.0025					2046
POL	LVGPTPVNII	163	10	52	81	0.0015					2047
POL	PVNIIGRNLL	168	10	26	41	0.0002					2048
POL	PVNIIGRNML	168	10	24	38						2049
POL	IIGRNLLTQI	171	10	21	33						2050
POL	IIGRNMLTQI	171	10	18	28						2051
POL	IIGRNMLTQL	171	10	11	17						2052
POL	NLLTQIGCTL	175	10	21	33	0.0007					2053
POL	NMLTQIGCTL	175	10	18	28						2054
POL	NMLTQLGCTL	175	10	10	16						2055
POL	QIGCTLNFPI	179	10	41	64	0.0025					2056
POL	QLGCTLNFPI	179	10	16	25						2057
POL	CTLNFPISPI	182	10	60	94	0.0340	0.1800	0.3300	0.4400	0.4000	2058
POL	PISPIETVPV	187	10	56	88	0.0002					2059
POL	TVPVKLKPGM	193	10	54	84						2060
POL	KQWPLTEEKI	209	10	56	88						2061
POL	PLTEEKIKAL	212	10	54	84	0.0002					2062
POL	LTEEKIKALT	213	10	37	58						2063
POL	LTEEKIKALV	213	10	15	23						2064
POL	KIKALTEICT	217	10	12	19						2065
POL	KIKALVEICT	217	10	15	23						2066
POL	KALVEICTEM	219	10	15	24						2067
POL	CTEMEKEGKI	225	10	27	42						2068
POL	KIGPENPYNT	238	10	50	78						2069
POL	RIGPENPYNT	238	10	10	16						2070
POL	RTQDFWEVQL	272	10	53	83						2071
POL	EVQLGIPHPA	278	10	54	84						2072
POL	QLGIPHPAGL	280	10	56	89	0.0002					2073
POL	PAGLKKKKSV	286	10	50	78						2074
POL	GLKKKKSVTV	288	10	49	77	0.0002					2075
POL	SVTVLDVGDA	294	10	57	89						2076
POL	PLDKDFRKYT	308	10	19	30						2077
POL	FTIPSINNET	319	10	37	58						2078

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	FTIPSTNNET	319	10	13	20						2079
POL	PQGWKGSPAI	339	10	59	92						2080
POL	AIFQSSMTKI	347	10	36	56						2081
POL	IVIYQYMDDL	367	10	42	66	0.0007					2082
POL	DLYVGSDLEI	375	10	58	91	0.0001					2083
POL	GQIIRAKIEEL	385	10	25	39						2084
POL	GQHRTKIEEL	385	10	20	31						2085
POL	KIEELREHLL	390	10	19	30						2086
POL	KIEELRQHLL	390	10	17	27	0.0002					2087
POL	RQHLLRWGFT	395	10	12	19						2088
POL	HQKEPPFLWM	410	10	62	97						2089
POL	IQLPEKDSWT	433	10	13	20						2090
POL	IVLPEKDSWT	433	10	13	20						2091
POL	QLPEKDSWTV	434	10	13	20						2092
POL	VLPEKDSWTV	434	10	13	20	0.0056					2093
POL	WTVNDIQKLV	441	10	61	95	0.0001					2094
POL	KLNWASQIYA	452	10	27	42	0.0230	0.0011	0.0250	0.0006	0.0130	2095
POL	GIKVKQLCKL	462	10	28	44						2096
POL	GIKVRQLCKL	462	10	18	28						2097
POL	KQLCKLLRGA	466	10	12	19						2098
POL	KQLCKLLRGT	466	10	14	22						2099
POL	RQLCKLLRGA	466	10	13	21						2100
POL	KLLRGAKALT	470	10	25	40						2101
POL	KLLRGTKALT	470	10	24	38						2102
POL	KALTDIVPLT	476	10	21	33						2103
POL	KALTEVIPLT	476	10	16	25						2104
POL	IVPLTEEAEL	481	10	13	20						2105
POL	VIPLTEEAEL	481	10	11	17						2106
POL	PLTEEAELEL	483	10	30	47						2107
POL	LTEEAELELA	484	10	36	56						2108
POL	ELELAENREI	489	10	53	83						2109
POL	EILKEPVHGV	497	10	41	64	0.0007					2110
POL	GVYYDPSKDL	508	10	38	59						2111
POL	IQKQGQDQWT	521	10	12	19						2112
POL	IQKQGQGQWT	521	10	15	23						2113
POL	QIYQEPFKNL	532	10	40	63	0.0002					2114
POL	YQEPFKNLKT	534	10	43	67						2115
POL	NLKTGKYAKM	540	10	18	29						2116
POL	NLKTGKYARM	540	10	13	21						2117
POL	KTGKYAKMRT	542	10	10	16						2118
POL	RMRGAHTNDV	548	10	12	19						2119
POL	GAHTNDVKQL	551	10	19	30						2120
POL	SAHTNDVKQL	551	10	16	25						2121
POL	TAHTNDVKQL	551	10	11	17						2122
POL	KQLTEAVQKI	558	10	32	51						2123
POL	QLTEAVQKIA	559	10	26	41						2124
POL	LTEAVQKIAT	560	10	11	17						2125
POL	AVQKIATESI	563	10	10	16						2126
POL	VQKIATESIV	564	10	14	22						2127
POL	ETWWTDYWQA	591	10	10	16						2128

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	WTDYWQATWI	594	10	14	22						2129
POL	WTEYWQATWI	594	10	24	38						2130
POL	ATWIPEWEFV	600	10	51	80	0.0013					2131
POL	WIPEWEFVNT	602	10	50	81						2132
POL	FVNTPPLVKL	608	10	54	86	0.0002					2133
POL	LVKLWYQLET	614	10	11	17						2134
POL	QLEKEPIVGA	620	10	16	25						2135
POL	PIVGAETFYV	625	10	28	44	0.0002					2136
POL	GAETFYVDGA	628	10	48	75						2137
POL	YVDGAANRET	633	10	45	70						2138
POL	ETKLGKAGYV	641	10	35	55						2139
POL	YVTDRGRQKV	649	10	29	45	0.0002					2140
POL	VTDRGRQKVV	650	10	28	44						2141
POL	RQKVVSLTET	655	10	10	16						2142
POL	SLTDTTNQKT	660	10	11	17						2143
POL	SLTETTNQKT	660	10	19	30						2144
POL	TTNQKTELHA	664	10	12	19						2145
POL	TTNQKTELQA	664	10	42	66						2146
POL	KTELQAIHLA	668	10	15	23						2147
POL	KTELQAIYLA	668	10	12	19						2148
POL	LALQDSGLEV	676	10	27	42	0.0006					2149
POL	LALQDSGSEV	676	10	25	39						2150
POL	LQDSGLEVNI	678	10	27	42						2151
POL	LQDSGSEVNI	678	10	25	39						2152
POL	NIVTDSQYAL	686	10	59	92	0.0004					2153
POL	VTDSQYALGI	688	10	58	91						2154
POL	SQYALGIIQA	691	10	58	91						2155
POL	AQPDKSESEL	700	10	36	56						2156
POL	ELVNQIIEQL	708	10	18	28						2157
POL	ELVSQIIEQL	708	10	19	30						2158
POL	LVNQIIEQLI	709	10	19	30						2159
POL	LVSQIIEQLI	709	10	19	30						2160
POL	QLIKKEKVYL	716	10	28	44	0.0006					2161
POL	LIKKEKVYLA	717	10	20	31						2162
POL	LAWVPAHKGI	725	10	22	34						2163
POL	QVDKLVSAGI	739	10	15	23						2164
POL	QVDKLVSSGI	739	10	29	45						2165
POL	KLVSAGIRKV	742	10	15	23	0.0074					2166
POL	KLVSSGIRKV	742	10	26	41						2167
POL	LVSAGIRKVL	743	10	15	23	0.0002					2168
POL	LVSSGIRKVL	743	10	26	41						2169
POL	SAGIRKVLFL	745	10	15	23						2170
POL	VLFLDGIDKA	751	10	51	80	0.0007					2171
POL	MASDFNLPPI	774	10	22	34						2172
POL	MASDFNLPPV	774	10	25	39	0.0800	0.1900	0.1800	0.1100	2.2000	2173
POL	NLPPIVAKEI	779	10	26	41						2174
POL	NLPPVVAKEI	779	10	27	42	0.0007					2175
POL	IVASCDKCQL	788	10	43	67	0.0006					2176
POL	GIWQLDCTHL	811	10	59	92	0.0003					2177
POL	CTHLEGKIIL	817	10	31	48						2178

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	CTHLEGKVIL	817	10	23	36						2179
POL	HLEGKIILVA	819	10	31	48						2180
POL	HLEGKVILVA	819	10	23	36						2181
POL	KIILVAVHVA	823	10	30	47						2182
POL	KVILVAVHVA	823	10	22	34						2183
POL	VAVHVASGYI	827	10	53	83						2184
POL	VASGYIEAEV	831	10	52	81						2185
POL	VIPAETGQET	840	10	58	91						2186
POL	ETGQETAYFI	844	10	31	48						2187
POL	ETGQETAYFL	844	10	26	41						2188
POL	ETAYFILKLA	848	10	31	48						2189
POL	ETAYFLLKLA	848	10	27	42						2190
POL	ILKLAGRWPV	853	10	34	53						2191
POL	LLKLAGRWPV	853	10	25	39	0.0004					2192
POL	KLAGRWPVKT	855	10	14	22						2193
POL	KLAGRWPVKV	855	10	30	47						2194
POL	LAGRWPVKTI	856	10	13	20						2195
POL	LAGRWPVKVI	856	10	22	34						2196
POL	AAVKAACWWA	876	10	28	44						2197
POL	TTVKAACWWA	876	10	14	22						2198
POL	WAGIKQEFGI	884	10	21	33						2199
POL	WAGIQQEFGI	884	10	11	17						2200
POL	PQSQGVVESM	897	10	53	83						2201
POL	GVVESMNKEL	901	10	48	75						2202
POL	SMNKELKKII	905	10	53	83						2203
POL	KIIGQVRDQA	912	10	43	67						2204
POL	KIIGQVREQA	912	10	13	20						2205
POL	GQVRDQAEHL	915	10	44	69						2206
POL	GQVREQAEHL	915	10	13	20						2207
POL	DQAEHLKTAV	919	10	46	72						2208
POL	EQAEHLKTAV	919	10	13	20						2209
POL	HLKTAVQMAV	923	10	57	89	0.0005					2210
POL	KTAVQMAVFI	925	10	56	88	0.0002					2211
POL	SAGERIIDII	947	10	41	64						2212
POL	SAGERIVDII	947	10	14	22						2213
POL	RIIDIIASDI	951	10	12	19						2214
POL	RIIDIIATDI	951	10	29	45						2215
POL	RIVDIIATDI	951	10	12	19						2216
POL	IASDIQTKEL	956	10	14	22						2217
POL	IATDIQTKEL	956	10	35	55						2218
POL	IQTKELQKQI	960	10	44	69						2219
POL	QTKELQKQII	961	10	10	16						2220
POL	QTKELQKQIT	961	10	32	50						2221
POL	QIIKIQNFRV	968	10	12	19						2222
POL	QITKIQNFRV	968	10	35	55	0.0002					2223
POL	PIWKGPAKLL	985	10	35	55						2224
POL	PLWKGPAKLL	985	10	18	28						2225
POL	KLLWKGEGAV	992	10	60	94	0.0006					2226
POL	LLWKGEGAVV	993	10	61	95	0.0360					2227
POL	AVVIQDNSDI	1000	10	37	58						2228

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	AVVIQDNSEI	1000	10	12	19						2229
POL	VIQDNSDIKV	1003	10	37	58	0.0013					2230
POL	VIQDNSEIKV	1003	10	12	19						2231
POL	IQDNSDIKVV	1004	10	38	59						2232
POL	IQDNSEIKVV	1004	10	12	19						2233
POL	DIKVVPRRKA	1009	10	39	61						2234
POL	EIKVVPRRKA	1009	10	13	20						2235
POL	KVVPRRKAKI	1011	10	51	80						2236
POL	KVVPRRKVKI	1011	10	11	17						2237
POL	VVPRRKAKII	1012	10	50	78						2238
POL	VVPRRKVKII	1012	10	11	17						2239
POL	KIIKDYGKQM	1019	10	11	17						2240
POL	KIIRDYGKQM	1019	10	50	78						2241
POL	IIKDYGKQMA	1020	10	11	17						2242
POL	IIRDYGKQMA	1020	10	49	77						2243
POL	KQMAGDDCVA	1026	10	44	69						2244
POL	GAISLSLPQIT	79	11	01	17						2245
POL	AISLSLPQITL	80	11	01	33						2246
POL	PQITLWQRPLV	88	11	47	73						2247
POL	QITLWQRPLVT	89	11	37	58						2248
POL	ITLWQRPLVTI	90	11	19	30						2249
POL	ITLWQRPLVTV	90	11	18	28						2250
POL	PLVTIKIGGQL	96	11	13	20						2251
POL	TIKIGGQLKEA	99	11	17	27						2252
POL	KIGGQLKEALL	101	11	23	36						2253
POL	QLIEALLDTGA	105	11	10	16						2254
POL	QLKEALLDTGA	105	11	34	53						2255
POL	EALLDTGADDT	108	11	60	94						2256
POL	ALLDTGADDTV	109	11	61	95						2257
POL	LLDTGADDTVL	110	11	61	95						2258
POL	NLPGKWKPKMI	124	11	35	55						2259
POL	MIGGIGGFIKV	133	11	62	97						2260
POL	FIKVRQYDQIL	140	11	21	33						2261
POL	QILIEICGKKA	148	11	13	20						2262
POL	ILIEICGKKAI	149	11	13	20						2263
POL	EICGHKAIGTV	152	11	19	30						2264
POL	EICGKKAIGTV	152	11	23	36						2265
POL	KAIGTVLVGPT	157	11	48	75						2266
POL	TVLVGPTPVNI	161	11	53	83						2267
POL	VLVGPTPVNII	162	11	51	80						2268
POL	PTPVNIIGRNL	166	11	26	41						2269
POL	PTPVNIIGRNM	166	11	24	38						2270
POL	PVNIIGRNLLT	168	11	26	41						2271
POL	PVNIIGRNMLT	168	11	23	36						2272
POL	NIIGRNLLTQI	170	11	21	33						2273
POL	NIIGRNMLTQI	170	11	18	28						2274
POL	NIIGRNMLTQL	170	11	11	17						2275
POL	TQIGCTLNFPI	178	11	41	64						2276
POL	TQLGCTLNFPI	178	11	15	23						2277
POL	TLNFPISPIET	183	11	54	86						2278

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	ETVPVKLKPGM	192	11	51	80						2279
POL	KLKPGMDGPKV	197	11	47	73						2280
POL	PLTEEKIKALT	212	11	35	55						2281
POL	PLTEEKIKALV	212	11	15	23						2282
POL	EMEKEGKISKI	229	11	32	50						2283
POL	PIFAIKKKDST	248	11	22	34						2284
POL	PVFAIKKKDST	248	11	37	58						2285
POL	LVDFRELNKRT	263	11	60	94						2286
POL	TQDFWEVQLGI	273	11	55	86						2287
POL	VQLGIPHPAGL	279	11	54	84						2288
POL	PAGLKKKKSVT	286	11	47	73						2289
POL	GLKKKKSVTVL	288	11	49	77						2290
POL	VLDVGDAYFSV	297	11	53	83	0.0150					2291
POL	DVGDAYFSVPL	299	11	54	84						2292
POL	FLDKDFRKYTA	308	11	19	30						2293
POL	ETPGIRYQYNV	327	11	51	80						2294
POL	VLPQGWKGSPA	337	11	58	92						2295
POL	PAIFQSSMTKI	346	11	36	56						2296
POL	AIFQSSMTKIL	347	11	36	56						2297
POL	DIVIYQYMDDL	366	11	18	28						2298
POL	EIVIYQYMDDL	366	11	24	38						2299
POL	VIYQYMDDLYV	368	11	51	80						2300
POL	YMDDLYVGSDL	372	11	61	95						2301
POL	DLEIGQHRAKI	381	11	26	41						2302
POL	DLEIGQHRTKI	381	11	20	31						2303
POL	RAKIEELREHL	388	11	13	20						2304
POL	RTKIEELRQHL	388	11	14	22						2305
POL	RQHLLRWGFTT	395	11	12	19						2306
POL	PIQLPEKDSWT	432	11	13	20						2307
POL	PIVLPEKDSWT	432	11	13	20						2308
POL	IQLPEKDSWTV	433	11	13	20						2309
POL	IVLPEKDSWTV	433	11	13	20						2310
POL	IQKLVGKLNWA	446	11	61	95						2311
POL	LVGKLNWASQI	449	11	60	94						2312
POL	WASQIYAGIKV	455	11	26	41						2313
POL	WASQIYPGIKV	455	11	27	42						2314
POL	QIYAGIKVKQL	458	11	18	29						2315
POL	QIYPGIKVKQL	458	11	11	17						2316
POL	QIYPGIKVRQL	458	11	14	22						2317
POL	GIKVKQLCKLL	462	11	27	42						2318
POL	GIKVRQLCKLL	462	11	18	28						2319
POL	QLCKLLRGAKA	467	11	24	38						2320
POL	QLCKLLRGTKA	467	11	21	33						2321
POL	LLRGAKALTDI	471	11	22	34						2322
POL	LLRGTKALTEV	471	11	18	28						2323
POL	GAKALTDIVPL	474	11	17	27						2324
POL	GTKALTEVIPL	474	11	11	17						2325
POL	LTDIVPLTEEA	478	11	13	20						2326
POL	LTEVIPLTEEA	478	11	11	17						2327
POL	DIVPLTEEAEL	480	11	13	20						2328

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	EVIPLTEEAEL	480	11	11	17						2329
POL	PLTEEAELELA	483	11	29	45						2330
POL	ELELAENREIL	489	11	53	83						2331
POL	GVYYDPSKDLI	508	11	31	48						2332
POL	EIQKQGQDQWT	520	11	12	19						2333
POL	EIQKQGQGQWT	520	11	15	23						2334
POL	KQGQDQWTYQI	523	11	13	20						2335
POL	KQGQGQWTYQI	523	11	25	39						2336
POL	YQIYQEPFKNL	531	11	40	63						2337
POL	KTGKYAKMRTA	542	11	10	16						2338
POL	KTGKYARMRGA	542	11	13	21						2339
POL	GAHTNDVKQLT	551	11	18	28						2340
POL	SAHTNDVKQLT	551	11	12	19						2341
POL	TAHTNDVKQLT	551	11	10	16						2342
POL	HTNDVKQLTEA	553	11	32	50						2343
POL	KQLTEAVQKIA	558	11	24	38						2344
POL	QLTEAVQKIAT	559	11	11	17						2345
POL	EAVQKIATESI	562	11	10	16						2346
POL	AVQKIATESIV	563	11	10	16						2347
POL	VQKIATESIVI	564	11	14	22						2348
POL	ATESIVIWGKT	568	11	16	25						2349
POL	VIWGKTPKFKL	573	11	17	27						2350
POL	VIWGKTPKFRL	573	11	29	45						2351
POL	RLPIQKETWET	582	11	18	28						2352
POL	IQKETWEAWWT	585	11	11	17						2353
POL	IQKETWETWWT	585	11	21	33						2354
POL	ETWWTDYWQAT	591	11	10	16						2355
POL	QATWIPEWEFV	599	11	51	81						2356
POL	KLWYQLEKDPI	616	11	14	22						2357
POL	KLWYQLEKEPI	616	11	31	48						2358
POL	KLWYQLETEPI	616	11	11	17						2359
POL	YQLEKEPIVGA	619	11	16	25						2360
POL	GAETFYVDGAA	628	11	44	69						2361
POL	AANRETKLGKA	637	11	30	47						2362
POL	ETKLGKAGYVT	641	11	35	55						2363
POL	YVTDRGRQKVV	649	11	27	42						2364
POL	RQKVVSLTETT	655	11	10	16						2365
POL	LTDTTNQKTEL	661	11	19	30						2366
POL	LTETTNQKTEL	661	11	25	39						2367
POL	DTTNQKTELQA	663	11	25	39						2368
POL	ETTNQKTELHA	663	11	11	17						2369
POL	ETTNQKTELQA	663	11	17	27						2370
POL	TTNQKTELHAI	664	11	12	19						2371
POL	TTNQKTELQAI	664	11	42	66						2372
POL	NQKTELQAIHL	666	11	15	23						2373
POL	NQKTELQAIYL	666	11	12	19						2374
POL	KTELQAIHLAL	668	11	15	23						2375
POL	KTELQAIYLAL	668	11	12	19						2376
POL	AIHLALQDSGL	673	11	15	23						2377
POL	HLALQDSGLEV	675	11	15	23						2378

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	ALQDSGLEVNI	677	11	27	42						2379
POL	ALQDSGSEVNI	677	11	25	39						2380
POL	LQDSGLEVNIV	678	11	27	42						2381
POL	LQDSGSEVNIV	678	11	25	39						2382
POL	EVNIVTDSQYA	684	11	59	92						2383
POL	IVTDSQYALGI	687	11	58	91						2384
POL	VTDSQYALGII	688	11	58	91						2385
POL	QAQPDKSESEL	699	11	36	56						2386
POL	AQPDKSESELV	700	11	36	56						2387
POL	ELVNQIIEQLI	708	11	18	28						2388
POL	ELVSQIIEQLI	708	11	19	30						2389
POL	IIEQLIKKEKV	713	11	28	44						2390
POL	EQLIKKEKVYL	715	11	28	44						2391
POL	QLIKKEKVYLA	716	11	19	30						2392
POL	YLAWVPAHKGI	724	11	22	34						2393
POL	YLSWVPAHKGI	724	11	37	58						2394
POL	GIGGNEQVDKL	733	11	58	91						2395
POL	EQVDKLVSAGI	738	11	15	23						2396
POL	EQVDKLVSSGI	738	11	29	45						2397
POL	KLVSAGIRKVL	742	11	15	23						2398
POL	KLVSSGIRKVL	742	11	26	41						2399
POL	GIRKVLFLDGI	747	11	49	77						2400
POL	KVLFLDGIDKA	750	11	48	75						2401
POL	AMASDFNLPPI	773	11	18	28						2402
POL	AMASDFNLPPV	773	11	25	39						2403
POL	MASDFNLPPIV	774	11	20	31						2404
POL	MASDFNLPPVV	774	11	25	39						2405
POL	NLPPIVAKEIV	779	11	26	41						2406
POL	NLPPVVAKEIV	779	11	27	42						2407
POL	EIVASCDKCQL	787	11	43	67						2408
POL	QLKGEAMHGQV	796	11	53	83						2409
POL	QVDCSPGIWQL	805	11	56	88						2410
POL	QLDCTHLEGKI	814	11	33	52						2411
POL	QLDCTHLEGKV	814	11	26	41						2412
POL	CTHLEGKIILV	817	11	31	48						2413
POL	CTHLEGKVILV	817	11	23	36						2414
POL	HLEGKIILVAV	819	11	31	48						2415
POL	HLEGKVILVAV	819	11	23	36						2416
POL	LVAVHVASGYI	826	11	47	73						2417
POL	AVHVASGYIEA	828	11	52	81						2418
POL	HVASGYIEAEV	830	11	52	81						2419
POL	VASGYIEAEVI	831	11	52	81						2420
POL	YIEAEVIPAET	835	11	53	83						2421
POL	EVIPAETGQET	839	11	58	91						2422
POL	VIPAETGQETA	840	11	58	91						2423
POL	ETGQETAYFIL	844	11	31	48						2424
POL	ETGQETAYFLL	844	11	26	41						2425
POL	GQETAYFILKL	846	11	31	48						2426
POL	GQETAYFLLKL	846	11	26	41						2427
POL	FILKLAGRWPV	852	11	32	50						2428

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	FLLKLAGRWPV	852	11	25	39						2429
POL	KLAGRWPVKTI	855	11	13	20						2430
POL	KLAGRWPVKVI	855	11	22	34						2431
POL	TIHTDNGSNFT	864	11	13	20						2432
POL	VIHTDNGSNFT	864	11	23	36						2433
POL	HTDNGSNFTSA	866	11	33	52						2434
POL	HTDNGSNFTST	866	11	11	17						2435
POL	SAAVKAACWWA	875	11	28	44						2436
POL	STTVKAACWWA	875	11	14	22						2437
POL	AVKAACWWAGI	877	11	10	16						2438
POL	TVKAACWWAGI	877	11	20	31						2439
POL	GIPYNPQSQGV	892	11	63	98						2440
POL	QVRDQAEHLKT	916	11	43	67						2441
POL	QVREQAEHLKT	916	11	13	20						2442
POL	QAEHLKTAVQM	920	11	57	89						2443
POL	FHNFKRKGGI	933	11	58	91						2444
POL	GIGGYSAGERI	942	11	57	89						2445
POL	SAGERIIDIIA	947	11	40	63						2446
POL	SAGERIVDIIA	947	11	14	22						2447
POL	IIDIIASDIQT	952	11	12	19						2448
POL	IIDIIATDIQT	952	11	27	42						2449
POL	IVDIIATDIQT	952	11	12	19						2450
POL	IIASDIQTKEL	955	11	14	22						2451
POL	IIATDIQTKEL	955	11	34	53						2452
POL	DIQTKELQKQI	959	11	44	69						2453
POL	IQTKELQKQII	960	11	10	16						2454
POL	IQTKELQKQIT	960	11	30	47						2455
POL	KQIIKIQNFRV	967	11	12	19						2456
POL	KQITKIQNFRV	967	11	34	54						2457
POL	RVYYRDSRDPI	976	11	34	53						2458
POL	RVYYRDSRDPL	976	11	14	22						2459
POL	PAKLLWKGEGA	990	11	59	92						2460
POL	KLLWKGEGAVV	992	11	59	92						2461
POL	LLWKGEGAVVI	993	11	59	92						2462
POL	GAVVIQDNSDI	999	11	37	58						2463
POL	GAVVIQDNSEI	999	11	12	19						2464
POL	VVIQDNSDIKV	1002	11	37	58						2465
POL	VVIQDNSEIKV	1002	11	12	19						2466
POL	VIQDNSDIKVV	1003	11	37	58						2467
POL	VIQDNSEIKVV	1003	11	12	19						2468
POL	KVVPRRKAKII	1011	11	50	78						2469
POL	KVVPRRKVKII	1011	11	11	17						2470
POL	KIIKDYGKQMA	1019	11	11	17						2471
POL	KIIRDYGKQMA	1019	11	49	77						2472
REV	LLKTVRLI	12	8	11	17						2473
REV	AVRIIKIL	17	8	13	20						2474
REV	RQRQIHSI	52	8	11	17						2475
REV	QLPPIERL	78	8	14	22						2476
REV	QLPPLERL	78	8	37	58						2477
REV	GTSGTQGV	94	8	21	33						2478

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
REV	GTQQSQGT	97	8	10	16						2479
REV	PQGTETGV	101	8	05	18						2480
REV	SQGTETGV	101	8	05	18						2481
REV	LVESPAVL	114	8	11	17						2482
REV	SISERILST	58	9	10	16						2483
REV	CLGRPAEPV	67	9	10	16						2484
REV	PAEPVPLQL	71	9	21	33						2485
REV	SAEPVPLQL	71	9	12	19						2486
REV	PVPLQLPPI	74	9	11	17						2487
REV	PVPLQLPPL	74	9	35	55						2488
REV	LQLPPIERL	77	9	11	17						2489
REV	LQLPPLERL	77	9	36	56						2490
REV	QLPPLERLT	78	9	18	28						2491
REV	TQGVGSPQI	98	9	11	18						2492
REV	RARQRQIHSI	50	10	10	16						2493
REV	PLQLPPIERL	76	10	11	17						2494
REV	PLQLPPLERL	76	10	34	53						2495
REV	LQLPPLERLT	77	10	17	27						2496
REV	QLPPLERLTL	78	10	18	28	0.0001					2497
REV	GTQGVGSPQI	97	10	11	18						2498
REV	PLQLPPLERLT	76	11	15	23						2499
REV	LQLPPLERLTL	77	11	17	27						2500
REV	GTSGTQQSQGT	94	11	10	16						2501
TAT	SQPKTACT	19	8	13	20						2502
TAT	FLNKGLGI	41	8	14	22						2503
TAT	SQPRGDPT	80	8	13	20						2504
TAT	KVERETET	97	8	12	19						2505
TAT	PTGPKESKKKV	88	11	12	19						2506
VIF	QVMIVWQV	6	8	43	67						2507
VIF	IVWQVDRM	9	8	59	92						2508
VIF	WQVDRMKI	11	8	13	20						2509
VIF	WQVDRMRI	11	8	48	75						2510
VIF	KIRTWNSL	17	8	12	19						2511
VIF	RIRTWKSL	17	8	15	23						2512
VIF	RIRTWNSL	17	8	15	23						2513
VIF	LVKHHMYI	24	8	19	30						2514
VIF	LVKHHMYV	24	8	21	33						2515
VIF	HMYVSKKA	28	8	13	20						2516
VIF	KISSEVHI	50	8	15	23						2517
VIF	KVSSEVHI	50	8	20	31						2518
VIF	RISSEVHI	50	8	15	23						2519
VIF	PLGDARLV	58	8	11	17						2520
VIF	PLGEARLV	58	8	19	30						2521
VIF	VIKTYWGL	67	8	10	16						2522
VIF	VITTYWGL	67	8	22	34						2523
VIF	VVRTYWGL	67	8	10	16						2524
VIF	VVTTYWGL	67	8	11	17						2525
VIF	TTYWGLHT	69	8	24	38						2526
VIF	HLGHGVSI	83	8	25	39						2527
VIF	HLGQGVSI	83	8	26	41						2528

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VIF	GVSHEWRL	87	8	18	28						2529
VIF	STQIDPDL	100	8	12	19						2530
VIF	STQVDPGL	100	8	11	17						2531
VIF	TQHDPDLA	101	8	12	19						2532
VIF	TQVDPDLA	101	8	11	17						2533
VIF	TQVDPGLA	101	8	16	25						2534
VIF	LADQLIHL	107	8	25	39						2535
VIF	LADQLIHM	107	8	17	27						2536
VIF	SAIRKAIL	123	8	35	55						2537
VIF	SAIRNAIL	123	8	12	19						2538
VIF	YQAGHNKV	140	8	38	59						2539
VIF	KVGSLQYL	146	8	52	81						2540
VIF	SLQYLALA	149	8	12	19						2541
VIF	SLQYLALT	149	8	31	48						2542
VIF	LQYLALAA	150	8	12	19						2543
VIF	LQYLALKA	150	8	11	17						2544
VIF	LQYLALTA	150	8	34	53						2545
VIF	YLALTALI	152	8	28	44						2546
VIF	ALIKPKKI	157	8	10	16						2547
VIF	PLPSVKKL	168	8	21	33						2548
VIF	PLPSVRKL	168	8	14	22						2549
VIF	WQVMIVWQV	5	9	43	67						2550
VIF	MIVWQVDRM	8	9	46	72						2551
VIF	QVDRMKIRT	12	9	12	19						2552
VIF	QVDRMRINT	12	9	10	16						2553
VIF	QVDRMRIRT	12	9	31	48						2554
VIF	KIRTWNSLV	17	9	12	19						2555
VIF	RIRTWKSLV	17	9	15	23						2556
VIF	RIRTWNSLV	17	9	15	23						2557
VIF	SLVKHHMYI	23	9	19	30						2558
VIF	SLVKHHMYV	23	9	21	33						2559
VIF	EVHIPLGDA	54	9	24	38						2560
VIF	EVHIPLGEA	54	9	25	39						2561
VIF	HIPLGDARL	56	9	13	20						2562
VIF	HIPLGEARL	56	9	20	31						2563
VIF	PLGEARLVI	58	9	10	16						2564
VIF	LVIKTYWGL	66	9	10	16						2565
VIF	LVITTYWGL	66	9	22	34	0.0031					2566
VIF	ITTYWGLHT	68	9	16	25						2567
VIF	HTGERDWHL	75	9	21	33						2568
VIF	QTGERDWHL	75	9	12	19						2569
VIF	STQIDPDLA	100	9	12	19						2570
VIF	STQVDPGLA	100	9	11	17						2571
VIF	DLADQLIHL	106	9	18	28						2572
VIF	GLADQLIHM	106	9	15	23						2573
VIF	KVGSLQYLA	146	9	52	81						2574
VIF	SLQYLALAA	149	9	12	19						2575
VIF	SLQYLALKA	149	9	11	17						2576
VIF	SLQYLALTA	149	9	31	48						2577
VIF	LQYLALAAL	150	9	12	19						2578

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VIF	LQYLALKAL	150	9	11	17						2579
VIF	LQYLALTAL	150	9	33	52						2580
VIF	KIKPPLPSV	164	9	19	30						2581
VIF	KTKPPLPSV	164	9	12	19						2582
VIF	PLPSVKKLT	168	9	13	20						2583
VIF	VMIVWQVDRM	7	10	44	69						2584
VIF	IVWQVDRMKI	9	10	12	19						2585
VIF	IVWQVDRMRI	9	10	47	73						2586
VIF	WQVDRMKIRT	11	10	12	19						2587
VIF	WQVDRMRINT	11	10	10	16						2588
VIF	WQVDRMRIRT	11	10	31	48						2589
VIF	RMKIRTWNSL	15	10	12	19						2590
VIF	RMRIRTWKSL	15	10	15	23						2591
VIF	RMRIRTWNSL	15	10	15	23						2592
VIF	KISSEVHIPL	50	10	14	22						2593
VIF	KVSSEVHIPL	50	10	19	30						2594
VIF	RISSEVHIPL	50	10	13	20						2595
VIF	HIPLGDARLV	56	10	10	16						2596
VIF	HIPLGEARLV	56	10	19	30						2597
VIF	RLVITTYWGL	65	10	12	19						2598
VIF	VITTYWGLHT	67	10	16	25						2599
VIF	LQTGERDWHL	74	10	12	19						2600
VIF	QIDPDLADQL	102	10	10	16						2601
VIF	QVDPGLADQL	102	10	14	22						2602
VIF	IVSPRCEYQA	133	10	11	17						2603
VIF	QAGHNKVGSL	141	10	38	59						2604
VIF	KVGSLQYLAL	146	10	51	80	0.0008					2605
VIF	SLQYLALAAL	149	10	12	19						2606
VIF	SLQYLALKAL	149	10	11	17						2607
VIF	SLQYLALTAL	149	10	31	48						2608
VIF	LQYLALTALI	150	10	28	44						2609
VIF	KTKGHRGSHT	188	10	16	25						2610
VIF	QVMIVWQVDRM	6	11	43	67						2611
VIF	MIVWQVDRMRI	8	11	43	67						2612
VIF	RMKIRTWNSLV	15	11	12	19						2613
VIF	RMRIRTWKSLV	15	11	15	23						2614
VIF	RMRIRTWNSLV	15	11	15	23						2615
VIF	RTWKSLVKHHM	19	11	14	22						2616
VIF	RTWNSLVKHHM	19	11	24	38						2617
VIF	EVHIPLGDARL	54	11	13	20						2618
VIF	EVHIPLGEARL	54	11	20	31						2619
VIF	HIPLGEARLVI	56	11	10	16						2620
VIF	LVITTYWGLHT	66	11	16	25						2621
VIF	GLHTGERDWHL	73	11	21	33						2622
VIF	GLQTGERDWHL	73	11	12	19						2623
VIF	TQIDPDLADQL	101	11	10	16						2624
VIF	TQVDPGLADQL	101	11	13	20						2625
VIF	QIDPDLADQLI	102	11	10	16						2626
VIF	QVDPGLADQLI	102	11	14	22						2627
VIF	YQAGHNKVGSL	140	11	38	59						2628

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VIF	KVGSLQYLALA	146	11	12	19						2629
VIF	KVGSLQYLALT	146	11	28	44						2630
VIF	SLQYLALTALI	149	11	27	42						2631
VIF	LIKPKKIKPPL	158	11	10	16						2632
VIF	KTKGHRGSHTM	188	11	15	23						2633
VPR	ALELLEEL	19	8	10	16						2634
VPR	TLELLEEL	19	8	44	69						2635
VPR	AVRHFPRI	30	8	14	22						2636
VPR	ETYGDTWA	48	8	16	25						2637
VPR	ETYGDTWT	48	8	11	17						2638
VPR	DTWAGVEA	52	8	16	25						2639
VPR	DTWEGVEA	52	8	23	36						2640
VPR	WAGVEAII	54	8	16	25						2641
VPR	GVEAHRI	56	8	34	53						2642
VPR	HRILQQL	60	8	42	66						2643
VPR	ILQQLLFI	63	8	37	58						2644
VPR	LLFHIFRI	67	8	44	69						2645
VPR	LLFVHFRI	67	8	12	19						2646
VPR	CQHSRIGI	77	8	45	70						2647
VPR	WALELLEEL	18	9	09	15						2648
VPR	WTLELLEEL	18	9	42	69	0.0035					2649
VPR	LLEELKNEA	22	9	17	27						2650
VPR	LLEELKSEA	22	9	16	25						2651
VPR	EAVRHFPRI	29	9	14	22	0.0001					2652
VPR	WLHGLGQHI	38	9	20	31						2653
VPR	HYETYGDT	45	9	17	27						2654
VPR	HYNTYGDT	45	9	14	22						2655
VPR	YIYETYGDT	45	9	14	22						2656
VPR	DTWAGVEAI	52	9	16	25						2657
VPR	DTWEGVEAI	52	9	20	31						2658
VPR	GVEAHRIL	56	9	34	53						2659
VPR	AHRILQQL	59	9	39	61	0.0150	0.1900	0.2400	0.0960	0.0730	2660
VPR	HRILQQLL	60	9	42	66	0.0004					2661
VPR	RILQQLLFI	62	9	36	56	0.2600	0.0028	0.0800	0.1000	0.0220	2662
VPR	QLLFHIFRI	66	9	44	69	0.0530	0.0002	0.0004	0.0023	0.0840	2663
VPR	QLLFVHFRI	66	9	10	16						2664
VPR	RIGCQHSRI	74	9	47	73						2665
VPR	RIGCRHSRI	74	9	12	19						2666
VPR	CQHSRIGII	77	9	16	25						2667
VPR	CQHSRIGIT	77	9	14	22						2668
VPR	RQRRARNGA	90	9	13	20						2669
VPR	PQREPYNEWT	10	10	29	45						2670
VPR	ELLEELKNEA	21	10	16	25						2671
VPR	ELLEELKSEA	21	10	16	25						2672
VPR	LLEELKNEAV	22	10	17	27						2673
VPR	LLEELKSEAV	22	10	16	25						2674
VPR	AVRHFPRIWL	30	10	14	22	0.0002					2675
VPR	AVRHFPRPWL	30	10	34	53						2676
VPR	ETYGDTWAGV	48	10	16	25	0.0009					2677
VPR	ETYGDTWTGV	48	10	11	17						2678

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VPR	NTYGDTWEGV	48	10	16	25						2679
VPR	DTWAGVEAH	52	10	16	25						2680
VPR	DTWEGVEAH	52	10	19	30						2681
VPR	WAGVEAHRI	54	10	15	23						2682
VPR	EAHRILQQL	58	10	33	52						2683
VPR	AHRILQQLL	59	10	39	61	0.0014					2684
VPR	QQLLFIHFRI	65	10	44	69						2685
VPR	QQLLFVHFRI	65	10	10	16						2686
VPR	PQREPYNEWTL	10	11	29	45						2687
VPR	ELLEELKNEAV	21	11	16	25						2688
VPR	ELLEELKSEAV	21	11	16	25						2689
VPR	EAVRHFPRIWL	29	11	14	22						2690
VPR	EAVRHFPRPWL	29	11	34	53						2691
VPR	GQHIYETYGDT	43	11	17	27						2692
VPR	GQHIYNTYGDT	43	11	13	20						2693
VPR	GQYIYETYGDT	43	11	13	20						2694
VPR	WAGVEAHRIL	54	11	15	23						2695
VPR	EAHRILQQLL	58	11	33	52						2696
VPR	HRILQQLLFI	60	11	33	52						2697
VPR	LQQLLFIHFRI	64	11	44	69						2698
VPR	LQQLLFVHFRI	64	11	10	16						2699
VPR	RIGCQHSRIGI	74	11	45	70						2700
VPR	RIGCRHSRIGI	74	11	11	17						2701
VPR	#LPGRRGRNGA	85	11	01	50						2702
VPU	LAKVDYRI	5	8	01	25						2703
VPU	LAKVDYRL	5	8	01	25						2704
VPU	KVDYRIVI	7	8	01	33						2705
VPU	KVDYRLGV	7	8	01	33						2706
VPU	RIDYRLGV	7	8	01	33						2707
VPU	ILAIVALV	12	8	12	19						2708
VPU	LAIVALVV	13	8	12	20						2709
VPU	AIVALVVA	14	8	12	19						2710
VPU	HAIVVWT	27	8	23	36						2711
VPU	IAIVVWTI	28	8	23	36						2712
VPU	AIVVWTIV	29	8	29	45						2713
VPU	VVWTIVFI	31	8	15	23						2714
VPU	KILRQRKI	45	8	15	23						2715
VPU	RQRKIDRL	48	8	20	31						2716
VPU	DQEELSAL	79	8	13	22						2717
VPU	GVEMGHHA	91	8	01	50						2718
VPU	LAKVDYRIV	5	9	01	25						2719
VPU	KVDYRIVIV	7	9	01	33						2720
VPU	ILAIVALVV	12	9	11	17						2721
VPU	LAIVALVVA	13	9	09	15						2722
VPU	HAIVVWTI	27	9	23	36						2723
VPU	IAIVVWTIV	28	9	20	31						2724
VPU	IVVWTIVFI	30	9	15	23						2725
VPU	IVFIEYRKI	36	9	12	19						2726
VPU	RQRKIDRLI	48	9	17	27						2727
VPU	KIDRLIDRI	52	9	14	22						2728

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VPU	LIDRIRERA	58	9	12	19						2729
VPU	DQEELSALV	79	9	11	18						2730
VPU	VTLLSSSKL	94	9	01	50						2731
VPU	LAKVDYRIVI	5	10	01	25						2732
VPU	LAKVDYRLGV	5	10	01	25						2733
VPU	KVDYRIVIVA	7	10	01	33						2734
VPU	KVDYRLGVGA	7	10	01	33						2735
VPU	RIDYRLGVGA	7	10	01	33						2736
VPU	HAIVVWTIV	27	10	20	31						2737
VPU	AIVVWTIVFI	29	10	14	22						2738
VPU	ILRQRKIDRL	46	10	15	23						2739
VPU	LVTLLSSSKL	91	10	01	50						2740
VPU	LAKVDYRIVIV	5	11	01	25						2741
VPU	KVDYRLGVGAL	7	11	01	33						2742
VPU	RIDYRLGVGAL	7	11	01	33						2743
VPU	KILRQRKIDRL	45	11	15	23						2744
VPU	ILRQRKIDRLI	46	11	13	20						2745

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
ENV	SLWDQSLK	123	8	47	75						2746
ENV	QSLKPCVK	127	8	48	75						2747
ENV	AITQACPK	244	8	14	22						2748
ENV	TITQACPK	244	8	11	17						2749
ENV	VITQACPK	244	8	17	27						2750
ENV	PAGFAILK	266	8	38	59						2751
ENV	PAGYAILK	266	8	15	23						2752
ENV	AILKCNDK	270	8	20	31						2753
ENV	ILKCNDKK	271	8	12	19						2754
ENV	SVEINCTR	340	8	13	20						2755
ENV	GTAGNSSR	375	8	01	33						2756
ENV	TTHSFNCR	432	8	12	19						2757
ENV	ITLPCRIK	483	8	26	41						2758
ENV	NMWQEVGK	494	8	15	23						2759
ENV	FGLLLTR	520	8	37	58						2760
ENV	RSELYKYK	558	8	54	84						2761
ENV	PLGVAPTK	571	8	26	41						2762
ENV	PLGVAPTR	571	8	10	16						2763
ENV	GVAPTKAK	573	8	19	30						2764
ENV	VAPTKAKR	574	8	19	30						2765
ENV	VISTRTHR	584	8	01	50						2766
ENV	STRTHREK	586	8	01	50						2767
ENV	RVVEREKR	587	8	32	50						2768
ENV	RVVQREKR	587	8	17	27	0.0003	0.0001				2769
ENV	ITLTVQAR	621	8	32	50						2770
ENV	EAQQHLLK	646	8	12	19						2771
ENV	KLTVWGIK	653	8	13	20						2772
ENV	QLTVWGIK	653	8	44	69						2773
ENV	GIKQLQAR	658	8	49	77						2774
ENV	LAVERYLK	667	8	26	41						2775
ENV	LAVERYLR	667	8	11	17						2776
ENV	GIWGCSGK	680	8	52	81						2777
ENV	MTWMEWER	721	8	12	19						2778
ENV	ESQNQQEK	743	8	27	42						2779
ENV	AVLSIVNR	795	8	31	48						2780
ENV	LSIVNRVR	797	8	38	59						2781
ENV	ALAWDDLR	851	8	25	39						2782
ENV	RIVELLGR	878	8	22	34						2783
ENV	IVELLGRR	879	8	22	34						2784
ENV	RLGWEGLK	894	8	10	32						2785
ENV	AVAEGTDR	928	8	31	48						2786
ENV	RAILHIPR	945	8	13	20						2787
ENV	AILHIPRR	946	8	13	20						2788
ENV	RIRQGLER	953	8	44	69						2789
ENV	TLFCASDAK	64	9	52	81	0.0930	0.5300	0.0017	0.0013	0.0420	2790
ENV	VTENFNMWK	102	9	31	48						2791
ENV	ISLWDQSLK	122	9	47	73	0.0048	0.0890	0.0017	0.0013	0.0021	2792
ENV	SAITQACPK	243	9	14	22						2793
ENV	STITQACPK	243	9	10	16						2794
ENV	SVITQACPK	243	9	17	27						2795

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
ENV	FAILKCNDK	269	9	14	22	0.0002	0.0002	0.0004	0.0015	0.0027	2796
ENV	AILKCNDKK	270	9	12	19						2797
ENV	TVQCTHGIK	290	9	28	44	0.0021	0.0460	0.0042	0.0017	0.0190	2798
ENV	TVQCTHGIR	290	9	23	36	0.0008	0.0008	0.0880	0.0330	0.0120	2799
ENV	LAEEEVVIR	312	9	12	19	0.0002	0.0002	0.0004	0.0007	0.0002	2800
ENV	CTRPNNNTR	345	9	28	44						2801
ENV	ITTHSFNCR	431	9	11	17						2802
ENV	NANITIPCR	478	9	01	50						2803
ENV	NITLPCRIK	482	9	11	17						2804
ENV	TITLFCRIK	482	9	14	22						2805
ENV	NITGLLLTR	519	9	35	55	0.0004	0.0001				2806
ENV	STNGTETFR	537	9	01	17						2807
ENV	ELYKYKVVK	560	9	32	51						2808
ENV	GVAPTKAKR	573	9	19	30						2809
ENV	VAPTKAKRR	574	9	17	27	0.0002	0.0002	0.0004	0.0006	0.0002	2810
ENV	KAKRRVVQR	579	9	13	20	0.0002	0.0002	0.0800	0.0095	0.0002	2811
ENV	HNHITPHR	584	9	01	50						2812
ENV	ISTRTHREK	585	9	01	50						2813
ENV	NHTPHREK	586	9	01	50						2814
ENV	STRTHREKR	586	9	01	50						2815
ENV	SITLTVQAR	620	9	32	50						2816
ENV	QARVLAVER	663	9	33	52	0.0009	0.0003	0.0320	0.0320	0.0007	2817
ENV	VLAVERYLK	666	9	18	28						2818
ENV	VLAVERYLR	666	9	11	17						2819
ENV	NMTWMEWER	720	9	12	19						2820
ENV	ISNWLWYIK	770	9	11	17						2821
ENV	ITKWLWYIK	770	9	16	25						2822
ENV	ITNWLWYIK	770	9	15	23						2823
ENV	IVGGLIGLR	783	9	42	66						2824
ENV	FAVLSIVNR	794	9	31	48						2825
ENV	VLSIVNRVR	796	9	38	59						2826
ENV	GIEEEGGER	829	9	12	19						2827
ENV	LALAWDDLR	850	9	25	39						2828
ENV	NLCLFSYHR	859	9	11	17						2829
ENV	SLCLFSYHR	859	9	31	48						2830
ENV	CLFSYHRLR	861	9	42	66						2831
ENV	RIVELLGRR	878	9	22	34	0.0550	0.0100	0.1300	0.0021	0.0180	2832
ENV	IAVAEGTDR	927	9	31	48	0.0004	0.0003	0.0003	0.0004	0.0030	2833
ENV	RAILHIPRR	945	9	13	20						2834
ENV	ILHIPRRIR	947	9	13	20						2835
ENV	TVYYGVPVWK	48	10	41	64	3.8000	7.8000				2836
ENV	TTLFCASDAK	61	10	50	78	0.0920	0.2200	0.0019	0.0020	0.0570	2837
ENV	NVTENFNMWK	101	10	31	48						2838
ENV	IISLWDQSLK	121	10	38	59	0.0410	0.0540	0.0017	0.0020	0.0029	2839
ENV	TSAITQACPK	242	10	14	22						2840
ENV	TSVITQACPK	242	10	14	22						2841
ENV	CAPAGFAILK	264	10	29	45						2842
ENV	FAILKCNDKK	269	10	10	16						2843
ENV	STVQCTHGIK	289	10	28	44						2844
ENV	STVQCTHGIR	289	10	23	36						2845

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
ENV	SLAEEEVVIR	311	10	12	19						2846
ENV	CTRPNNNTRK	345	10	22	34						2847
ENV	ATGDIIGDIR	369	10	12	19						2848
ENV	EITTHSFNCR	430	10	11	17						2849
ENV	IINMWQEVGK	492	10	12	19						2850
ENV	GSENGTETFR	538	10	02	18						2851
ENV	PLGVAPTKAK	571	10	19	30						2852
ENV	GVAPTKAKRR	573	10	17	27						2853
ENV	VISTRTHREK	584	10	01	50						2854
ENV	ISTRTHREKR	585	10	01	50						2855
ENV	NIITPHREKR	586	10	01	50						2856
ENV	ASITLTVQAR	619	10	28	44						2857
ENV	IVQQQNNLLR	634	10	25	39	0.0024	0.0190	0.0130	0.0072	0.0035	2858
ENV	IVQQQSNLLR	634	10	26	41						2859
ENV	AIEAQQHLLK	644	10	12	19						2860
ENV	LLKLTVWGIK	651	10	13	20						2861
ENV	LLQLTVWGIK	651	10	34	53	0.0055	0.0110				2862
ENV	MLQLTVWGIK	651	10	10	16						2863
ENV	RVLAVERYLK	665	10	18	28						2864
ENV	RVLAVERYLR	665	10	10	16						2865
ENV	LLGIWGCSGK	678	10	50	78	0.1200	0.0120	0.0017	0.0020	0.0001	2866
ENV	MIVGGLIGLR	782	10	36	56						2867
ENV	AVLSIVNRVR	795	10	31	48						2868
ENV	FLALAWDDLR	849	10	25	39						2869
ENV	RSLCLFSYHR	858	10	31	48						2870
ENV	GLRLGWEGLK	892	10	10	32						2871
ENV	LLQYWSQELK	906	10	12	19						2872
ENV	AIAVAEGTDR	926	10	31	48						2873
ENV	AILHIPRRIR	946	10	12	19						2874
ENV	PTRIRQGLER	951	10	12	19						2875
ENV	VTVYYGVPVWK	47	11	41	64	0.8600	4.1000				2876
ENV	KTTLFCASDAK	60	11	12	19						2877
ENV	TTTLFCASDAK	60	11	22	34						2878
ENV	DIISLWDQSLK	120	11	38	59						2879
ENV	NTSAITQACPK	241	11	14	22						2880
ENV	NTSVITQACPK	241	11	13	20						2881
ENV	VSTVQCTHGIK	288	11	28	44						2882
ENV	VSTVQCTHGIR	288	11	23	36						2883
ENV	GSLAEEEVVIR	310	11	12	19						2884
ENV	YATGDIIGDIR	368	11	11	17						2885
ENV	KLREIRQFENK	405	11	01	25						2886
ENV	HTEGNITLQCR	478	11	01	50						2887
ENV	NANITIPCRIK	478	11	01	50						2888
ENV	QIINMWQEVGK	491	11	12	19						2889
ENV	SSNITGLLLTR	516	11	19	30						2890
ENV	NTETNKTETFR	537	11	01	17						2891
ENV	NTTGNTTETFR	537	11	01	17						2892
ENV	EIFRPGGGDMR	544	11	15	23						2893
ENV	ETFRPGGGDMR	544	11	20	31						2894
ENV	RSELYKYKVVK	558	11	29	45						2895

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
ENV	KIEPLGVAPTK	568	11	15	24						2896
ENV	PLGVAPTKAKR	571	11	19	30						2897
ENV	PTKAKRRVVQR	576	11	13	20						2898
ENV	KAKRRVVQREK	579	11	13	20						2899
ENV	IINIITPHREK	584	11	01	50						2900
ENV	VISTRTHREKR	584	11	01	50						2901
ENV	AASITLTVQAR	618	11	28	44						2902
ENV	GIVQQQNNLLR	633	11	25	39						2903
ENV	GIVQQQSNLLR	633	11	26	41						2904
ENV	HLLKLTVWGIK	650	11	13	20						2905
ENV	HLLQLTVWGIK	650	11	34	53						2906
ENV	TVWGIKQLQAR	655	11	48	75						2907
ENV	QLQARVLAVER	661	11	33	52						2908
ENV	QLLGIWGCSGK	677	11	50	78						2909
ENV	NVPWNSSWSNK	693	11	10	16						2910
ENV	LIEESQNQQEK	740	11	20	31						2911
ENV	IMIVGGLIGLR	781	11	34	54						2912
ENV	IIFAVLSIVNR	792	11	14	22						2913
ENV	IVFAVLSIVNR	792	11	17	27						2914
ENV	FAVLSIVNRVR	794	11	31	48						2915
ENV	GIEEEGGERDR	829	11	12	19						2916
ENV	NLCLFSYHRLR	859	11	11	17						2917
ENV	SLCLFSYHRLR	859	11	31	48						2918
ENV	LLGRRGWEALK	882	11	09	15						2919
ENV	NLLQYWSQELK	905	11	12	19						2920
ENV	IAIAVAEGTDR	925	11	10	16						2921
ENV	TAIAVAEGTDR	925	11	21	33						2922
ENV	RAILHIPRRIR	945	11	12	19						2923
GAG	GARASILR	2	8	10	16						2924
GAG	ASVLSGGK	5	8	29	45						2925
GAG	RLRPGGKK	20	8	49	77						2926
GAG	WASRELER	37	8	48	75						2927
GAG	QTGSEELR	71	8	12	19						2928
GAG	TLYCVHQK	86	8	12	19						2929
GAG	TLYCVHQR	86	8	15	23						2930
GAG	RIEVKDTK	93	8	13	20						2931
GAG	DTKEALDK	98	8	36	56	0.0003	0.0001				2932
GAG	DTKEALEK	98	8	12	19						2933
GAG	KIEEEQNK	105	8	23	36						2934
GAG	PAAADKEK	123	8	01	50						2935
GAG	RTLNAWVK	171	8	63	98	0.0410	0.0560				2936
GAG	WVKVIEEK	176	8	29	45						2937
GAG	WVKVVEEK	176	8	31	48	0.0003	0.0001				2938
GAG	QAAMQMLK	216	8	61	95						2939
GAG	PIAPGQMR	243	8	19	30						2940
GAG	PIPPGQMR	243	8	17	27						2941
GAG	PVAPGQMR	243	8	10	16						2942
GAG	PVGDIYKR	281	8	18	28						2943
GAG	PVGEIYKR	281	8	40	63	0.0003	0.0001				2944
GAG	WIILGLNK	289	8	57	89						2945

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	PTSILDIR	303	8	12	19						2946
GAG	PVSILDIK	303	8	16	25						2947
GAG	PVSILDIR	303	8	25	39						2948
GAG	GVGGPGHK	376	8	37	58	0.0012	0.0018				2949
GAG	GVGGPSHK	376	8	23	36						2950
GAG	ASAQQDLK	392	8	01	50						2951
GAG	ATAQQDLK	392	8	01	50						2952
GAG	AAAIMMQK	400	8	04	19						2953
GAG	AAAIMMQK	405	8	01	25						2954
GAG	SATIMMQR	405	8	01	25						2955
GAG	YTAVFMQR	405	8	02	50						2956
GAG	MMQKSNFK	409	8	10	16						2957
GAG	MMQRGNFK	409	8	10	16						2958
GAG	MMQRGNFR	409	8	23	36						2959
GAG	QMKDCTER	455	8	49	77						2960
GAG	RASVLSGGK	4	9	29	45						2961
GAG	KLDAWEKIR	12	9	16	25						2962
GAG	KLDKWEKIR	12	9	10	16						2963
GAG	DAWEKIRLR	14	9	17	27						2964
GAG	KIRLRPGGK	18	9	44	69						2965
GAG	RLRPGGKKK	20	9	34	53						2966
GAG	LLETSEGCR	52	9	17	27						2967
GAG	ATLYCVHQK	85	9	12	19						2968
GAG	ATLYCVHQR	85	9	15	23	0.0150	0.7100				2969
GAG	MVHQAISPR	163	9	27	42	0.1800	0.0670	1.0000	2.1000	0.8400	2970
GAG	PIPVGEIYK	279	9	35	55	0.0002	0.0012	0.0006	0.0005	0.0003	2971
GAG	ILGLNKIVR	291	9	58	91	0.0008	0.0001	0.0032	0.0100	0.0004	2972
GAG	ILDIKQGPK	306	9	19	30						2973
GAG	ILDIRQGPK	306	9	42	66	0.0420	0.0048	0.0006	0.0006	0.0002	2974
GAG	NSATIMMQR	404	9	01	33						2975
GAG	IMMQKSNFK	408	9	10	16						2976
GAG	IMMQRGNFR	408	9	20	31						2977
GAG	IVKCFNCGK	422	9	13	20						2978
GAG	TIKCFNCGK	422	9	11	17						2979
GAG	TVKCFNCGK	422	9	11	17						2980
GAG	IAKNCRAPR	434	9	18	29	0.0009	0.0003	0.0330	0.0500	0.0039	2981
GAG	IARNCRAPR	434	9	13	21						2982
GAG	LARNCRAPR	434	9	20	32						2983
GAG	KIWPSHKGR	472	9	22	35	0.0770	0.0005	0.4400	0.0087	0.0001	2984
GAG	KIWPSNKGR	472	9	13	21						2985
GAG	KIWPSSKGR	472	9	10	16						2986
GAG	TAPPEESFR	496	9	15	23						2987
GAG	TAPPAESFR	508	9	02	67						2988
GAG	TAPPPESFR	508	9	01	33						2989
GAG	KIRLRPGGKK	18	10	44	69	1.9000	0.0010	0.0008	0.0005	0.0001	2990
GAG	KLKHIVWASR	31	10	13	20						2991
GAG	RLKHLVWASR	31	10	17	27						2992
GAG	IVWASRELER	35	10	20	31	0.0099	0.0066				2993
GAG	LVWASRELER	35	10	26	41						2994
GAG	GLLETSEGCR	51	10	16	25						2995

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	VATLYCVHQK	84	10	12	19						2996
GAG	VATLYCVHQR	84	10	15	23						2997
GAG	KIEEEQNKSK	105	10	15	23						2998
GAG	QMVHQAISPR	162	10	27	42	0.0260	0.0010	0.0740	0.1000	0.0430	2999
GAG	NAWVKVIEEK	174	10	29	45						3000
GAG	NAWVKVVEEK	174	10	30	47	0.0004	0.0002				3001
GAG	IAPGQMREPR	244	10	19	30						3002
GAG	PIPVGEIYKR	279	10	34	53	0.0003	0.0001	0.0009	0.0010	0.0005	3003
GAG	IILGLNKIVR	290	10	57	89	0.0003	0.0006	0.0110	0.0260	0.0073	3004
GAG	YSPTSILDIR	301	10	12	19						3005
GAG	YSPVSILDIK	301	10	16	25						3006
GAG	YSPVSILDIR	301	10	24	38						3007
GAG	SILDIKQGPK	305	10	18	28						3008
GAG	SILDIRQGPK	305	10	40	63	0.3100	0.7100	0.0017	0.0020	0.0060	3009
GAG	YVDRFFKTLR	320	10	27	42						3010
GAG	YVDRFYKTLR	320	10	28	44	0.0003	0.0006				3011
GAG	RAEQASQEVK	329	10	12	19						3012
GAG	RAEQATQDVK	329	10	15	23						3013
GAG	RAEQATQEVK	329	10	27	42						3014
GAG	LVQNANPDCK	346	10	59	92	0.0002	0.0110				3015
GAG	GVGGPGHKAR	376	10	37	58	0.0003	0.0001				3016
GAG	GVGGPSHKAR	376	10	22	34						3017
GAG	TIMMQRGNFR	407	10	12	21						3018
GAG	KTVKCFNCGK	421	10	08	16						3019
GAG	HAKNCRAPR	433	10	18	28						3020
GAG	HARNCRAPR	433	10	13	20						3021
GAG	HLARNCRAPR	433	10	20	31						3022
GAG	IAKNCRAPRK	434	10	16	25						3023
GAG	IARNCRAPRK	434	10	13	21						3024
GAG	LARNCRAPRK	434	10	20	32						3025
GAG	RAPRKKGCWK	439	10	51	80						3026
GAG	FLGKIWPSHK	469	10	23	36	0.0200	0.0013				3027
GAG	FLGKIWPSNK	469	10	13	20						3028
GAG	FLGKIWPSSK	469	10	10	16						3029
GAG	GTRPGNYVQK	480	10	01	50						3030
GAG	GTRPGNYVQR	480	10	01	50						3031
GAG	PTAPPEESFR	495	10	15	23						3032
GAG	PTAPPAESFR	507	10	02	67						3033
GAG	PTAPPPESFR	507	10	01	33						3034
GAG	ITSLPKQEQK	526	10	01	50						3035
GAG	PSQKQEPIDK	528	10	11	18						3036
GAG	GARASVLSGGK	2	11	29	46						3037
GAG	LSGGKLDAWEK	8	11	15	23						3038
GAG	KLDAWEKIRLR	12	11	16	25						3039
GAG	KLDKWEKIRLR	12	11	10	16						3040
GAG	KIRLRPGGKKK	18	11	30	47						3041
GAG	RLRPGGKKKYK	20	11	12	19						3042
GAG	RLRPGGKKKYR	20	11	19	30						3043
GAG	HIVWASRELER	34	11	20	31						3044
GAG	HLVWASRELER	34	11	26	41						3045

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	TVATLYCVHQK	83	11	12	19						3046
GAG	TVATLYCVHQR	83	11	14	22						3047
GAG	EVKDTKEALDK	95	11	13	20						3048
GAG	ALDKIEEEQNK	102	11	17	27						3049
GAG	KIEEEQNKSKK	105	11	15	23						3050
GAG	PAAADKEKDSK	123	11	01	50						3051
GAG	ISPRTLNAWVK	168	11	36	56						3052
GAG	LSPRTLNAWVK	168	11	17	27						3053
GAG	TINEEAAEWDR	225	11	53	83						3054
GAG	HAGPIAPGQMR	240	11	18	28						3055
GAG	HAGPIPPGQMR	240	11	17	27						3056
GAG	PIAPGQMREPR	243	11	19	30						3057
GAG	PIPPGQMREPR	243	11	17	27						3058
GAG	WIILGLNKIVR	289	11	57	89						3059
GAG	TSILDIRQGPK	304	11	12	19						3060
GAG	VSILDIKQGPK	304	11	16	25						3061
GAG	VSILDIRQGPK	304	11	25	39						3062
GAG	DIKQGPKEPFR	308	11	19	30						3063
GAG	DIRQGPKEPFR	308	11	41	64						3064
GAG	LLVQNANPDCK	345	11	58	91						3065
GAG	NANPDCKTILK	349	11	27	42						3066
GAG	NANPDCKTILR	349	11	18	28						3067
GAG	AAIMMQKSNFK	406	11	06	15						3068
GAG	ATIMMQRGNFR	406	11	11	28						3069
GAG	MMQRGNFRNQR	409	11	15	23						3070
GAG	HIAKNCRAPRK	433	11	16	25						3071
GAG	HIARNCRAPRK	433	11	13	20						3072
GAG	HLARNCRAPRK	433	11	20	31						3073
GAG	IAKNCRAPRKK	434	11	14	22						3074
GAG	IARNCRAPRKK	434	11	13	21						3075
GAG	LARNCRAPRKK	434	11	19	30						3076
GAG	CTERQANFLGK	459	11	52	83						3077
GAG	EITSLPKQEQK	525	11	01	50						3078
NEF	AVSQDLDK	48	8	10	16						3079
NEF	AVSRDLEK	48	8	11	17						3080
NEF	PLRPMTFK	102	8	10	16						3081
NEF	PLRPMTYK	102	8	49	77	0.0010	0.0003				3082
NEF	LSFFLKEK	114	8	22	34						3083
NEF	LSHFLKEK	114	8	27	42						3084
NEF	GLIYSKKR	173	8	23	36						3085
NEF	YTPGPGIR	207	8	20	31						3086
NEF	YTPGPGTR	207	8	21	33						3087
NEF	YTPGPGVR	207	8	12	19						3088
NEF	LTFGWCFK	221	8	39	61						3089
NEF	KLVPVDPR	228	8	11	17						3090
NEF	ELHPEFYK	324	8	14	22						3091
NEF	ELHPEYYK	324	8	22	34						3092
NEF	GAVSQDLDK	47	9	10	16						3093
NEF	GAVSRDLEK	47	9	11	17	0.0002	0.0009	0.0004	0.0006	0.0001	3094
NEF	PVRPQVPLR	95	9	48	75						3095

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
NEF	AVDLSHFLK	111	9	14	22	0.0740	1.1000	0.0009	0.0008	0.0025	3096
NEF	DLSFFLKEK	113	9	22	34						3097
NEF	DLSHFLKEK	113	9	27	42						3098
NEF	GLDGLIYSK	125	9	16	25						3099
NEF	GLEGLIYSK	125	9	10	16						3100
NEF	PLTFGWCFK	219	9	39	61						3101
NEF	AADGVGAVSR	42	10	09	15						3102
NEF	QVPLRPMTFK	100	10	10	16						3103
NEF	QVPLRPMTYK	100	10	46	72	0.6100	0.6300	0.0098	0.0130	0.0600	3104
NEF	GAFDLSFFLK	110	10	10	16						3105
NEF	GLDGLIYSKK	125	10	14	22						3106
NEF	GVGAVSQDLDK	45	11	10	16						3107
NEF	GVGAVSRDLEK	45	11	11	17						3108
NEF	AVDLSHFLKEK	111	11	13	20						3109
NEF	GLDGLIYSKKR	125	11	14	22						3110
NEF	MARELHPEYYK	321	11	10	16						3111
POL	RANSPTRR	26	8	16	25						3112
POL	RANSPTSR	26	8	17	27						3113
POL	STNSPTSR	32	8	01	33						3114
POL	RANSPSSR	35	8	01	33						3115
POL	RANSPTTR	37	8	01	50						3116
POL	ILIEICGK	149	8	14	22						3117
POL	LIEICGHK	150	8	10	16						3118
POL	LIEICGKK	150	8	14	22						3119
POL	PIETVPVK	190	8	53	83						3120
POL	ETVPVKLK	192	8	53	83	0.0049	0.0001				3121
POL	GMDGPKVK	201	8	51	80	0.0007	0.0004				3122
POL	PLTEEKIK	212	8	55	86						3123
POL	EICTEMEK	223	8	27	42						3124
POL	NTPIFAIK	246	8	24	38						3125
POL	NTPVFAIK	246	8	37	58	0.0003	0.0003				3126
POL	PIFAIKKK	248	8	25	39						3127
POL	PVFAIKKK	248	8	37	58	0.0003	0.0001				3128
POL	PAGLKKKK	286	8	52	81						3129
POL	PLDKDFRK	308	8	19	30						3130
POL	NVLPQGWK	336	8	63	100	0.0003	0.0012				3131
POL	KILEPFRK	355	8	23	36						3132
POL	DLEIGQHR	381	8	52	81						3133
POL	EIGQHRAK	383	8	27	42						3134
POL	EIGQHRTK	383	8	22	34						3135
POL	RAKIEELR	388	8	26	41						3136
POL	RTKIEELR	388	8	22	34						3137
POL	ELREHLLK	393	8	17	27						3138
POL	ELRQHLLR	393	8	15	23						3139
POL	WTVNDIQK	441	8	62	97	0.0003	0.0001				3140
POL	DIQKLVGK	445	8	62	97						3141
POL	ELELAENR	489	8	53	83						3142
POL	GVYYDPSK	508	8	43	67						3143
POL	DLIAEIQK	516	8	28	44						3144
POL	QIYQEPFK	532	8	41	64	0.0010	0.0013				3145

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	GAHTNDVK	551	8	19	30						3146
POL	SAHTNDVK	551	8	16	25						3147
POL	TAHTNDVK	551	8	11	17						3148
POL	QLTEAVQK	559	8	37	58						3149
POL	QLTEVVQK	559	8	11	17						3150
POL	ESIVIWGK	570	8	50	79						3151
POL	VIWGKTPK	573	8	48	75						3152
POL	KLWYQLEK	616	8	46	72						3153
POL	YVDGAANR	633	8	50	78	0.0003	0.0001				3154
POL	GAANRETK	636	8	45	70						3155
POL	KAGYVTDR	646	8	42	66						3156
POL	VTDRGRQK	650	8	40	63	0.0090	0.0065				3157
POL	LTDTTNQK	661	8	19	30						3158
POL	LTETTNQK	661	8	30	47						3159
POL	IIQAQPDK	697	8	40	63						3160
POL	IIQAQPDR	697	8	16	25						3161
POL	QIIEQLIK	712	8	37	58						3162
POL	IIEQLIKK	713	8	37	58						3163
POL	LAWVPAHK	725	8	22	34						3164
POL	LSWVPAHK	725	8	37	58						3165
POL	KLVSAGIR	742	8	16	25						3166
POL	KLVSSGIR	742	8	29	45						3167
POL	LVSAGIRK	743	8	16	25	0.0091	0.0054				3168
POL	LVSSGIRK	743	8	27	42						3169
POL	KAQEEHEK	759	8	27	43						3170
POL	KAQEEHER	759	8	16	25						3171
POL	NLPPIVAK	779	8	26	41						3172
POL	NLPPVVAK	779	8	27	42						3173
POL	EIVASCDK	787	8	45	70						3174
POL	ETAYFILK	848	8	31	48						3175
POL	ETAYFLLK	848	8	27	42	0.0037	0.0430				3176
POL	FILKLAGR	852	8	32	50						3177
POL	FLLKLAGR	852	8	25	39						3178
POL	LAGRWPVK	856	8	50	78						3179
POL	GVVESMNK	901	8	49	77						3180
POL	ESMNKELK	904	8	53	83						3181
POL	SMNKELKK	905	8	53	83						3182
POL	AVFIHNFK	931	8	62	97	0.0280	0.0380				3183
POL	FIHNFKRK	933	8	58	91						3184
POL	IASDIQTK	956	8	14	22						3185
POL	IATDIQTK	956	8	36	56						3186
POL	ELQKQIIK	964	8	13	21						3187
POL	ELQKQITK	964	8	35	56						3188
POL	IIKIQNFR	969	8	12	19						3189
POL	ITKIQNFR	969	8	36	57						3190
POL	RVYYRDSR	976	8	58	91						3191
POL	DSRDPIWK	981	8	35	55						3192
POL	DSRDPLWK	981	8	14	22						3193
POL	PIWKGPAK	985	8	36	56						3194
POL	PLWKGPAK	985	8	19	30						3195

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	DIKVVPRR	1009	8	48	75						3196
POL	EIKVVPRR	1009	8	16	25						3197
POL	VVPRRKAK	1012	8	52	81	0.0027	0.0001				3198
POL	VVPRRKVK	1012	8	11	17						3199
POL	KIKDYGK	1019	8	11	17						3200
POL	KIRDYGK	1019	8	50	78						3201
POL	LAFPQGEAR	6	9	12	19						3202
POL	LAFQQGEAR	6	9	16	25						3203
POL	QTRANSPTR	21	9	15	24						3204
POL	NSTNSPTSR	31	9	01	33						3205
POL	PTSRELQVR	36	9	01	33						3206
POL	PSSRELQVR	39	9	01	50						3207
POL	TIKIGGQLK	99	9	17	27	0.2700	0.0330	0.0010	0.0008	0.1100	3208
POL	DINLPGKWK	122	9	13	20						3209
POL	EINLPGKWK	122	9	12	19						3210
POL	NLPGKWKPK	124	9	36	56						3211
POL	GIGGFIKVK	136	9	11	17						3212
POL	GIGGFIKVR	136	9	53	83	0.0008	0.0005	0.0062	0.0120	0.0001	3213
POL	QILIEICGK	148	9	14	22						3214
POL	ILIEICGKK	149	9	14	22						3215
POL	PTPVNIIGR	166	9	54	84	0.0008	0.0001	0.0007	0.0120	0.0002	3216
POL	CTEMEKEGK	225	9	28	44	0.0002	0.0001	0.0006	0.0006	0.0002	3217
POL	NTPIFAIKK	246	9	24	38						3218
POL	NTPVFAIKK	246	9	37	58	0.0330	0.0600	0.0006	0.0006	1.7000	3219
POL	AIKKKDSTK	251	9	57	89	0.0017	0.0086	0.0018	0.0005	0.0001	3220
POL	LVDFRELNK	263	9	62	97	0.0110	0.0300	0.0006	0.0006	0.0002	3221
POL	GIPHPAGLK	282	9	56	89	0.2300	0.0650	0.0007	0.0005	0.0110	3222
POL	SVPLDKDFR	306	9	18	28						3223
POL	AIFQSSMTK	347	9	36	56	1.1000	0.9600	0.0076	0.0005	0.0230	3224
POL	MTKILEPFR	353	9	43	67	0.0008	0.0160	0.2200	0.4200	0.3100	3225
POL	TTPDKKHQK	404	9	57	89	0.0002	0.0042	0.0021	0.0029	0.0053	3226
POL	ASQIYAGIK	456	9	27	43	0.0013	0.3400	0.0005	0.0018	0.0001	3227
POL	ASQIYPGIK	456	9	28	44						3228
POL	QIYAGIKVK	458	9	20	32						3229
POL	QIYPGIKVK	458	9	12	19						3230
POL	QIYPGIKVR	458	9	14	22						3231
POL	GIKVKQLCK	462	9	28	44						3232
POL	GIKVRQLCK	462	9	19	30						3233
POL	LAENREILK	492	9	54	84	0.0002	0.0003	0.0004	0.0006	0.0001	3234
POL	NLKTGKYAK	540	9	28	44						3235
POL	NLKTGKYAR	540	9	29	46	0.0008	0.0001	0.0130	0.4400	0.0033	3236
POL	KTGKYAKMR	542	9	19	30						3237
POL	KTGKYARMR	542	9	13	21						3238
POL	RSAHTNDVK	550	9	10	16						3239
POL	IVIWGKTPK	572	9	48	75	0.0850	0.3700	0.9900	0.3000	0.0330	3240
POL	FVNTPPLVK	608	9	54	86	0.0120	0.0660	0.0009	0.0099	0.0380	3241
POL	YVTDRGRQK	649	9	39	61	0.0011	0.0010	0.0006	0.0006	0.0039	3242
POL	SLTDTTNQK	660	9	11	17						3243
POL	SLTETTNQK	660	9	21	33						3244
POL	GIIQAQPDK	696	9	40	63	0.0009	0.0400	0.0006	0.0005	0.0003	3245

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	GHQAQPDR	696	9	16	25						3246
POL	QHEQLIKK	712	9	37	58	0.0091	0.1600	0.0006	0.0005	0.0120	3247
POL	YLAWVPAHK	724	9	22	34	0.0770	0.0570	0.0550	0.8800	4.0000	3248
POL	YLSWVPAHK	724	9	37	58						3249
POL	KLVSAGIRK	742	9	16	25	0.1300	0.0770	0.0017	0.0020	0.0001	3250
POL	KLVSSGIRK	742	9	27	42						3251
POL	VLFLDGIDK	751	9	51	80	0.0380	0.0320	0.0006	0.0006	0.0004	3252
POL	ASCDKCQLK	790	9	43	67	0.0027	0.0140	0.0020	0.0009	0.0001	3253
POL	KLAGRWPVK	855	9	50	78	2.7000	0.0690	0.2100	0.0006	0.0002	3254
POL	AACWWAGIK	880	9	21	33	0.0130	0.0470	0.0023	0.0041	0.0014	3255
POL	ESMNKELKK	904	9	53	83						3256
POL	MAVFIHNFK	930	9	60	94	0.0170	0.3000	0.0480	0.0560	3.2000	3257
POL	AVFIHNFKR	931	9	62	97	0.1700	1.8000	3.5000	0.2700	1.9000	3258
POL	HASDIQTK	955	9	14	22						3259
POL	HATDIQTK	955	9	35	55	0.0250	0.0980	0.0007	0.0005	0.0002	3260
POL	DIQTKELQK	959	9	46	72	0.0009	0.0006	0.0006	0.0018	0.0001	3261
POL	QHKIQNFR	968	9	12	19						3262
POL	QTTKIQNFR	968	9	35	55	0.0021	0.0015	0.2400	0.0660	0.2600	3263
POL	VIQDNSDIK	1003	9	37	58	0.0009	0.0068	0.0006	0.0005	0.0001	3264
POL	VIQDNSEIK	1003	9	12	19						3265
POL	NSDIKVVPR	1007	9	40	63						3266
POL	NSEIKVVPR	1007	9	12	19						3267
POL	DIKVVPRRK	1009	9	48	75	0.0002	0.0001	0.0006	0.0069	0.0065	3268
POL	EIKVVPRRK	1009	9	15	23						3269
POL	KVVPRRKAK	1011	9	52	81	0.0290	0.0039	0.3100	0.0008	0.0002	3270
POL	KVVPRRKVK	1011	9	11	17						3271
POL	NLAFPQGEAR	5	10	10	16						3272
POL	NLAFQQGEAR	5	10	16	25						3273
POL	QTRANSPTRR	21	10	11	18						3274
POL	QTRANSPTSR	21	10	12	19						3275
POL	PSRANSPTSR	24	10	01	50						3276
POL	QTRANSPSSR	33	10	01	33						3277
POL	QTRANSPTTR	35	10	01	33						3278
POL	VTIKIGGQLK	98	10	17	27	0.0370	0.2100	0.0017	0.0025	0.0640	3279
POL	VLEDINLPGK	119	10	13	20						3280
POL	VLEEINLPGK	119	10	12	19						3281
POL	MIGGIGGFIK	133	10	62	97	0.0099	0.0550	0.0052	0.0012	0.3100	3282
POL	QILIEICGKK	148	10	14	22						3283
POL	ISPIETVPVK	188	10	53	83	0.0003	0.0310	0.0017	0.0025	0.0001	3284
POL	PIETVPVKLK	190	10	53	83	0.0002	0.0001	0.0009	0.0009	0.0003	3285
POL	KLKPGMDGPK	197	10	49	77	0.3900	0.0760				3286
POL	LVEICTEMEK	221	10	15	24	0.0002	0.0120	0.0010	0.0013	0.0024	3287
POL	EMEKEGKISK	229	10	33	52	0.0004	0.0001	0.0009	0.0009	0.0003	3288
POL	NTPIFAIKKK	246	10	24	38						3289
POL	NTPVFAIKKK	246	10	37	58	0.0006	0.0046				3290
POL	FAIKKKDSTK	250	10	57	89	0.0004	0.0002				3291
POL	KLVDFRELNK	262	10	62	97	0.5100	0.0900				3292
POL	LVDFRELNKR	263	10	60	94						3293
POL	GIPHPAGLKK	282	10	54	86	0.0110	0.1700	0.0009	0.0009	0.0007	3294
POL	DAYFSVPLDK	302	10	21	33						3295

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	FSVPLDKDFR	305	10	18	28						3296
POL	SVPLDKDFRK	306	10	18	28						3297
POL	SINNETPGIR	323	10	32	50						3298
POL	STNNETPGIR	323	10	11	17						3299
POL	PAIFQSSMTK	346	10	36	56	0.0760	0.0830	0.0017	0.0025	0.0046	3300
POL	SMTKILEPFR	352	10	42	66	0.0004	0.0004				3301
POL	MTKILEPFRK	353	10	22	34	0.0150	0.0380	0.0150	0.0060	0.1100	3302
POL	GSDLEIGQHR	379	10	52	81						3303
POL	DLEIGQHRAK	381	10	27	42						3304
POL	DLEIGQHRTK	381	10	21	33						3305
POL	FTTPDKKHQK	403	10	51	80	0.0002	0.0150	0.0010	0.0013	0.0273	3306
POL	WMGYELHPDK	418	10	60	94	0.0005	0.0004	0.0009	0.0016	0.0003	3307
POL	TVQPIQLPEK	429	10	17	27						3308
POL	TVQPIVLPEK	429	10	13	20	0.1600	5.6000				3309
POL	DSWTVNDIQK	439	10	43	67	0.0007	0.0002				3310
POL	ESWTVNDIQK	439	10	11	17						3311
POL	WASQIYAGIK	455	10	27	42						3312
POL	WASQIYPGIK	455	10	28	44						3313
POL	KVKQLCKLLR	464	10	27	42						3314
POL	KVRQLCKLLR	464	10	19	30						3315
POL	QLCKLLRGAK	467	10	25	39						3316
POL	QLCKLLRGTK	467	10	21	33						3317
POL	EAELELAENR	487	10	53	83						3318
POL	ELAENREILK	491	10	54	84	0.0002	0.0003				3319
POL	ATESIVIWGK	568	10	19	30						3320
POL	SIVIWGKTPK	571	10	42	66						3321
POL	VIWGKTPKFK	573	10	17	27						3322
POL	VIWGKTPKFR	573	10	29	45						3323
POL	LVKLWYQLEK	614	10	46	72	0.0560	0.0820	0.0075	0.0081	0.0097	3324
POL	AANRETKLGK	637	10	30	47	0.0007	0.0016				3325
POL	KAGYVTDRGR	646	10	39	61						3326
POL	VSLTDTTNQK	659	10	10	16						3327
POL	VSLTETTNQK	659	10	20	31						3328
POL	VSQIIEQLIK	710	10	19	30	0.0007	0.0370	0.0017	0.0025	0.0007	3329
POL	IIEQLIKKEK	713	10	30	47	0.0004	0.0003	0.0009	0.0008	0.0003	3330
POL	GIGGNEQVDK	733	10	58	91	0.0005	0.0001	0.0009	0.0009	0.0003	3331
POL	KVLFLDGIDK	750	10	48	75	0.3600	0.7800				3332
POL	VASCDKCQLK	789	10	43	67	0.0004	0.0004				3333
POL	QLDCTHLEGK	814	10	60	95	0.0010	0.0003				3334
POL	GSNFTSAAVK	870	10	26	41						3335
POL	GSNFTSTTVK	870	10	11	17						3336
POL	KAACWWAGIK	879	10	20	32	0.0300	0.0740	0.0017	0.0025	0.0002	3337
POL	VVESMNKELK	902	10	48	75						3338
POL	ELKKIIGQVR	909	10	56	88						3339
POL	QVRDQAEHLK	916	10	44	69	0.0089	0.0093				3340
POL	QVREQAEHLK	916	10	13	20						3341
POL	QMAVFIHNFK	929	10	60	94	0.6100	0.6400	0.0240	0.0083	0.0610	3342
POL	MAVFIHNFKR	930	10	60	94	0.0068	0.0083				3343
POL	AVFIHNFKRK	931	10	58	91	0.6600	0.8500				3344
POL	GIGGYSAGER	942	10	58	91	0.0003	0.0001	0.0010	0.0029	0.0003	3345

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	DIIASDIQTK	954	10	14	22						3346
POL	DIIATDIQTK	954	10	34	53	0.0056	0.0130	0.0017	0.0025	0.0170	3347
POL	KIQNFRVYYR	971	10	52	81	0.0320	0.2100	6.6000	0.0850	0.0380	3348
POL	VVIQDNSDIK	1002	10	37	58	0.0005	0.0210	0.0010	0.0013	0.0018	3349
POL	VVIQDNSEIK	1002	10	12	19						3350
POL	NSDIKVVPRR	1007	10	40	63	0.0007	0.0001				3351
POL	NSEIKVVPRR	1007	10	12	19						3352
POL	KAKIIRDYGK	1017	10	41	64	0.0048	0.0018				3353
POL	MAGDDCVAGR	1028	10	24	38						3354
POL	MAGDECVASR	1028	10	19	30						3355
POL	NSPTSRELQVR	34	11	01	33						3356
POL	NSPSSRELQVR	37	11	01	50						3357
POL	NSPTTRELQVR	39	11	01	50						3358
POL	FSFPQITLWQR	85	11	14	22						3359
POL	TLWQRPLVTIK	91	11	17	27						3360
POL	TLWQRPLVTVK	91	11	13	20						3361
POL	LVTIKIGGQLK	97	11	13	20						3362
POL	TVLEDINLPGK	118	11	13	20						3363
POL	TVLEEINLPGK	118	11	12	19						3364
POL	DINLPGKWKPK	122	11	13	20						3365
POL	EINLPGKWKPK	122	11	12	19						3366
POL	KMIGGIGGFIK	132	11	62	97	2.3000	0.7000				3367
POL	PISPIETVPVK	187	11	53	83						3368
POL	KVKQWPLTEEK	207	11	46	72	0.0750	0.0330				3369
POL	ALVEICTEMEK	220	11	15	23						3370
POL	EICTEMEKEGK	223	11	27	42						3371
POL	AIKKKDSTKWR	251	11	57	89						3372
POL	STKWRKLVDFR	257	11	58	91						3373
POL	KLVDFRELNKR	262	11	60	94						3374
POL	QLGIPHPAGLK	280	11	56	89						3375
POL	GIPHPAGLKKK	282	11	53	84						3376
POL	FSVPLDKDFRK	305	11	18	28						3377
POL	PSINNETPGIR	322	11	31	48						3378
POL	PSTNNETPGIR	322	11	11	17						3379
POL	SSMTKILEPFR	351	11	32	50						3380
POL	SMTKILEPFRK	352	11	22	34						3381
POL	KIEELREHLLK	390	11	13	20						3382
POL	KIEELRQHLLR	390	11	15	23						3383
POL	LLKWGFTTPDK	398	11	23	36						3384
POL	LLRWGFTTPDK	398	11	23	36						3385
POL	WTVQPIQLPEK	428	11	17	27						3386
POL	WTVQPIVLPEK	428	11	13	20	0.0011	0.0510				3387
POL	TVNDIQKLVGK	442	11	61	95	0.0400	0.1700				3388
POL	ASQIYAGIKVK	456	11	20	32						3389
POL	ASQIYPGIKVK	456	11	12	19						3390
POL	ASQIYPGIKVR	456	11	14	22						3391
POL	YAGIKVKQLCK	460	11	18	28						3392
POL	PVIIGVYYDPSK	505	11	39	61						3393
POL	PSKDLIAEIQK	513	11	25	39						3394
POL	WTYQIYQEPFK	529	11	40	63	0.9200	0.0540				3395

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	QIYQEPFKNLK	532	11	40	63	0.2800	0.2900				3396
POL	NLKTGKYAKMR	540	11	18	29						3397
POL	NLKTGKYARMR	540	11	13	21						3398
POL	RMRGAHTNDVK	548	11	12	19						3399
POL	DVKQLTEAVQK	556	11	33	52	0.0048	0.0240				3400
POL	IATESIVIWGK	567	11	14	22						3401
POL	ESIVIWGKTPK	570	11	41	65						3402
POL	IVIWGKTPKFK	572	11	17	27						3403
POL	IVIWGKTPKFR	572	11	29	45						3404
POL	KTPKFKLPIQK	577	11	14	22						3405
POL	KTPKFRLPIQK	577	11	22	34						3406
POL	PLVKLWYQLEK	613	11	45	70						3407
POL	ETFYVDGAANR	630	11	43	67						3408
POL	YVDGAANRETK	633	11	44	69						3409
POL	GAANRETKLGK	636	11	30	47						3410
POL	KLGKAGYVTDR	643	11	24	38						3411
POL	VVSLTDTTNQK	658	11	10	16						3412
POL	VVSLTETTNQK	658	11	11	17						3413
POL	ALGIIQAQPDK	694	11	39	61						3414
POL	ALGIIQAQPDR	694	11	15	23						3415
POL	LVNQIIEQLIK	709	11	15	23						3416
POL	LVSQIIEQLIK	709	11	18	28						3417
POL	VSQIIEQLIKK	710	11	19	30						3418
POL	QIIEQLIKKEK	712	11	30	47						3419
POL	KVYLAWVPAHK	722	11	20	32	8.6000	2.3000				3420
POL	KVYLSWVPAHK	722	11	23	37						3421
POL	QVDKLVSAGIR	739	11	15	23						3422
POL	QVDKLVSSGIR	739	11	29	45						3423
POL	GIDKAQEEHEK	756	11	25	39						3424
POL	GIDKAQEEHER	756	11	14	22						3425
POL	VAKEIVASCDK	784	11	45	71						3426
POL	IVASCDKCQLK	788	11	43	67	0.0970	0.1000				3427
POL	TAYFILKLAGR	849	11	31	48						3428
POL	TAYFLLKLAGR	849	11	24	38						3429
POL	ILKLAGRWPVK	853	11	30	47						3430
POL	LLKLAGRWPVK	853	11	20	31						3431
POL	QSQGVVESMNK	898	11	49	77						3432
POL	GVVESMNKELK	901	11	48	75						3433
POL	VVESMNKELKK	902	11	48	75						3434
POL	QMAVFIHNFKR	929	11	60	94						3435
POL	MAVFIHNFKRK	930	11	57	89						3436
POL	ASDIQTKELQK	957	11	11	17						3437
POL	ATDIQTKELQK	957	11	35	55	0.0051	0.1800				3438
POL	QTKELQKQIIK	961	11	10	16						3439
POL	QTKELQKQITK	961	11	32	50	0.0050	0.0100				3440
POL	AVVIQDNSDIK	1000	11	37	58	0.0004	0.0150				3441
POL	AVVIQDNSEIK	1000	11	12	19						3442
POL	NSDIKVVPRRK	1007	11	40	63						3443
POL	NSEIKVVPRRK	1007	11	11	17						3444
POL	DIKVVFRRKAK	1009	11	39	61						3445

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	EIKVVPRRKAK	1009	11	13	20						3446
POL	VVPRRKAKIIR	1012	11	42	66						3447
POL	QMAGDDCVAGR	1027	11	24	38						3448
POL	QMAGDDCVASR	1027	11	19	30						3449
REV	DSDEELLK	7	8	12	19						3450
REV	QARKNRRR	40	8	17	27						3451
REV	QARRNRRR	40	8	38	59						3452
REV	RARQRQIR	50	8	12	19						3453
REV	ILSTCLGR	63	8	12	19						3454
REV	GTETGVGR	103	8	06	19						3455
REV	LLKTVRLIK	12	9	10	16						3456
REV	GTRQARKNR	36	9	15	23						3457
REV	GTRQARRNR	36	9	34	53						3458
REV	GTRQTRKNR	37	9	01	50						3459
REV	TTRQARRNR	37	9	01	50						3460
REV	QARKNRRRR	40	9	16	25						3461
REV	QARRNRRRR	40	9	38	59						3462
REV	RILSTCLGR	62	9	12	19						3463
REV	PLQLPPIER	76	9	11	17						3464
REV	PLQLPPLER	76	9	35	55						3465
REV	PSPEGTRQAR	31	10	13	20						3466
REV	GTRQARKNRR	36	10	15	23						3467
REV	GTRQARRNRR	36	10	34	53						3468
REV	GTRQTRKNRR	37	10	01	50						3469
REV	TTRQARRNRR	37	10	01	50						3470
REV	RSGDSDEELLK	4	11	11	17						3471
REV	PSPEGTRQARR	31	11	13	20						3472
REV	GTRQARKNRRR	36	11	14	22						3473
REV	GTRQARRNRRR	36	11	34	53						3474
REV	GTRQTRKNRRR	37	11	01	50						3475
REV	TTRQARRNRRR	37	11	01	50						3476
REV	QARKNRRRRWR	40	11	16	25						3477
REV	QARRNRRRRWR	40	11	37	58						3478
REV	PVPLQLPPIER	74	11	11	17						3479
REV	PVPLQLPPLER	74	11	34	53						3480
TAT	GLGISYGR	45	8	55	87						3481
TAT	GISYGRKK	47	8	58	91						3482
TAT	ISYGRKKR	48	8	58	91						3483
TAT	PTGPKESK	88	8	20	31						3484
TAT	TACNNCYCK	23	9	17	27						3485
TAT	TACTNCYCK	23	9	10	16						3486
TAT	GLGISYGRK	45	9	55	87	0.0340	0.0006	0.0017	0.0020	0.0001	3487
TAT	GISYGRKKR	47	9	57	89	0.0008	0.0005	0.0018	0.0014	0.0001	3488
TAT	ISYGRKKRR	48	9	46	72	0.0008	0.0005	0.3900	0.1300	0.0032	3489
TAT	PTGPKESKK	88	9	18	28						3490
TAT	ESKKKVESK	93	9	12	19						3491
TAT	PVDPRLEPWK	3	10	11	17	0.0005	0.0001				3492
TAT	TACNNCYCKK	23	10	11	17						3493
TAT	GLGISYGRKK	45	10	55	87						3494
TAT	GISYGRKKRR	47	10	45	70	0.0003	0.0001				3495

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
TAT	PTGPKESKKK	88	10	12	19						3496
TAT	KAGPGGYPRR	101	10	01	50						3497
TAT	GLGISYGRKKR	45	11	54	86						3498
TAT	ISYGRKKRRQR	48	11	39	61						3499
TAT	KAGPGGYPRRK	101	11	01	50						3500
VIF	LIVWQVDR	8	8	10	16						3501
VIF	MIVWQVDR	8	8	46	72						3502
VIF	QVDRMKIR	12	8	13	20						3503
VIF	QVDRMRIR	12	8	34	53						3504
VIF	RMRINTWK	15	8	10	16						3505
VIF	RMRIRTWK	15	8	15	23						3506
VIF	RTWKSLVK	19	8	15	23						3507
VIF	RTWNSLVK	19	8	27	42						3508
VIF	HIPLGDAR	56	8	13	20						3509
VIF	HIPLGEAR	56	8	20	31						3510
VIF	GVSIEWRK	87	8	16	25						3511
VIF	VSIEWRLR	88	8	15	23						3512
VIF	SIEWRLRR	89	8	11	17						3513
VIF	FSDSAIRK	120	8	13	20						3514
VIF	FSESAIRK	120	8	14	22						3515
VIF	SLQYLALK	149	8	13	20						3516
VIF	LALTALIK	153	8	16	25						3517
VIF	LTALIKPK	155	8	13	20						3518
VIF	TALIKPKK	156	8	11	17						3519
VIF	LIKPKKIK	158	8	10	16						3520
VIF	LTEDRWNK	178	8	31	48	0.0003	0.0045				3521
VIF	LVEDRWNK	178	8	11	17						3522
VIF	VMIVWQVDR	7	9	44	69	0.0034	0.0220	4.8000	5.5000	0.0010	3523
VIF	IVWQVDRMK	9	9	12	19						3524
VIF	IVWQVDRMR	9	9	47	73	0.0008	0.0007	0.4500	0.5600	0.0048	3525
VIF	GVSIEWRLR	87	9	14	22						3526
VIF	VSIEWRLRR	88	9	11	17						3527
VIF	GSLQYLALK	148	9	13	20						3528
VIF	YLALTALIK	152	9	16	25						3529
VIF	ALTALIKPK	154	9	13	20						3530
VIF	LTALIKPKK	155	9	11	17						3531
VIF	ALIKPKKIK	157	9	10	16						3532
VIF	SVKKLTEDR	174	9	13	20						3533
VIF	KLTEDRWNK	177	9	29	45	0.0130	0.2700	0.0680	0.0006	0.0002	3534
VIF	KLVEDRWNK	177	9	11	17						3535
VIF	QVMIVWQVDR	6	10	43	67						3536
VIF	MIVWQVDRMR	8	10	43	67	0.0062	0.0001				3537
VIF	KIRTWNSLVK	17	10	12	19						3538
VIF	RIRTWKSLVK	17	10	15	23						3539
VIF	RIRTWNSLVK	17	10	15	23						3540
VIF	LVKHHMYVSK	24	10	12	19						3541
VIF	EVHHPLGDAR	54	10	13	20						3542
VIF	EVHHPLGEAR	54	10	20	31						3543
VIF	GVSIEWRLRR	87	10	10	16						3544
VIF	LALTALIKPK	153	10	13	20						3545

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
VIF	ALTALIKPKK	154	10	11	17						3546
VIF	PSVKKLTEDR	173	10	13	20						3547
VIF	VMIVWQVDRMR	7	11	41	64						3548
VIF	IVWQVDRMKIR	9	11	12	19						3549
VIF	IVWQVDRMRIR	9	11	33	52						3550
VIF	QVDRMRINTWK	12	11	10	16						3551
VIF	QVDRMRIRTWK	12	11	14	22						3552
VIF	SLVKHHMYVSK	23	11	12	19						3553
VIF	LVKHHMYVSKK	24	11	12	19						3554
VIF	TTYWGLHTGER	69	11	22	34						3555
VIF	HLGHGVSIEWR	83	11	22	34						3556
VIF	HLGQGVSIEWR	83	11	25	39						3557
VIF	YLALTALIKPK	152	11	13	20						3558
VIF	LALTALIKPKK	153	11	11	17						3559
VIF	LTEDRWNKPQK	178	11	21	33	0.0390	0.0130				3560
VIF	LVEDRWNKPQK	178	11	10	16						3561
VPR	ELKNEAVR	25	8	17	27						3562
VPR	ELKSEAVR	25	8	16	25						3563
VPR	EAVRHFPR	29	8	59	92						3564
VPR	QLLFIHFR	66	8	44	69						3565
VPR	QLLFVHFR	66	8	10	16						3566
VPR	RIGCQHSR	74	8	47	73						3567
VPR	RIGCRHSR	74	8	12	19						3568
VPR	HSRIGIIR	79	8	10	16						3569
VPR	HSRIGITR	79	8	11	17						3570
VPR	RIGITRQR	81	8	10	16						3571
VPR	#LPGRRGR	85	8	01	50						3572
VPR	NIRGRRVR	85	8	01	50						3573
VPR	RARNGASR	93	8	19	30						3574
VPR	ALELLEELK	19	9	10	16						3575
VPR	TLELLEELK	19	9	44	69						3576
VPR	WAGVEAIIR	54	9	16	25						3577
VPR	FIHFRIGCR	69	9	11	17						3578
VPR	RIGITRQRR	81	9	10	16						3579
VPR	QAPEDQGPQR	3	10	39	62						3580
VPR	WALELLEELK	18	10	09	15						3581
VPR	WTLELLEELK	18	10	42	69						3582
VPR	KSEAVRHFPR	27	10	14	22						3583
VPR	HSRIGITRQR	79	10	10	16						3584
VPR	LLEELKNEAVR	22	11	17	27						3585
VPR	LLEELKSEAVR	22	11	16	25						3586
VPR	DTWAGVEAIIR	52	11	16	25						3587
VPR	DTWEGVEAIIR	52	11	18	28						3588
VPR	ILQQLLFIHFR	63	11	35	55						3589
VPR	LLFIHFRIGCR	67	11	11	17						3590
VPR	HSRIGITRQRR	79	11	10	16						3591
VPU	TIVFIEYR	35	8	10	16						3592
VPU	IVFIEYRK	36	8	12	19						3593
VPU	LVQRKQDR	43	8	01	50						3594
VPU	KIDRLIDR	52	8	15	23						3595

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
VPU	LIDRIRER	58	8	14	22						3596
VPU	VTLLSSSK	94	8	01	50						3597
VPU	WTIVFIEYR	34	9	10	16						3598
VPU	LVQRKQDRR	43	9	01	50						3599
VPU	ILRQRKIDR	46	9	15	23						3600
VPU	RLIDRIRER	56	9	10	16						3601
VPU	LVTLLSSSK	91	9	01	50						3602
VPU	KILRQRKIDR	45	10	15	23	0.0039	0.0001				3603
VPU	KIDRLIDRIR	52	10	10	16						3604
VPU	VVWTIVFIEYR	31	11	10	16						3605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	LILGLVII	21	8	09	15		3606
ENV	KLWVTVYY	44	8	11	17		3607
ENV	NLWVTVYY	44	8	35	56		3608
ENV	VYYGVPVW	49	8	55	86		3609
ENV	DTEVHNVW	75	8	19	30		3610
ENV	NVTENFNM	101	8	34	53		3611
ENV	VTENFNMW	102	8	34	53		3612
ENV	SLKPCVKL	128	8	55	86		3613
ENV	LTPLCVTL	135	8	54	84		3614
ENV	HYCAPAGF	262	8	27	42		3615
ENV	HYCTPAGF	262	8	11	17		3616
ENV	CTPAGFAI	264	8	10	16		3617
ENV	TVQCTHGI	290	8	51	80		3618
ENV	PVVSTQLL	300	8	60	94		3619
ENV	VVSTQLLL	301	8	60	94		3620
ENV	QLLLNGSL	305	8	57	89		3621
ENV	NTRKSIRI	351	8	10	16		3622
ENV	RIGPGQTF	357	8	11	17		3623
ENV	GIGPGQTF	360	8	01	33		3624
ENV	SIGSGQAF	360	8	01	33		3625
ENV	FYATGDII	367	8	12	19		3626
ENV	KLREHRQF	405	8	01	25		3627
ENV	SFNCGGEF	437	8	36	56		3628
ENV	SFNCRGEF	437	8	16	25		3629
ENV	FYCNTSGL	445	8	21	33		3630
ENV	HTEGNITL	478	8	01	50		3631
ENV	NITLPCRI	482	8	11	17		3632
ENV	TITLPCRI	482	8	14	22		3633
ENV	RIKQIINM	488	8	30	47		3634
ENV	RIKQIVNM	488	8	12	19		3635
ENV	QIRCSSNI	512	8	11	17		3636
ENV	STNGTETF	537	8	01	17		3637
ENV	KVVKIEPL	565	8	25	39		3638
ENV	AVGIGAVF	595	8	11	17		3639
ENV	STMGAASI	614	8	39	61		3640
ENV	LTVQARQL	623	8	38	59		3641
ENV	TVQARQLL	624	8	36	56		3642
ENV	IVQQQNNL	634	8	26	41		3643
ENV	IVQQQSNL	634	8	32	50		3644
ENV	AIEAQQHL	644	8	49	77		3645
ENV	HLLKLTVW	650	8	13	20		3646
ENV	HLLQLTVW	650	8	34	53		3647
ENV	HMLQLTVW	650	8	10	16		3648
ENV	TVWGIKQL	655	8	59	92		3649
ENV	RVLAVERY	665	8	33	52		3650
ENV	VLAVERYL	666	8	34	53		3651
ENV	RYLKDQQL	671	8	30	47		3652
ENV	RYLRDQQL	671	8	18	28		3653
ENV	YLKDQQLL	672	8	31	48	0.0001	3654
ENV	YLRDQQLL	672	8	18	28		3655

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	IWGCSGKL	681	8	48	75		3656
ENV	NVPWNSSW	693	8	13	20		3657
ENV	EIWDNMTW	716	8	13	20		3658
ENV	IWDNMTWM	717	8	11	17		3659
ENV	IWNNMTWM	717	8	17	27		3660
ENV	WMEWEREI	723	8	12	19		3661
ENV	DLLALDKW	754	8	21	33		3662
ENV	ELLELDKW	754	8	20	31		3663
ENV	ALDKWASL	757	8	11	17		3664
ENV	ELDKWASL	757	8	18	28		3665
ENV	KWASLWNW	760	8	26	41		3666
ENV	SLWNWFDI	763	8	17	27		3667
ENV	WFDITNWL	767	8	10	16		3668
ENV	DITNWLWY	769	8	10	16		3669
ENV	ITKWLWYI	770	8	16	25		3670
ENV	ITNWLWYI	770	8	19	30		3671
ENV	KWLWYIKI	772	8	19	30		3672
ENV	NWLWYIKI	772	8	25	39		3673
ENV	WLWYIKIF	773	8	50	78		3674
ENV	LWYIKIFI	774	8	49	77		3675
ENV	WYIKIFIM	775	8	43	67		3676
ENV	YIKIFIMI	776	8	43	67		3677
ENV	FIMIVGGL	780	8	44	69		3678
ENV	IMIVGGLI	781	8	35	56		3679
ENV	IVGGLIGL	783	8	42	66		3680
ENV	IVGGLVGL	783	8	10	16		3681
ENV	GLIGLRII	786	8	15	23		3682
ENV	LIGLRIIF	787	8	16	25		3683
ENV	LIGLRIVF	787	8	29	45		3684
ENV	IIFAVLSI	792	8	15	23		3685
ENV	IVFAVLSI	792	8	20	31		3686
ENV	PLSFQTLL	809	8	10	16		3687
ENV	SIRLVNGF	842	8	13	20		3688
ENV	SIRLVSGF	842	8	13	20		3689
ENV	LVNGFLAL	845	8	14	22		3690
ENV	LVSGFLAL	845	8	19	30		3691
ENV	AWDDLRSL	853	8	20	31		3692
ENV	DLRNLCLF	856	8	17	27		3693
ENV	DLRSLCLF	856	8	38	59		3694
ENV	CLFSYHRL	861	8	42	66		3695
ENV	SYHRLRDF	864	8	18	28		3696
ENV	SYHRLRDL	864	8	23	36		3697
ENV	RLRDLLLI	867	8	13	20		3698
ENV	ELLGHSSL	881	8	09	15		3699
ENV	ELLGRRGW	881	8	23	37		3700
ENV	GWEALKYL	896	8	12	19		3701
ENV	GWEGLKYL	896	8	12	19		3702
ENV	YWWNLLQY	902	8	15	23		3703
ENV	WWNLLQYW	903	8	15	23		3704
ENV	SLLNATAI	920	8	14	22		3705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	ILIIPRRI	947	8	13	20		3706
ENV	PTRIRQGL	951	8	12	19		3707
ENV	TVYYGVPVW	48	9	55	86		3708
ENV	VWKEATTTL	55	9	22	34	0.0300	3709
ENV	PTDPNPQEI	89	9	25	39		3710
ENV	NVTENFNMW	101	9	34	53		3711
ENV	NFNMWKNDM	105	9	12	19		3712
ENV	NFNMWKNNM	105	9	18	28		3713
ENV	MVEQMHEDI	113	9	23	36		3714
ENV	QMHEDHSL	116	9	29	45		3715
ENV	IISLWDQSL	121	9	38	59		3716
ENV	VISLWDQSL	121	9	10	16		3717
ENV	KLTPLCVTL	134	9	52	81		3718
ENV	EIKNCSFNI	181	9	13	20		3719
ENV	LINCNTSAI	237	9	15	23		3720
ENV	KVSFEPIPI	252	9	30	47		3721
ENV	SFEPIPIIY	254	9	31	48		3722
ENV	ILKCNDKKF	271	9	12	19		3723
ENV	STVQCTHGI	289	9	51	80		3724
ENV	PVVSTQLLL	300	9	60	94		3725
ENV	SLAEEEVVI	311	9	13	20		3726
ENV	RIGPGQTFY	357	9	11	17		3727
ENV	GIGPGQTFY	360	9	01	33		3728
ENV	SIGSGQAFY	360	9	01	33		3729
ENV	ATGDIIGDI	369	9	12	19		3730
ENV	DIRQAHCNI	380	9	15	23		3731
ENV	DLEITTHSF	428	9	21	33		3732
ENV	SFNCGGEFF	437	9	35	55		3733
ENV	SFNCRGEFF	437	9	16	25		3734
ENV	FFYCNTSGL	444	9	21	33		3735
ENV	FYCNTSGLF	445	9	21	33		3736
ENV	TLPCRIKQI	484	9	26	41		3737
ENV	RIKQIINMW	488	9	30	47		3738
ENV	RIKQIVNMW	488	9	12	19		3739
ENV	MWQEVGKAM	495	9	15	23		3740
ENV	MWQRVGQAM	495	9	10	16		3741
ENV	IFRPGGGDM	545	9	17	27		3742
ENV	TFRPGGGDM	545	9	25	39		3743
ENV	NWRSELYKY	556	9	54	84		3744
ENV	LYKYKVVEI	561	9	13	20		3745
ENV	LYKYKVVKI	561	9	29	45	0.0200	3746
ENV	AVGIGAVFL	595	9	11	17		3747
ENV	GIGAVFLGF	598	9	11	18		3748
ENV	MLGAMFLGF	599	9	04	36		3749
ENV	TIGAMFLGF	599	9	03	27		3750
ENV	FLGAAGSTM	608	9	55	86		3751
ENV	TMGAASITL	615	9	39	61		3752
ENV	TLTVQARQL	622	9	37	58		3753
ENV	LTVQARQLL	623	9	36	56		3754
ENV	GIVQQQNNL	633	9	26	41		3755

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	GIVQQQSNL	633	9	32	50		3756.
ENV	IVQQQNNLL	634	9	26	41		3757
ENV	IVQQQSNLL	634	9	32	50		3758
ENV	AIEAQQHLL	644	9	48	75		3759
ENV	LLKLTVWGI	651	9	13	20		3760
ENV	LLQLTVWGI	651	9	34	53		3761
ENV	MLQLTVWGI	651	9	10	16		3762
ENV	LTVWGIKQL	654	9	59	92		3763
ENV	RVLAVERYL	665	9	33	52		3764
ENV	RYLKDQQLL	671	9	29	45	0.7600	3765
ENV	RYLRDQQLL	671	9	17	27	0.2300	3766
ENV	GIWGCSGKL	680	9	48	75		3767
ENV	IWGCSGKLI	681	9	48	75	0.0270	3768
ENV	LICTTAVPW	688	9	19	30		3769
ENV	LICTTNVPW	688	9	17	27		3770
ENV	LICTTTVPW	688	9	12	19		3771
ENV	TWMEWEREI	722	9	12	19		3772
ENV	EWEREIDNY	725	9	11	17		3773
ENV	ALDKWASLW	757	9	11	17		3774
ENV	ELDKWASLW	757	9	18	28		3775
ENV	KWASLWNWF	760	9	26	41		3776
ENV	WFDITNWLW	767	9	10	16		3777
ENV	DITNWLWYI	769	9	10	16		3778
ENV	KWLWYIKIF	772	9	16	25		3779
ENV	NWLWYIKIF	772	9	25	39		3780
ENV	WLWYIKIFI	773	9	49	77		3781
ENV	LWYIKIFIM	774	9	43	67		3782
ENV	WYIKIFIMI	775	9	43	67		3783
ENV	IFIMIVGGL	779	9	41	64		3784
ENV	FIMIVGGLI	780	9	35	55		3785
ENV	MIVGGLIGL	782	9	36	56		3786
ENV	GLIGLRIIF	786	9	15	23		3787
ENV	GLIGLRIVF	786	9	29	45		3788
ENV	GLRIIFAVL	789	9	17	27		3789
ENV	GLRIVFAVL	789	9	28	44		3790
ENV	RIIFAVLSI	791	9	14	22		3791
ENV	RIVFAVLSI	791	9	19	30		3792
ENV	IVNRVRQGY	799	9	38	59		3793
ENV	RVRQGYSPL	802	9	55	86		3794
ENV	SIRLVNGFL	842	9	11	17		3795
ENV	SIRLVSGFL	842	9	13	20		3796
ENV	RLVNGFLAL	844	9	12	19		3797
ENV	RLVSGFLAL	844	9	19	30		3798
ENV	FLALAWDDL	849	9	25	39		3799
ENV	SYHRLRDFI	864	9	13	20		3800
ENV	SYHRLRDLL	864	9	14	22		3801
ENV	LIAARTVEL	873	9	12	19		3802
ENV	SLKGLRLGW	889	9	11	39		3803
ENV	SLRGLQRGW	889	9	05	18		3804
ENV	GLRLGWEGL	892	9	10	32		3805

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	HLGWEGLKY	894	9	09	29		3806
ENV	KYWWNLLQY	901	9	14	22		3807
ENV	YWWNLLQYW	902	9	15	23		3808
ENV	LLQYWSQEL	906	9	16	25		3809
ENV	ELKNSAINL	913	9	10	16		3810
ENV	ELKNSAISL	913	9	10	16		3811
ENV	ELKNSAVSL	913	9	12	19		3812
ENV	AVAEGTDRI	928	9	16	25		3813
ENV	AILHHPRRI	946	9	12	19		3814
ENV	VTVYYGVPVW	47	10	55	86		3815
ENV	PVWKEATTTL	54	10	22	34		3816
ENV	VWKEATTTLF	55	10	22	34	0.2700	3817
ENV	LFCASDAKAY	65	10	42	66		3818
ENV	AYDTEVHNVW	73	10	18	28		3819
ENV	MWKNNMVEQ	108	10	35	55		3820
ENV	NMVEQMHEDI	112	10	20	31	0.0004	3821
ENV	MVEQMHEDII	113	10	23	36		3822
ENV	QMHEDIISLW	116	10	29	45		3823
ENV	DIISLWDQSL	120	10	38	59		3824
ENV	DVISLWDQSL	120	10	10	16		3825
ENV	RLINCNTSAI	236	10	15	24		3826
ENV	ITQACPKVSF	245	10	29	45		3827
ENV	PHHYCAPAGF	260	10	27	42		3828
ENV	PHHYCTPAGF	260	10	10	16		3829
ENV	HYCAPAGFAI	262	10	27	42		3830
ENV	HYCTPAGFAI	262	10	10	16		3831
ENV	AILKCNDKKF	270	10	12	19		3832
ENV	GIKPVVSTQL	297	10	33	52		3833
ENV	GIRPVVSTQL	297	10	26	41		3834
ENV	STQLLLNGSL	303	10	57	89		3835
ENV	NTSPRSRVAY	376	10	01	33		3836
ENV	SFNCGGEFFY	437	10	35	55		3837
ENV	SFNCRGEFFY	437	10	16	25		3838
ENV	EFFYCNTSGL	443	10	21	33		3839
ENV	FFYCNTSGLF	444	10	21	33		3840
ENV	ITLPCRIKQI	483	10	25	39		3841
ENV	TLPCRIKQII	484	10	15	23		3842
ENV	NMWQEVGKA	494	10	15	23	0.0001	3843
ENV	MWQEVGKAM	495	10	15	23		3844
ENV	MWQRVGQAM	495	10	10	16		3845
ENV	NTETNKTETF	537	10	01	17		3846
ENV	NTTGNTTETF	537	10	01	17		3847
ENV	EIFRPGGGDM	544	10	17	27		3848
ENV	ETFRPGGGDM	544	10	21	33		3849
ENV	DMRDNWRSEL	552	10	37	58		3850
ENV	ELYKYKVVEI	560	10	13	21		3851
ENV	ELYKYKVVKI	560	10	29	46		3852
ENV	KYKVVKIEPL	563	10	25	39		3853
ENV	GIGAVFLGFL	598	10	11	18		3854
ENV	MLGAMFLGFL	599	10	04	36		3855

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	TIGAMFLGFL	599	10	03	27		3856
ENV	GFLGAAGSTM	606	10	55	86		3857
ENV	STMGAASITL	614	10	39	61		3858
ENV	ITLTVQARQL	621	10	27	42		3859
ENV	TLTVQARQLL	622	10	35	55		3860
ENV	GIVQQQNNLL	633	10	26	41		3861
ENV	GIVQQQSNLL	633	10	32	50		3862
ENV	HLLKLTVWGI	650	10	13	20		3863
ENV	HLLQLTVWGI	650	10	34	53		3864
ENV	KLTVWGIKQL	653	10	13	20		3865
ENV	QLTVWGIKQL	653	10	44	69		3866
ENV	GIKQLQARVL	658	10	40	63		3867
ENV	YLKDQQLLGI	672	10	27	42		3868
ENV	YLRDQQLLGI	672	10	18	28		3869
ENV	GIWGCSGKLI	680	10	48	75		3870
ENV	KLICTTAVPW	687	10	19	30		3871
ENV	KLICTTNVPW	687	10	17	27		3872
ENV	KLICTTTVPW	687	10	12	19		3873
ENV	TTNVPWNSS	691	10	11	17		3874
ENV	IWNNMTWME	717	10	10	16		3875
ENV	MTWMEWERE	721	10	12	19		3876
ENV	LLALDKWASL	755	10	11	17		3877
ENV	LLELDKWASL	755	10	18	28		3878
ENV	WFDITNWLW	767	10	10	16		3879
ENV	ITKWLWYIKI	770	10	15	23		3880
ENV	ITNWLWYIKI	770	10	14	22		3881
ENV	KWLWYIKIFI	772	10	16	25		3882
ENV	NWLWYIKIFI	772	10	25	39		3883
ENV	WLWYIKIFIM	773	10	43	67		3884
ENV	LWYIKIFIMI	774	10	43	67		3885
ENV	KIFIMIVGGL	778	10	38	59		3886
ENV	IFIMIVGGLI	779	10	33	52		3887
ENV	IMIVGGLIGL	781	10	34	54		3888
ENV	IVGGLIGLRI	783	10	42	66		3889
ENV	SIVNRVRQGY	798	10	36	56		3890
ENV	GYSPLSFQTL	806	10	29	45		3891
ENV	LVSGFLALAW	845	10	16	25		3892
ENV	GFLALAWDDL	848	10	25	39		3893
ENV	ALAWDDLRSL	851	10	19	30		3894
ENV	AWDDLRSLCL	853	10	20	31		3895
ENV	DLRNLCLFSY	856	10	16	25		3896
ENV	DLRSLCLFSY	856	10	35	55		3897
ENV	NLCLFSYHRL	859	10	11	17		3898
ENV	SLCLFSYHRL	859	10	31	48		3899
ENV	LFSYHRLRDF	862	10	18	28		3900
ENV	LFSYHRLRDL	862	10	22	34		3901
ENV	SYHRLRDFIL	864	10	13	20		3902
ENV	SYHRLRDLLL	864	10	12	19		3903
ENV	LIAARTVELL	873	10	11	17		3904
ENV	IVELLGRRGW	879	10	22	34		3905

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	LLGRRGWEAL	882	10	09	15		3906
ENV	RLGWEGLKYL	894	10	09	29		3907
ENV	KYWWNLLQY	901	10	14	22		3908
ENV	NLLQYWSQEL	905	10	16	25		3909
ENV	ELKNSAVSLL	913	10	10	16		3910
ENV	AVSLLNATAI	918	10	11	17		3911
ENV	AVAEGTDRII	928	10	15	23		3912
ENV	AVAEGTDRVI	928	10	14	22		3913
ENV	HIPRRIRQGL	949	10	13	21		3914
ENV	NIPRRIRQGL	949	10	11	17		3915
ENV	RIRQGLERAL	953	10	34	53		3916
ENV	WVTVYYGVPV	46	11	55	86		3917
ENV	PVWKEATTTL	54	11	22	34		3918
ENV	TLFCASDAKA	64	11	40	63		3919
ENV	CVPTDPNPQEI	87	11	25	39		3920
ENV	PTDPNPQEVVL	89	11	12	19		3921
ENV	NMWKNNMVE	107	11	30	47		3922
ENV	NMVEQMHEDII	112	11	20	31		3923
ENV	SLKPCVKLTPL	128	11	54	84		3924
ENV	CVKLTPLCVT	132	11	52	81		3925
ENV	VITQACPKVSF	244	11	14	22		3926
ENV	KVSFEPIPIHY	252	11	28	44		3927
ENV	HYCAPAGFAIL	262	11	27	42		3928
ENV	NVSTVQCTHGI	287	11	51	80		3929
ENV	GIKPVVSTQLL	297	11	33	52		3930
ENV	GIRPVVSTQLL	297	11	26	41		3931
ENV	FYATGDIIGDI	367	11	11	17		3932
ENV	GTAGNSSRAA	375	11	01	33		3933
ENV	TTHSFNCGGE	432	11	16	25		3934
ENV	TTHSFNCRGE	432	11	12	19		3935
ENV	VMHSFNCGGE	432	11	13	20		3936
ENV	EFFYCNTSGLF	443	11	21	33		3937
ENV	NITLPCRIKQI	482	11	11	17		3938
ENV	TITLPCRIKQI	482	11	13	20		3939
ENV	ITLPCRIKQII	483	11	15	23		3940
ENV	NMWQEVGKA	494	11	15	23		3941
ENV	EVGKAMYAPPI	498	11	18	28		3942
ENV	RVGQAMYAPP	498	11	10	16		3943
ENV	QIRCSSNITGL	512	11	11	17		3944
ENV	DMRDNWRSEL	552	11	37	58		3945
ENV	VVEREKRAVGI	588	11	11	17		3946
ENV	AVGIGAVFLGF	595	11	11	17		3947
ENV	SITLTVQARQL	620	11	27	42		3948
ENV	ITLTVQARQLL	621	11	27	42		3949
ENV	TVQARQLLSGI	624	11	36	56		3950
ENV	LLRAIEAQQHL	641	11	45	70		3951
ENV	AIEAQQHLLKL	644	11	12	19		3952
ENV	AIEAQQHLLQL	644	11	35	55		3953
ENV	AVERYLKDQQ	668	11	23	36		3954
ENV	AVERYLRDQQ	668	11	11	17		3955

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RYLKDQQLLGI	671	11	25	39		3956
ENV	RYLRDQQLLGI	671	11	17	27		3957
ENV	YLKDQQLLGI	672	11	27	42		3958
ENV	YLRDQQLLGI	672	11	18	28		3959
ENV	LLGIWGCSGKL	678	11	46	72		3960
ENV	CTTNVPWNSS	690	11	11	17		3961
ENV	NMTWMEWER	720	11	12	19		3962
ENV	WMEWEREIDN	723	11	10	16		3963
ENV	ELLELDKWAS	754	11	15	23		3964
ENV	LLALDKWASL	755	11	11	17		3965
ENV	LLELDKWASL	755	11	18	28		3966
ENV	ALDKWASLW	757	11	10	16		3967
ENV	ELDKWASLWN	757	11	16	25		3968
ENV	KWASLWNWF	760	11	15	23		3969
ENV	WFDITNWLW	767	11	10	16		3970
ENV	ITKWLWYIKIF	770	11	12	19		3971
ENV	ITNWLWYIKIF	770	11	14	22		3972
ENV	KWLWYIKIFIM	772	11	15	23		3973
ENV	NWLWYIKIFIM	772	11	22	34		3974
ENV	WLWYIKIFIMI	773	11	43	67		3975
ENV	KIFIMIVGGLI	778	11	31	48		3976
ENV	FIMIVGGLIGL	780	11	34	53		3977
ENV	MIVGGLIGLRI	782	11	36	56		3978
ENV	IVGGLIGLRII	783	11	12	19		3979
ENV	LIGLRIIFAVL	787	11	15	23		3980
ENV	LIGLRIVFAVL	787	11	20	31		3981
ENV	GLRIIFAVLSI	789	11	14	22		3982
ENV	GLRIVFAVLSI	789	11	19	30		3983
ENV	RVRQGYSPLSF	802	11	47	73		3984
ENV	SIRLVSGFLAL	842	11	11	17		3985
ENV	RLVSGFLALA	844	11	16	25		3986
ENV	AWDDLRSLCL	853	11	20	31		3987
ENV	CLFSYHRLRDF	861	11	18	28		3988
ENV	CLFSYHRLRDL	861	11	20	31		3989
ENV	LFSYHRLRDFI	862	11	13	20		3990
ENV	LFSYHRLRDLL	862	11	13	20		3991
ENV	SYHRLRDLLLI	864	11	10	16		3992
ENV	RIVELLGRRG	878	11	22	34		3993
ENV	ELLGRRGWEA	881	11	09	15		3994
ENV	GLRLGWEGLK	892	11	09	29		3995
ENV	RLGWEGLKYL	894	11	07	23		3996
ENV	YWGQELKNSA	909	11	12	19		3997
ENV	AIAVAEGTDRI	926	11	16	25		3998
ENV	RIRQGLERALL	953	11	33	52		3999
GAG	SVLSGGEL	6	8	11	17		4000
GAG	SVLSGGKL	6	8	28	44		4001
GAG	KLDAWEKI	12	8	18	28		4002
GAG	KLDKWEKI	12	8	10	16		4003
GAG	IVWASREL	35	8	21	33		4004
GAG	LVWASREL	35	8	36	56		4005

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	RFALNPGL	45	8	20	31		4006
GAG	RFAVNPGL	45	8	16	25		4007
GAG	GTEELRSL	73	8	12	19		4008
GAG	LFNTVATL	80	8	16	25		4009
GAG	LYNTVATL	80	8	22	34		4010
GAG	LYCVHQKI	87	8	13	20		4011
GAG	LYCVHQRI	87	8	18	28		4012
GAG	KVSQNYPI	148	8	15	27		4013
GAG	QVSQNYPI	148	8	27	48		4014
GAG	NYPIVQNL	152	8	31	48		4015
GAG	KVIEEKAF	178	8	24	38		4016
GAG	KVVEEKAF	178	8	28	44		4017
GAG	VIPMFSAL	189	8	46	72		4018
GAG	VIPMFTAL	189	8	14	22		4019
GAG	ATPQDLNM	200	8	12	19		4020
GAG	DLNMMLNI	204	8	12	19		4021
GAG	TLQEQIAW	263	8	12	19		4022
GAG	TLQEQIGW	263	8	27	42		4023
GAG	WMTNNPPI	270	8	20	31		4024
GAG	WMTSNPPI	270	8	16	25		4025
GAG	PIPVGDIY	279	8	11	17		4026
GAG	PIPVGEIY	279	8	35	55		4027
GAG	DIYKRWII	284	8	17	27		4028
GAG	EIYKRWII	284	8	39	61		4029
GAG	IYKRWIIL	285	8	54	84		4030
GAG	IILGLNKI	290	8	57	89		4031
GAG	GLNKIVRM	293	8	60	94		4032
GAG	RMYSPTSI	299	8	14	22		4033
GAG	RMYSPVSI	299	8	40	63		4034
GAG	MYSPTSIL	300	8	14	22		4035
GAG	MYSPVSIL	300	8	42	66		4036
GAG	ATQDVKNW	333	8	15	23		4037
GAG	ATQEVKNW	333	8	18	28		4038
GAG	NWMTDTLL	339	8	16	25		4039
GAG	NWMTETLL	339	8	36	56		4040
GAG	ALGPAATL	360	8	16	25		4041
GAG	ALGPGATL	360	8	18	28		4042
GAG	IMMQKSNF	408	8	11	17		4043
GAG	IMMQRGNF	408	8	27	42		4044
GAG	CTERQANF	459	8	55	87		4045
GAG	ETIDKDLY	537	8	01	25		4046
GAG	ELYPLASL	543	8	14	22		4047
GAG	ELYPLTSL	543	8	11	17		4048
GAG	PLASLKSL	548	8	15	23		4049
GAG	PLTSLKSL	548	8	12	19		4050
GAG	PLTSLRSL	548	8	12	19		4051
GAG	LTSLKSLF	549	8	13	20		4052
GAG	LTSLRSLF	549	8	12	19		4053
GAG	SLFGNDPL	554	8	12	19		4054
GAG	SLFGSDPL	554	8	11	17		4055

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	KYKLKHIVW	29	9	10	16		4056
GAG	KYRLKHLVW	29	9	16	25		4057
GAG	HIVWASREL	34	9	21	33		4058
GAG	HLVWASREL	34	9	36	56		4059
GAG	RFALNPGLL	45	9	20	31		4060
GAG	RFAVNPGLL	45	9	16	25	0.0100	4061
GAG	ETSEGCRQI	54	9	16	25		4062
GAG	ILGQLQPSL	62	9	11	17		4063
GAG	SLQTGSEEL	69	9	14	22		4064
GAG	SLFNTVATL	79	9	16	25		4065
GAG	SLYNTVATL	79	9	22	34		4066
GAG	LFNTVATLY	80	9	15	23		4067
GAG	LYNTVATLY	80	9	22	34		4068
GAG	TLYCVHQKI	86	9	12	19		4069
GAG	TLYCVHQRI	86	9	15	23		4070
GAG	DVKDTKEAL	95	9	11	17		4071
GAG	EVKDTKEAL	95	9	20	31		4072
GAG	DTKEALDKI	98	9	32	50		4073
GAG	DTKEALEKI	98	9	10	16		4074
GAG	IVQNAQGQM	155	9	21	33		4075
GAG	IVQNLQGQM	155	9	29	45		4076
GAG	TLNAWVKVI	172	9	30	47		4077
GAG	AFSPEVIPM	184	9	50	78		4078
GAG	EVIPMFSAL	188	9	46	72		4079
GAG	EVIPMFTAL	188	9	14	22		4080
GAG	ATPQDLNMM	200	9	12	19		4081
GAG	ATPQDLNTM	200	9	42	66		4082
GAG	IVGGHQAAM	211	9	12	19		4083
GAG	TVGGHQAAM	211	9	47	73		4084
GAG	AMQMLKDTI	218	9	33	52		4085
GAG	AMQMLKETI	218	9	26	41		4086
GAG	TINEEAAEW	225	9	53	83		4087
GAG	DIAGTTSTL	256	9	48	75		4088
GAG	TTSTLQEQI	260	9	45	71		4089
GAG	STLQEQIAW	262	9	12	19		4090
GAG	STLQEQIGW	262	9	27	42		4091
GAG	TLQEQIAWM	263	9	12	19		4092
GAG	TLQEQIGWM	263	9	27	42		4093
GAG	GWMTNNPPI	269	9	18	28	0.0140	4094
GAG	GWMTSNPPI	269	9	10	16		4095
GAG	PVGDIYKRW	281	9	18	28		4096
GAG	PVGEIYKRW	281	9	40	63		4097
GAG	DIYKRWIIL	284	9	17	27		4098
GAG	EIYKRWIIL	284	9	37	58		4099
GAG	WIILGLNKI	289	9	57	89		4100
GAG	GLNKIVRMY	293	9	60	94		4101
GAG	RMYSPTSIL	299	9	14	22		4102
GAG	RMYSPVSIL	299	9	40	63		4103
GAG	PFRDYVDRF	316	9	63	98		4104
GAG	YVDRFFKTL	320	9	27	42		4105

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	YVDRFYKTL	320	9	28	44		4106
GAG	ATQDVKNWM	333	9	15	23		4107
GAG	ATQEVKNWM	333	9	18	28		4108
GAG	NIMMQRGNF	407	9	10	17		4109
GAG	TIMMQRGNF	407	9	13	22		4110
GAG	CTERQANFL	459	9	55	87		4111
GAG	PTAPPAESF	495	9	20	31		4112
GAG	PTAPPEESF	495	9	15	23		4113
GAG	PTAPPAESF	507	9	02	67		4114
GAG	PTAPPPESF	507	9	01	33		4115
GAG	PIDKELYPL	534	9	12	19		4116
GAG	PIDKELYPL	538	9	01	25		4117
GAG	TIDKDLYPL	538	9	01	25		4118
GAG	PLASLKSLF	548	9	15	23		4119
GAG	PLTSLKSLF	548	9	12	19		4120
GAG	PLTSLRSLF	548	9	12	19		4121
GAG	VLSGGKLDAW	7	10	15	23		4122
GAG	KLDAWEKIRL	12	10	16	25		4123
GAG	KLDKWEKIRL	12	10	10	16		4124
GAG	RLRPGGKKKY	20	10	34	53		4125
GAG	VWASRELERF	36	10	45	70		4126
GAG	ETSEGCRQIL	54	10	14	22		4127
GAG	QILGQLQPSL	61	10	11	17		4128
GAG	QTGSEELRSL	71	10	12	19		4129
GAG	SLFNTVATLY	79	10	15	23		4130
GAG	SLYNTVATLY	79	10	22	34		4131
GAG	ATLYCVHQKI	85	10	12	19		4132
GAG	ATLYCVHQRI	85	10	15	23		4133
GAG	PIVQNAQGQM	154	10	21	33		4134
GAG	PIVQNLQGQM	154	10	29	45		4135
GAG	AISPRTLNAW	167	10	29	45		4136
GAG	ALSPRTLNAW	167	10	10	16		4137
GAG	RTLNAWVKVI	171	10	30	47		4138
GAG	WVKVIEEKAF	176	10	24	38		4139
GAG	WVKVVEEKAF	176	10	28	44		4140
GAG	AFSPEVIPMF	184	10	50	78	0.0078	4141
GAG	ATPQDLNMML	200	10	12	19		4142
GAG	ATPQDLNTML	200	10	42	66		4143
GAG	NIVGGHQAAM	210	10	12	19		4144
GAG	NTVGGHQAAM	210	10	47	73		4145
GAG	DTINEEAAEW	224	10	31	48		4146
GAG	ETINEEAAEW	224	10	22	34		4147
GAG	RLHPVHAGPI	235	10	22	34		4148
GAG	RVHPVHAGPI	235	10	14	22		4149
GAG	QMREPRGSDI	248	10	44	69		4150
GAG	GTTSTLQEQI	259	10	45	70		4151
GAG	STLQEQIAWM	262	10	12	19		4152
GAG	STLQEQIGWM	262	10	27	42		4153
GAG	PVGDIYKRWI	281	10	17	27		4154
GAG	PVGEIYKRWI	281	10	40	63		4155

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IYKRWIILGL	285	10	54	84	0.0140	4156
GAG	RWIILGLNKI	288	10	56	88		4157
GAG	ILGLNKIVRM	291	10	57	89		4158
GAG	IVRMYSPTSI	297	10	14	22		4159
GAG	IVRMYSPVSI	297	10	40	63		4160
GAG	MYSPTSILDI	300	10	13	20		4161
GAG	MYSPVSILDI	300	10	40	63		4162
GAG	DIKQGPKEPF	308	10	19	30		4163
GAG	DIRQGPKEPF	308	10	41	64		4164
GAG	PFRDYVDRFF	316	10	35	55		4165
GAG	PFRDYVDRFY	316	10	28	44		4166
GAG	DYVDRFFKTL	319	10	27	42		4167
GAG	DYVDRFYKTL	319	10	28	44	0.0010	4168
GAG	DVKNWMTDT	336	10	12	19		4169
GAG	DVKNWMTET	336	10	11	17		4170
GAG	EVKNWMTETL	336	10	25	39		4171
GAG	ATIMMQRGNF	406	10	11	28		4172
GAG	CFNCGKEGHI	425	10	27	42		4173
GAG	CFNCGKEGHL	425	10	27	42		4174
GAG	TTPSQKQEPI	522	10	09	45		4175
GAG	ETIDKDLYPL	537	10	01	25		4176
GAG	RTENSLYPPL	538	10	01	25		4177
GAG	LYPLASLKSL	544	10	09	17		4178
GAG	SVLSGGKLDA	6	11	15	23		4179
GAG	IVWASRELERF	35	11	19	30		4180
GAG	LVWASRELER	35	11	25	39		4181
GAG	ELERFALNPGL	42	11	14	22		4182
GAG	ELERFAVNPGL	42	11	15	23		4183
GAG	LLETSEGCRQI	52	11	16	25		4184
GAG	RIEVKDTKEAL	93	11	12	19		4185
GAG	NLQGQMVHQA	158	11	15	23		4186
GAG	MVHQAISPRTL	163	11	27	42		4187
GAG	AWVKVIEEKA	175	11	24	38		4188
GAG	AWVKVVEEKA	175	11	28	44		4189
GAG	ALSEGATPQDL	195	11	58	91		4190
GAG	IVGGHQAAMQ	211	11	11	17		4191
GAG	TVGGHQAAMQ	211	11	47	73		4192
GAG	TTSTLQEQIA	260	11	11	17		4193
GAG	TTSTLQEQIG	260	11	27	43		4194
GAG	QIGWMTNNPPI	267	11	18	29		4195
GAG	QIGWMTSNPPI	267	11	10	16		4196
GAG	PIPVGEIYKRW	279	11	34	53		4197
GAG	PVGDIYKRWII	281	11	17	27		4198
GAG	PVGEIYKRWII	281	11	39	61		4199
GAG	DIYKRWIILGL	284	11	17	27		4200
GAG	EIYKRWIILGL	284	11	37	58		4201
GAG	IILGLNKIVRM	290	11	56	88		4202
GAG	ILGLNKIVRMY	291	11	57	89		4203
GAG	KIVRMYSPTSI	296	11	14	22		4204
GAG	KIVRMYSPVSI	296	11	39	61		4205

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IVRMYSPTSIL	297	11	14	22		4206
GAG	IVRMYSPVSIL	297	11	40	63		4207
GAG	RMYSPTSILDI	299	11	13	20		4208
GAG	RMYSPVSILDI	299	11	38	59		4209
GAG	DVKNWMTDT	336	11	12	19		4210
GAG	DVKNWMTET	336	11	11	17		4211
GAG	EVKNWMTETL	336	11	25	39		4212
GAG	ILKALGPAATL	357	11	16	25		4213
GAG	ALGPAATLEE	360	11	16	25		4214
GAG	ALGPGATLEE	360	11	17	27		4215
GAG	ATAQQDLKGG	392	11	01	50		4216
GAG	CWKCGKEGHQ	446	11	46	72		4217
GAG	PTAPPAESFGF	495	11	10	16		4218
GAG	PTAPPEESFRF	495	11	14	22		4219
GAG	PTAPPAESFRF	507	11	02	67		4220
GAG	PTAPPEESFRF	507	11	01	33		4221
GAG	LYPLASLKSLF	544	11	09	17		4222
GAG	SLKSLFGNDPL	551	11	12	19		4223
NEF	DLEKHGAI	57	8	14	22		4224
NEF	ATNADCAW	71	8	12	22		4225
NEF	PVRPQVPL	95	8	48	75		4226
NEF	PMTYKGAF	105	8	12	19		4227
NEF	TYKGAFDL	107	8	12	19		4228
NEF	AFDLSFFL	111	8	18	28		4229
NEF	ALDLSHFL	111	8	11	17		4230
NEF	AVDLSHFL	111	8	15	23		4231
NEF	FLKEKGGL	117	8	56	88		4232
NEF	DILDLWVY	185	8	20	31		4233
NEF	EILDLWVY	185	8	33	52		4234
NEF	WVYHTQGF	191	8	13	20		4235
NEF	WVYHTQGY	191	8	21	33		4236
NEF	VYHTQGFF	192	8	13	20		4237
NEF	VYHTQGYF	192	8	21	33		4238
NEF	FFPDWQNY	199	8	17	27		4239
NEF	YFPDWQNY	199	8	36	56		4240
NEF	NYTPGPGI	206	8	20	31		4241
NEF	GIRYPLTF	213	8	13	20		4242
NEF	GTRFPLTF	213	8	13	20		4243
NEF	RFPLTFGW	216	8	20	32		4244
NEF	RYPLTFGW	216	8	27	43		4245
NEF	PLTFGWCF	219	8	43	67		4246
NEF	TFGWCFKL	222	8	40	63		4247
NEF	GVGAASQDL	45	9	11	17		4248
NEF	GVGAVSQDL	45	9	21	33		4249
NEF	GVGAVSRDL	45	9	17	27		4250
NEF	ATNADCAWL	71	9	12	22		4251
NEF	QVPLRPMTF	100	9	10	16		4252
NEF	QVPLRPMTY	100	9	46	72		4253
NEF	MTYKGAFDL	106	9	12	19		4254
NEF	FFLKEKGGL	116	9	26	41		4255

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
NEF	HFLKEKGGL	116	9	29	45		4256
NEF	IYSKKRQEI	175	9	18	29		4257
NEF	LWVYHTQGF	190	9	13	20		4258
NEF	LWVYHTQGY	190	9	21	33		4259
NEF	WVYHTQGFF	191	9	13	20		4260
NEF	WVYHTQGYF	191	9	21	33		4261
NEF	HTQGFFPDW	194	9	14	22		4262
NEF	HTQGYFPDW	194	9	25	39		4263
NEF	NTQGYFPDW	194	9	12	19		4264
NEF	GFFPDWQNY	198	9	17	27		4265
NEF	GYFPDWQNY	198	9	36	56	0.0002	4266
NEF	YTPGPGIRY	207	9	17	27		4267
NEF	YTPGPGTRF	207	9	13	20		4268
NEF	LTFGWCFKL	221	9	39	61		4269
NEF	KWSKSSIVGW	4	10	20	31		4270
NEF	GFPVRPQVPL	93	10	48	75		4271
NEF	PMTYKGAFDL	105	10	12	19		4272
NEF	SFFLKEKGGL	115	10	22	34		4273
NEF	LIYSKKRQEI	174	10	18	28		4274
NEF	IYSKKRQEIL	175	10	18	29		4275
NEF	DLWVYHTQGF	188	10	13	20		4276
NEF	DLWVYHTQGY	188	10	21	33		4277
NEF	LWVYHTQGFF	190	10	13	20		4278
NEF	LWVYHTQGYF	190	10	21	33		4279
NEF	NYTPGPGIRY	206	10	17	27		4280
NEF	NYTPGPGTRF	206	10	13	20		4281
NEF	GIRYPLTFGW	213	10	13	20		4282
NEF	GTRFPLTFGW	213	10	12	19		4283
NEF	RFPLTFGWCF	216	10	17	27		4284
NEF	RYPLTFGWCF	216	10	21	33		4285
NEF	PLTFGWCFKL	219	10	39	61		4286
NEF	LLHPICQHGM	257	10	10	16		4287
NEF	LLHPMSQHGM	257	10	12	19		4288
NEF	HMARELHPEY	320	10	10	16		4289
NEF	NTAATNADCA	68	11	12	19		4290
NEF	PVRPQVPLRP	95	11	47	73		4291
NEF	PLRPMTYKGA	102	11	12	19		4292
NEF	FLKEKGGLDGL	117	11	26	41		4293
NEF	FLKEKGGLEGL	117	11	29	45		4294
NEF	GLIYSKKRQEI	173	11	18	28		4295
NEF	LIYSKKRQEIL	174	11	18	28		4296
NEF	DLWVYHTQGF	188	11	13	20		4297
NEF	DLWVYHTQGY	188	11	21	33		4298
NEF	VYHTQGFFPD	192	11	13	20		4299
NEF	VYHTQGYFPD	192	11	21	33		4300
NEF	DWQNYTPGPG	203	11	18	28		4301
NEF	YTPGPGIRYPL	207	11	16	25		4302
NEF	YTPGPGTRFPL	207	11	13	20		4303
NEF	CLLHPMSQHG	256	11	10	16		4304
NEF	HMARELHPEY	320	11	10	16		4305

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FFREDLAF	1	8	15	23		4306
POL	FFRENLAF	1	8	41	64		4307
POL	GTLNCPQI	80	8	01	33		4308
POL	PTFNFPQI	80	8	01	33		4309
POL	NFPQITLW	86	8	22	34		4310
POL	SFPQITLW	86	8	23	36		4311
POL	ITLWQRPL	90	8	47	73		4312
POL	TIKIGGQL	99	8	17	27		4313
POL	TVKIGGQL	99	8	11	17		4314
POL	TVLEDINL	118	8	13	20		4315
POL	TVLEEINL	118	8	15	23		4316
POL	DINLPGKW	122	8	13	20		4317
POL	EINLPGKW	122	8	12	19		4318
POL	MIGGIGGF	133	8	62	97		4319
POL	GFIKVRQY	139	8	53	83		4320
POL	KVRQYDQI	142	8	41	64		4321
POL	EICGHKAI	152	8	19	30		4322
POL	EICGKKAI	152	8	24	38		4323
POL	NIIGRNLL	170	8	26	41		4324
POL	NIIGRNML	170	8	31	48		4325
POL	LTQIGCTL	177	8	42	66		4326
POL	LTQLGCTL	177	8	15	23		4327
POL	QIGCTLNF	179	8	41	64		4328
POL	QLGCTLNF	179	8	16	25		4329
POL	PVKLKPGM	195	8	56	88		4330
POL	KIKALTEI	217	8	28	44		4331
POL	KIKALVEI	217	8	15	23		4332
POL	LVEICTEM	221	8	15	24		4333
POL	EMEKEGKI	229	8	42	66		4334
POL	KIGPENPY	238	8	51	80		4335
POL	RIGPENPY	238	8	11	17		4336
POL	KWRKLVDF	259	8	59	92		4337
POL	KLVDFREL	262	8	63	98		4338
POL	FWEVQLGI	276	8	57	89		4339
POL	GIPHPAGL	282	8	56	89		4340
POL	VLDVGDAY	297	8	60	94		4341
POL	SVPLDKDF	306	8	18	28		4342
POL	DFRKYTAF	312	8	42	66		4343
POL	GWKGSPAI	341	8	59	92		4344
POL	MTKILEPF	353	8	44	69		4345
POL	DIVIYQYM	366	8	18	28		4346
POL	EIVIYQYM	366	8	24	38		4347
POL	IYQYMDDL	369	8	61	95		4348
POL	DLYVGSDL	375	8	63	98		4349
POL	YVGSDLEI	377	8	58	91		4350
POL	FLWMGYEL	416	8	64	100		4351
POL	WTVQPIQL	428	8	28	44		4352
POL	WTVQPIVL	428	8	13	20		4353
POL	QLPEKDSW	434	8	13	20		4354
POL	VLPEKDSW	434	8	13	20		4355

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	TVNDIQKL	442	8	62	97		4356
POL	KLVGKLNW	448	8	62	97		4357
POL	KLNWASQI	452	8	61	95		4358
POL	KVKQLCKL	464	8	29	45		4359
POL	KVRQLCKL	464	8	19	30		4360
POL	LLRGAKAL	471	8	30	47		4361
POL	LLRGTKAL	471	8	24	38		4362
POL	ALTDIVPL	477	8	21	33		4363
POL	ALTEVIPL	477	8	16	25		4364
POL	PLTEEAEL	483	8	30	47		4365
POL	ELAENREI	491	8	57	89		4366
POL	YYDPSKDL	510	8	43	67		4367
POL	KTGKYAKM	542	8	19	30		4368
POL	KTGKYARM	542	8	13	21		4369
POL	HTNDVKQL	553	8	49	77		4370
POL	LTEAVQKI	560	8	34	53		4371
POL	ATESIVIW	568	8	19	30		4372
POL	IWGKIPKF	574	8	11	17		4373
POL	IWGKTPKF	574	8	48	75		4374
POL	ETWWTDYW	591	8	10	16		4375
POL	DYWQATWI	596	8	20	31		4376
POL	EYWQATWI	596	8	37	58		4377
POL	TWIPEWEF	601	8	52	81		4378
POL	EFVNTPPL	607	8	54	84		4379
POL	NTPPLVKL	610	8	57	89		4380
POL	LVKLWYQL	614	8	58	91		4381
POL	PIVGAETF	625	8	28	44		4382
POL	IVGAETFY	626	8	28	44		4383
POL	TTNQKTEL	664	8	55	86		4384
POL	KTELQAIY	668	8	12	19		4385
POL	NIVTDSQY	686	8	62	97		4386
POL	VTDSQYAL	688	8	59	92		4387
POL	LIKKEKVY	717	8	35	55		4388
POL	WVPAHKGI	727	8	63	98		4389
POL	GIRKVLFL	747	8	51	80		4390
POL	KVLFLDGI	750	8	50	78		4391
POL	AMASDFNL	773	8	45	70		4392
POL	QVDCSPGI	805	8	57	89		4393
POL	CTHLEGKI	817	8	35	55		4394
POL	HLEGKIIL	819	8	31	48		4395
POL	HLEGKVIL	819	8	23	36		4396
POL	AVHVASGY	828	8	59	92		4397
POL	GYIEAEVI	834	8	54	84		4398
POL	ETGQETAY	844	8	59	92		4399
POL	ILKLAGRW	853	8	34	53		4400
POL	LLKLAGRW	853	8	25	39		4401
POL	HTDNGSNF	866	8	51	80		4402
POL	TTVKAACW	876	8	15	23		4403
POL	AVKAACWW	877	8	32	50		4404
POL	TVKAACWW	877	8	24	38		4405

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	GIKQEFGI	886	8	22	34		4406
POL	GIQQEFGI	886	8	11	17		4407
POL	IILKTAVQM	923	8	57	89		4408
POL	AVQMAVFI	927	8	60	94		4409
POL	NFKRKGGI	936	8	60	94		4410
POL	GYSAGERI	945	8	57	89		4411
POL	QIIKIQNF	968	8	12	19		4412
POL	QITKIQNF	968	8	35	55		4413
POL	KIQNFRVY	971	8	52	81		4414
POL	IWKGPAKL	986	8	36	56		4415
POL	LWKGPAKL	986	8	19	30		4416
POL	VIQDNSDI	1003	8	37	58		4417
POL	VIQDNSEI	1003	8	12	19		4418
POL	PTRRELQVW	30	9	13	20		4419
POL	GTTLNFPQI	79	9	01	17		4420
POL	AISLSLPQI	80	9	01	33		4421
POL	SFSFPQITL	84	9	14	22		4422
POL	QITLWQRPL	89	9	47	73		4423
POL	LWQRPLVTI	92	9	21	33	0.0190	4424
POL	VTIKIGGQL	98	9	17	27		4425
POL	VTVKIGGQL	98	9	11	17		4426
POL	DTGADDTVL	112	9	61	95		4427
POL	DTVLEDINL	117	9	13	20		4428
POL	DTVLEEINL	117	9	14	22		4429
POL	KMIGGIGGF	132	9	62	97	0.0011	4430
POL	MIGGIGGFI	133	9	62	97		4431
POL	KVRQYDQIL	142	9	21	33		4432
POL	QYDQILIEI	145	9	27	42		4433
POL	QYDQIPIEI	145	9	12	19		4434
POL	LVGPTPVNI	163	9	54	84		4435
POL	PVNIIGRNL	168	9	26	41		4436
POL	PVNIIGRNM	168	9	24	38		4437
POL	LLTQIGCTL	176	9	21	33		4438
POL	MLTQIGCTL	176	9	18	28		4439
POL	MLTQLGCTL	176	9	10	16		4440
POL	TLNFPISPI	183	9	61	97		4441
POL	PIETVPVKL	190	9	53	83		4442
POL	QWPLTEEKI	210	9	56	88		4443
POL	LTEEKIKAL	213	9	56	88		4444
POL	ALVEICTEM	220	9	15	23		4445
POL	PYNTPIFAI	244	9	24	38		4446
POL	PYNTPVFAI	244	9	37	58	0.0310	4447
POL	ELNKRTQDF	268	9	57	89		4448
POL	DFWEVQLGI	275	9	56	88		4449
POL	TVLDVGDAY	296	9	57	89		4450
POL	VLDVGDAYF	297	9	60	94		4451
POL	PLDKDFRKY	308	9	19	30		4452
POL	YTAFTIPSI	316	9	37	58		4453
POL	SINNETPGI	323	9	32	50		4454
POL	STNNETPGI	323	9	11	17		4455

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	ETPGIRYQY	327	9	52	81		4456
POL	GIRYQYNVL	330	9	52	81		4457
POL	QYNVLPQGW	334	9	63	98	0.0036	4458
POL	GWKGSPAIF	341	9	59	92		4459
POL	IFQSSMTKI	348	9	38	59	0.0029	4460
POL	SMTKILEPF	352	9	43	67	0.0110	4461
POL	PFRKQNPDI	359	9	16	25		4462
POL	VIYQYMDDL	368	9	51	80		4463
POL	IYQYMDDLY	369	9	61	95	0.0130	4464
POL	LYVGSDLEI	376	9	58	91		4465
POL	EIGQHRAKI	383	9	26	41		4466
POL	EIGQHRTKI	383	9	21	33		4467
POL	KIEELREHL	390	9	19	30		4468
POL	KIEELRQHL	390	9	17	27		4469
POL	ELREHLLKW	393	9	17	27		4470
POL	ELRQHLLRW	393	9	15	23		4471
POL	PFLWMGYEL	415	9	64	100		4472
POL	GYELHPDKW	420	9	60	94	0.0001	4473
POL	KWTVQPIQL	427	9	28	44		4474
POL	KWTVQPIVL	427	9	12	19		4475
POL	IVLPEKDSW	433	9	13	20		4476
POL	WTVNDIQKL	441	9	62	97		4477
POL	DIQKLVGKL	445	9	62	97		4478
POL	KLNWASQIY	452	9	60	94		4479
POL	KVKQLCKLL	464	9	28	44		4480
POL	KVRQLCKLL	464	9	19	30		4481
POL	KLLRGAKAL	470	9	25	40		4482
POL	KLLRGTKAL	470	9	24	38		4483
POL	GTKALTEVI	474	9	11	17		4484
POL	LTEEAELEL	484	9	37	58		4485
POL	ELAENREIL	491	9	57	89		4486
POL	VYYDPSKDL	509	9	39	61	0.0004	4487
POL	YYDPSKDLI	510	9	35	55		4488
POL	TYQIYQEPF	530	9	42	66	0.3000	4489
POL	IYQEPFKNL	533	9	40	63	0.0520	4490
POL	QLTEAVQKI	559	9	34	53		4491
POL	KIATESIVI	566	9	14	22		4492
POL	VIWGKTPKF	573	9	47	73		4493
POL	KTPKFKLPI	577	9	17	27		4494
POL	KTPKFRLPI	577	9	29	45		4495
POL	KLPIQKETW	582	9	20	31		4496
POL	RLPIQKETW	582	9	26	41		4497
POL	TWETWWTDY	589	9	10	16		4498
POL	TWETWWTEY	589	9	10	16		4499
POL	WTDYWQATW	594	9	14	22		4500
POL	WTEYWQATW	594	9	24	38		4501
POL	ATWIPEWEF	600	9	52	81		4502
POL	NTPPLVKLW	610	9	57	89		4503
POL	PLVKLWYQL	613	9	54	84		4504
POL	WYQLEKDPI	618	9	14	22		4505

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	WYQLEKEPI	618	9	31	48	0.0001	4506
POL	WYQLETEPI	618	9	11	17		4507
POL	PIVGAETFY	625	9	28	44		4508
POL	ETKLGKAGY	641	9	35	55		4509
POL	DTTNQKTEL	663	9	26	41		4510
POL	ETTNQKTEL	663	9	29	45		4511
POL	KTELQAHIL	668	9	15	23		4512
POL	KTELQAIYL	668	9	12	19		4513
POL	ELQAHILAL	670	9	16	25		4514
POL	ELQAIYLAL	670	9	12	19		4515
POL	HLALQDSGL	675	9	15	23		4516
POL	IVTDSQYAL	687	9	59	92		4517
POL	LVNQIIEQL	709	9	19	30		4518
POL	LVSQIIEQL	709	9	19	30		4519
POL	QLIKKEKVY	716	9	28	44		4520
POL	LIKKEKVYL	717	9	35	55		4521
POL	AWVPAHKGI	726	9	22	34		4522
POL	SWVPAHKGI	726	9	37	58		4523
POL	KYHSNWRAM	766	9	28	44		4524
POL	RYHSNWRAM	766	9	11	17		4525
POL	NWRAMASDF	770	9	43	67	0.0016	4526
POL	QVDCSPGIW	805	9	57	89		4527
POL	IWQLDCTHL	812	9	59	92	0.0095	4528
POL	CTHLEGKII	817	9	35	55		4529
POL	CTHLEGKVI	817	9	26	41		4530
POL	AVHVASGYI	828	9	53	83		4531
POL	ETGQETAYF	844	9	57	89		4532
POL	ETAYFILKL	848	9	31	48		4533
POL	ETAYFLLKL	848	9	27	42		4534
POL	FILKLAGRW	852	9	32	50		4535
POL	FLLKLAGRW	852	9	25	39		4536
POL	STTVKAACW	875	9	15	23		4537
POL	TTVKAACWW	876	9	15	23		4538
POL	WWAGIKQEF	883	9	21	33	0.0120	4539
POL	WWAGIQQEF	883	9	11	17		4540
POL	VVESMNKEL	902	9	48	75		4541
POL	SMNKELKKI	905	9	53	83		4542
POL	QVRDQAEHL	916	9	48	75		4543
POL	QVREQAEHL	916	9	13	20		4544
POL	KTAVQMAVF	925	9	57	89		4545
POL	QMAVFIHNF	929	9	60	94	0.0190	4546
POL	GYSAGERII	945	9	41	64		4547
POL	IIDIIASDI	952	9	12	19		4548
POL	IIDIIATDI	952	9	29	45		4549
POL	IVDIIATDI	952	9	12	19		4550
POL	ATDIQTKEL	957	9	35	55		4551
POL	QTKELQKQI	961	9	46	72		4552
POL	ELQKQIIKI	964	9	13	21		4553
POL	ELQKQITKI	964	9	34	54		4554
POL	KIQNFRVYY	971	9	52	81		4555

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	YYRDSRDPI	978	9	34	53		4556
POL	YYRDSRDPL	978	9	14	22		4557
POL	PIWKGPAKL	985	9	36	56		4558
POL	PLWKGPAKL	985	9	19	30		4559
POL	IWKGPAKLL	986	9	35	55		4560
POL	LWKGPAKLL	986	9	18	28		4561
POL	VVIQDNSDI	1002	9	37	58		4562
POL	VVIQDNSEI	1002	9	12	19		4563
POL	VVPRRKAKI	1012	9	51	80		4564
POL	VVPRRKVKI	1012	9	11	17		4565
POL	IIKDYGKQM	1020	9	11	17		4566
POL	IIRDYGKQM	1020	9	50	78		4567
POL	AFPQGEAREF	7	10	10	16		4568
POL	STNSPTSREL	32	10	01	33		4569
POL	GTLNCPQITL	80	10	01	33		4570
POL	PTFNFPQITL	80	10	01	33		4571
POL	SFSFPQITLW	84	10	13	20		4572
POL	TLWQRPLVTI	91	10	21	33		4573
POL	LVTIKIGGQL	97	10	13	20		4574
POL	KIGGQLKEAL	101	10	23	36		4575
POL	NLPGKWKPKM	124	10	35	55		4576
POL	KWKPKMIGGI	128	10	42	66		4577
POL	RWKPKMIGGI	128	10	17	27		4578
POL	KMIGGIGGFI	132	10	62	97	0.0001	4579
POL	FIKVRQYDQI	140	10	41	64		4580
POL	KVRQYDQILI	142	10	20	31		4581
POL	KVRQYDQIPI	142	10	13	20		4582
POL	LIEICGHKAI	150	10	10	16		4583
POL	LIEICGKKAI	150	10	13	20		4584
POL	VLVGPTPVNI	162	10	53	83		4585
POL	LVGPTPVNII	163	10	52	81		4586
POL	PVNIIGRNLL	168	10	26	41		4587
POL	PVNIIGRNML	168	10	24	38		4588
POL	IIGRNLLTQI	171	10	21	33		4589
POL	IIGRNMLTQI	171	10	18	28		4590
POL	IIGRNMLTQL	171	10	11	17		4591
POL	NLLTQIGCTL	175	10	21	33		4592
POL	NMLTQIGCTL	175	10	18	28		4593
POL	NMLTQLGCTL	175	10	10	16		4594
POL	LTQIGCTLNF	177	10	41	64		4595
POL	LTQLGCTLNF	177	10	15	23		4596
POL	QIGCTLNFPI	179	10	41	64		4597
POL	QLGCTLNFPI	179	10	16	25		4598
POL	CTLNFPISPI	182	10	60	94		4599
POL	TVPVKLKPGM	193	10	54	84		4600
POL	GMDGPKVKQ	201	10	51	80		4601
POL	PLTEEKIKAL	212	10	54	84		4602
POL	CTEMEKEGKI	225	10	27	42		4603
POL	AIKKKDSTKW	251	10	57	89		4604
POL	STKWRKLVDF	257	10	58	91		4605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	ELNKRTQDFW	268	10	57	89		4606
POL	RTQDFWEVQL	272	10	53	83		4607
POL	QLGIPHPAGL	280	10	56	89		4608
POL	VTVLDVGDAY	295	10	56	88		4609
POL	TVLDVGDAYF	296	10	57	89		4610
POL	YFSVPLDKDF	304	10	18	29		4611
POL	DFRKYTAFTI	312	10	42	66		4612
POL	KYTAFTIPSI	315	10	37	58		4613
POL	AIFQSSMTKI	347	10	36	56		4614
POL	IFQSSMTKIL	348	10	38	59	0.0002	4615
POL	IVIYQYMDDL	367	10	42	66		4616
POL	VIYQYMDDLY	368	10	51	80		4617
POL	DLYVGSDLEI	375	10	58	91		4618
POL	KIEELREHLL	390	10	19	30		4619
POL	KIEELRQHLL	390	10	17	27		4620
POL	PIQLPEKDSW	432	10	13	20		4621
POL	PIVLPEKDSW	432	10	13	20		4622
POL	SWTVNDIQKL	440	10	54	84		4623
POL	NWASQIYAGI	454	10	27	42		4624
POL	NWASQIYPGI	454	10	29	45		4625
POL	IYAGIKVKQL	459	10	18	28		4626
POL	IYPGIKVKQL	459	10	11	17		4627
POL	IYPGIKVRQL	459	10	15	23		4628
POL	GIKVKQLCKL	462	10	28	44		4629
POL	GIKVRQLCKL	462	10	18	28		4630
POL	IVPLTEEAEL	481	10	13	20		4631
POL	VIPLTEEAEL	481	10	11	17		4632
POL	PLTEEAELEL	483	10	30	47		4633
POL	ELELAENREI	489	10	53	83		4634
POL	ILKEPVHGVY	498	10	40	63		4635
POL	GVYYDPSKDL	508	10	38	59		4636
POL	VYYDPSKDLI	509	10	31	48	0.0150	4637
POL	EIQKQGQDQW	520	10	13	20		4638
POL	EIQKQGQGQW	520	10	15	23		4639
POL	WTYQIYQEPF	529	10	42	66		4640
POL	QIYQEPFKNL	532	10	40	63		4641
POL	PFKNLKTGKY	537	10	45	70		4642
POL	NLKTGKYAKM	540	10	18	29		4643
POL	NLKTGKYARM	540	10	13	21		4644
POL	AVQKIATESI	563	10	10	16		4645
POL	KIATESIVIW	566	10	14	22		4646
POL	IVIWGKTPKF	572	10	47	73		4647
POL	IWGKTPKFKL	574	10	17	27		4648
POL	IWGKTPKFRL	574	10	30	47		4649
POL	PIQKETWEAW	584	10	15	23		4650
POL	PIQKETWETW	584	10	27	42		4651
POL	ETWETWWTD	588	10	10	16		4652
POL	ETWETWWTE	588	10	10	16		4653
POL	TWETWWTDY	589	10	10	16		4654
POL	WWTDYWQAT	593	10	14	22		4655

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	WWTEYWQAT	593	10	23	36		4656
POL	WTDYWQATW	594	10	14	22		4657
POL	WTEYWQATW	594	10	24	38		4658
POL	YWQATWIPE	597	10	52	81	0.0660	4659
POL	EWEFVNTPPL	605	10	50	78		4660
POL	FVNTPPLVKL	608	10	54	86		4661
POL	NTPPLVKLWY	610	10	57	89		4662
POL	LWYQLEKDPI	617	10	14	22		4663
POL	LWYQLEKEPI	617	10	31	48		4664
POL	LWYQLETEPI	617	10	11	17		4665
POL	EVNIVTDSQY	684	10	59	92		4666
POL	NIVTDSQYAL	686	10	59	92		4667
POL	VTDSQYALGI	688	10	58	91		4668
POL	ELVNQIIEQL	708	10	18	28		4669
POL	ELVSQIIEQL	708	10	19	30		4670
POL	LVNQIIEQLI	709	10	19	30		4671
POL	LVSQIIEQLI	709	10	19	30		4672
POL	QLIKKEKVYL	716	10	28	44		4673
POL	QVDKLVSAGI	739	10	15	23		4674
POL	QVDKLVSSGI	739	10	29	45		4675
POL	LVSAGIRKVL	743	10	15	23		4676
POL	LVSSGIRKVL	743	10	26	41		4677
POL	NLPPIVAKEI	779	10	26	41		4678
POL	NLPPVVAKEI	779	10	27	42		4679
POL	IVASCDKCQL	788	10	43	67		4680
POL	GIWQLDCTHL	811	10	59	92		4681
POL	CTHLEGKIIL	817	10	31	48		4682
POL	CTHLEGKVIL	817	10	23	36		4683
POL	LVAVHVASGY	826	10	53	83		4684
POL	ETGQETAYFI	844	10	31	48		4685
POL	ETGQETAYFL	844	10	26	41		4686
POL	YFILKLAGRW	851	10	31	48		4687
POL	YFLLKLAGRW	851	10	25	39		4688
POL	THTDNGSNF	864	10	14	22		4689
POL	VHTDNGSNF	864	10	24	38		4690
POL	STTVKAACW	875	10	15	23		4691
POL	CWWAGIKQEF	882	10	21	33		4692
POL	CWWAGIQQEF	882	10	11	17		4693
POL	GIKQEFGIPY	886	10	22	34		4694
POL	GIQQEFGIPY	886	10	11	17		4695
POL	GVVESMNKEL	901	10	48	75		4696
POL	SMNKELKKII	905	10	53	83		4697
POL	KTAVQMAVFI	925	10	56	88		4698
POL	RIDIIASDI	951	10	12	19		4699
POL	RIDIIATDI	951	10	29	45		4700
POL	RIVDIIATDI	951	10	12	19		4701
POL	QTKELQKQII	961	10	10	16		4702
POL	IIKIQNFRVY	969	10	12	19		4703
POL	ITKIQNFRVY	969	10	36	57		4704
POL	VYYRDSRDPI	977	10	34	53		4705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	VYYRDSRDPL	977	10	14	22		4706
POL	YYRDSRDPIW	978	10	34	53		4707
POL	YYRDSRDPLW	978	10	14	22		4708
POL	PIWKGPAKLL	985	10	35	55		4709
POL	PLWKGPAKLL	985	10	18	28		4710
POL	IWKGPAKLLW	986	10	35	55		4711
POL	LWKGPAKLLW	986	10	18	28		4712
POL	LWKGEGAVVI	994	10	59	92		4713
POL	AVVIQDNSDI	1000	10	37	58		4714
POL	AVVIQDNSEI	1000	10	12	19		4715
POL	KVVPRRKAKI	1011	10	51	80		4716
POL	KVVPRRKVKI	1011	10	11	17		4717
POL	VVPRRKAKII	1012	10	50	78		4718
POL	VVPRRKVKII	1012	10	11	17		4719
POL	KIIKDYGKQM	1019	10	11	17		4720
POL	KIIRDYGKQM	1019	10	50	78		4721
POL	GTTLNFPQITF	79	11	01	17		4722
POL	AISLSLPQITL	80	11	01	33		4723
POL	GTLNCPQITL	80	11	01	33		4724
POL	PTFNFPQITLW	80	11	01	33		4725
POL	ITLWQRPLVTI	90	11	19	30		4726
POL	LWQRPLVTIKI	92	11	14	22		4727
POL	LWQRPLVTVK	92	11	12	19		4728
POL	PLVTIKIGGQL	96	11	13	20		4729
POL	KIGGQLKEALL	101	11	23	36		4730
POL	LLDTGADDTV	110	11	61	95		4731
POL	VLEDINLPGKW	119	11	13	20		4732
POL	VLEEINLPGKW	119	11	12	19		4733
POL	NLPGKWKPKM	124	11	35	55		4734
POL	GIGGFIKVRQY	136	11	53	83		4735
POL	GFIKVRQYDQI	139	11	41	64		4736
POL	FIKVRQYDQIL	140	11	21	33		4737
POL	ILIEICGKKAI	149	11	13	20		4738
POL	TVLVGPTPVNI	161	11	53	83		4739
POL	VLVGPTPVNII	162	11	51	80		4740
POL	PTPVNIIGRNL	166	11	26	41		4741
POL	PTPVNIIGRNM	166	11	24	38		4742
POL	NIIGRNLLTQI	170	11	21	33		4743
POL	NIIGRNMLTQI	170	11	18	28		4744
POL	NIIGRNMLTQL	170	11	11	17		4745
POL	LLTQIGCTLNF	176	11	21	33		4746
POL	MLTQIGCTLNF	176	11	17	27		4747
POL	MLTQLGCTLN	176	11	10	16		4748
POL	ETVPVKLKPG	192	11	51	80		4749
POL	EMEKEGKISKI	229	11	32	50		4750
POL	KISKIGPENPY	235	11	41	64		4751
POL	KISRIGPENPY	235	11	11	17		4752
POL	KWRKLVDFRE	259	11	59	92		4753
POL	GLKKKKSVTV	288	11	49	77		4754
POL	SVTVLDVGDA	294	11	56	88		4755

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	VTVLDVGDAY	295	11	56	88		4756
POL	DVGDAYFSVP	299	11	54	84		4757
POL	AYFSVPLDKDF	303	11	18	28		4758
POL	SVPLDKDFRK	306	11	18	28		4759
POL	SINNETPGIRY	323	11	32	50		4760
POL	STNNETPGIRY	323	11	11	17		4761
POL	RYQYNVLPQG	332	11	63	98		4762
POL	AIFQSSMTKIL	347	11	36	56		4763
POL	PFRKQNPDIVI	359	11	14	22		4764
POL	DIVIYQYMDDL	366	11	18	28		4765
POL	EIVIYQYMDDL	366	11	24	38		4766
POL	IVIYQYMDDLY	367	11	42	66		4767
POL	YMDDLYVGSD	372	11	61	95		4768
POL	DLEIGQHRAKI	381	11	26	41		4769
POL	DLEIGQHRTKI	381	11	20	31		4770
POL	RTKIEELRQHL	388	11	14	22		4771
POL	ELREHLLKWG	393	11	14	22		4772
POL	ELRQHLLRWG	393	11	12	19		4773
POL	WMGYELHPDK	418	11	60	94		4774
POL	DIQKLVGKLN	445	11	62	97		4775
POL	LVGKLNWASQ	449	11	60	94		4776
POL	QIYAGIKVKQL	458	11	18	29		4777
POL	QIYPGIKVKQL	458	11	11	17		4778
POL	QIYPGIKVRQL	458	11	14	22		4779
POL	GIKVKQLCKLL	462	11	27	42		4780
POL	GIKVRQLCKLL	462	11	18	28		4781
POL	LLRGAKALTDI	471	11	22	34		4782
POL	GTKALTEVIPL	474	11	11	17		4783
POL	DIVPLTEEAEL	480	11	13	20		4784
POL	EVIPLTEEAEL	480	11	11	17		4785
POL	ELELAENREIL	489	11	53	83		4786
POL	EILKEPVHGVY	497	11	40	63		4787
POL	ILKEPVHGVYY	498	11	38	59		4788
POL	GVYYDPSKDLI	508	11	31	48		4789
POL	QWTYQIYQEP	528	11	42	66		4790
POL	SIVIWGKTPKF	571	11	41	64		4791
POL	VIWGKTPKFK	573	11	17	27		4792
POL	VIWGKTPKFR	573	11	29	45		4793
POL	KFKLPIQKETW	580	11	20	31		4794
POL	KFRLPIQKETW	580	11	26	41		4795
POL	PIQKETWEAW	584	11	15	23		4796
POL	PIQKETWETW	584	11	27	42		4797
POL	ETWETWWTD	588	11	10	16		4798
POL	TWWTDYWQA	592	11	10	16		4799
POL	TWWTEYWQA	592	11	12	19		4800
POL	WWTDYWQAT	593	11	14	22		4801
POL	WWTEYWQAT	593	11	23	36		4802
POL	DYWQATWIPE	596	11	19	30		4803
POL	EYWQATWIPE	596	11	33	52		4804
POL	EFVNTPPLVKL	607	11	54	84		4805

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FVNTPPLVKL	608	11	54	86		4806
POL	KLWYQLEKDPI	616	11	14	22		4807
POL	KLWYQLEKEPI	616	11	31	48		4808
POL	KLWYQLETEPI	616	11	11	17		4809
POL	LTDTTNQKTE	661	11	19	30		4810
POL	LTETTNQKTE	661	11	25	39		4811
POL	TTNQKTELHAI	664	11	12	19		4812
POL	TTNQKTELQAI	664	11	42	66		4813
POL	KTELQAIHLAL	668	11	15	23		4814
POL	KTELQAIYLAL	668	11	12	19		4815
POL	AIHLALQDSGL	673	11	15	23		4816
POL	ALQDSGLEVNI	677	11	27	42		4817
POL	ALQDSGSEVNI	677	11	25	39		4818
POL	IVTDSQYALGI	687	11	58	91		4819
POL	VTDSQYALGII	688	11	58	91		4820
POL	ELVNQIIEQLI	708	11	18	28		4821
POL	ELVSQIIEQLI	708	11	19	30		4822
POL	LIKKEKVYLA	717	11	20	31		4823
POL	LIKKEKVYLSW	717	11	13	20		4824
POL	YLAWVPAHKG	724	11	22	34		4825
POL	YLSWVPAHKG	724	11	37	58		4826
POL	GIGGNEQVDKL	733	11	58	91		4827
POL	KLVSAGIRKVL	742	11	15	23		4828
POL	KLVSSGIRKVL	742	11	26	41		4829
POL	LVSAGIRKVLF	743	11	15	23		4830
POL	LVSSGIRKVLF	743	11	26	41		4831
POL	GIRKVLFLDGI	747	11	49	77		4832
POL	NWRAMASDF	770	11	41	64		4833
POL	AMASDFNLPPI	773	11	18	28		4834
POL	EIVASCDKCQL	787	11	43	67		4835
POL	QVDCSPGIWQ	805	11	56	88		4836
POL	QLDCTHLEGKI	814	11	33	52		4837
POL	ILVAVHVASGY	825	11	53	83		4838
POL	LVAVHVASGYI	826	11	47	73		4839
POL	ETGQETAYFIL	844	11	31	48		4840
POL	ETGQETAYFLL	844	11	26	41		4841
POL	AYFILKLAGR	850	11	31	48		4842
POL	AYFLLKLAGR	850	11	25	39		4843
POL	KLAGRWPVKT	855	11	13	20		4844
POL	KLAGRWPVKV	855	11	22	34		4845
POL	KVIHTDNGSNF	863	11	21	33		4846
POL	FTSAAVKAAC	873	11	27	42		4847
POL	FTSTTVKAAC	873	11	14	22		4848
POL	AVKAACWWA	877	11	10	16		4849
POL	TVKAACWWA	877	11	20	31		4850
POL	WWAGIKQEFG	883	11	21	33		4851
POL	WWAGIQQEFG	883	11	11	17		4852
POL	IILKTAVQMAV	923	11	57	89		4853
POL	AVQMAVFIHN	927	11	60	94		4854
POL	FIHNFKRKGGI	933	11	58	91		4855

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	NFKRKGGIGGY	936	11	59	92		4856
POL	GIGGYSAGERI	942	11	57	89		4857
POL	GYSAGERIIDI	945	11	40	63		4858
POL	GYSAGERIVDI	945	11	14	22		4859
POL	IIASDIQTKEL	955	11	14	22		4860
POL	IIATDIQTKEL	955	11	34	53		4861
POL	DIQTKELQKQI	959	11	44	69		4862
POL	QIIKIQNFRVY	968	11	12	19		4863
POL	QITKIQNFRVY	968	11	35	55		4864
POL	IIKIQNFRVYY	969	11	12	19		4865
POL	ITKIQNFRVYY	969	11	36	57		4866
POL	RVYYRDSRDPI	976	11	34	53		4867
POL	RVYYRDSRDP	976	11	14	22		4868
POL	VYYRDSRDPI	977	11	34	53		4869
POL	VYYRDSRDPL	977	11	14	22		4870
POL	PIWKGPAKLL	985	11	35	55		4871
POL	PLWKGPAKLL	985	11	18	28		4872
POL	LLWKGEGAVV	993	11	59	92		4873
POL	KVVPRRKAKII	1011	11	50	78		4874
POL	KVVPRRKVKII	1011	11	11	17		4875
REV	LLKTVRLI	12	8	11	17		4876
REV	AVRIIKIL	17	8	13	20		4877
REV	ILYQSNPY	23	8	27	42		4878
REV	QLPPIERL	78	8	14	22		4879
REV	QLPPLERL	78	8	37	58		4880
REV	LVESPAVL	114	8	11	17		4881
REV	AVRIIKILY	17	9	13	20		4882
REV	KILYQSNPY	22	9	26	41		4883
REV	RWRARQRQI	48	9	35	55		4884
REV	RWRERQRQI	48	9	11	17		4885
REV	PVPLQLPPI	74	9	11	17		4886
REV	PVPLQLPPL	74	9	35	55		4887
REV	PLQLPPIERL	76	10	11	17		4888
REV	PLQLPPLERL	76	10	34	53		4889
REV	QLPPLERLTL	78	10	18	28		4890
REV	GTQGVGSPQI	97	10	11	18		4891
REV	IIKILYQSNPY	20	11	18	28		4892
TAT	CYCKKCCF	28	8	11	17		4893
TAT	CYCKKCCY	28	8	11	17		4894
TAT	CFHCQVCF	34	8	11	17		4895
TAT	FLNKGLGI	41	8	14	22		4896
TAT	PVDPNLEPW	3	9	20	31		4897
TAT	PVDPRLEPW	3	9	14	22		4898
TAT	CFLNKGLGI	40	9	14	22		4899
TAT	FLNKGLGISY	41	10	14	22		4900
TAT	CFLNKGLGISY	40	11	14	22		4901
VIF	RWQVLIVW	4	8	10	16		4902
VIF	RWQVMIVW	4	8	43	67		4903
VIF	IVWQVDRM	9	8	59	92		4904
VIF	KIRTWNSL	17	8	12	19		4905

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	RIRTWKSL	17	8	15	23		4906
VIF	RIRTWNSL	17	8	15	23		4907
VIF	SLVKHHMY	23	8	44	69		4908
VIF	LVKHHMYI	24	8	19	30		4909
VIF	GWFYRHHY	37	8	20	31		4910
VIF	KISSEVHI	50	8	15	23		4911
VIF	KVSSEVHI	50	8	20	31		4912
VIF	RISSEVHI	50	8	15	23		4913
VIF	RLVITTYW	65	8	12	19		4914
VIF	VIKTYWGL	67	8	10	16		4915
VIF	VITTYWGL	67	8	22	34		4916
VIF	VVRTYWGL	67	8	10	16		4917
VIF	VVTTYWGL	67	8	11	17		4918
VIF	HLGHGVSI	83	8	25	39		4919
VIF	HLGQGVSI	83	8	26	41		4920
VIF	GVSIEWRL	87	8	18	28		4921
VIF	STQIDPDL	100	8	12	19		4922
VIF	STQVDPGL	100	8	11	17		4923
VIF	QLIHLYYF	110	8	14	22		4924
VIF	QLIHMHYF	110	8	14	22		4925
VIF	HLYYFDCF	113	8	16	25		4926
VIF	HMHYFDCF	113	8	15	23		4927
VIF	IVSPRCEY	133	8	14	22		4928
VIF	KVGSLQYL	146	8	52	81		4929
VIF	QYLALAAL	151	8	12	19		4930
VIF	QYLALKAL	151	8	11	17		4931
VIF	QYLALTAL	151	8	33	52		4932
VIF	YLALTALI	152	8	28	44		4933
VIF	ALIKPKKI	157	8	10	16		4934
VIF	PLPSVKKL	168	8	21	33		4935
VIF	PLPSVRKL	168	8	14	22		4936
VIF	MIVWQVDRM	8	9	46	72		4937
VIF	VWQVDRMKI	10	9	13	20		4938
VIF	VWQVDRMRI	10	9	48	75		4939
VIF	SLVKHHMYI	23	9	19	30		4940
VIF	HIPLGDARL	56	9	13	20		4941
VIF	HIPLGEARL	56	9	20	31		4942
VIF	PLGEARLVI	58	9	10	16		4943
VIF	LVIKTYWGL	66	9	10	16		4944
VIF	LVITTYWGL	66	9	22	34		4945
VIF	GLHTGERDW	73	9	22	34		4946
VIF	GLQTGERDW	73	9	12	19		4947
VIF	HTGERDWHL	75	9	21	33		4948
VIF	QTGERDWHL	75	9	12	19		4949
VIF	SIEWRLRRY	89	9	11	17		4950
VIF	DLADQLIHL	106	9	18	28		4951
VIF	GLADQLIHM	106	9	15	23		4952
VIF	QYLALTALI	151	9	28	44		4953
VIF	VMIVWQVDR	7	10	44	69		4954
VIF	IVWQVDRMKI	9	10	12	19		4955

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	IVWQVDRMRI	9	10	47	73		4956
VIF	QVDRMKIRTW	12	10	12	19		4957
VIF	QVDRMRINTW	12	10	10	16		4958
VIF	QVDRMRIRTW	12	10	31	48		4959
VIF	RMKIRTWNSL	15	10	12	19		4960
VIF	RMRIRTWKSL	15	10	15	23		4961
VIF	RMRIRTWNSL	15	10	15	23		4962
VIF	TWKSLVKHHI	20	10	16	25		4963
VIF	TWNSLVKHHI	20	10	25	39		4964
VIF	KISSEVHIPL	50	10	14	22		4965
VIF	KVSSEVHIPL	50	10	19	30		4966
VIF	RISSEVHIPL	50	10	13	20		4967
VIF	RLVITTYWGL	65	10	12	19		4968
VIF	DWHLGHGVSI	81	10	21	33		4969
VIF	DWHLGQGVSI	81	10	18	28		4970
VIF	HLGHGVSIEW	83	10	25	39		4971
VIF	HLGQGVSIEW	83	10	26	41		4972
VIF	RYSTQVDPGL	98	10	10	16		4973
VIF	QIDPDLADQL	102	10	10	16		4974
VIF	QVDPGLADQL	102	10	14	22		4975
VIF	LIHLYYFDCF	111	10	16	25		4976
VIF	LIHMHYFDCF	111	10	15	23		4977
VIF	YFDCFSESAI	116	10	28	44		4978
VIF	KVGSLQYLAL	146	10	51	80		4979
VIF	SLQYLALAAL	149	10	12	19		4980
VIF	SLQYLALKAL	149	10	11	17		4981
VIF	SLQYLALTAL	149	10	31	48		4982
VIF	SVKKLTEDRW	174	10	13	20		4983
VIF	QVMIVWQVDR	6	11	43	67		4984
VIF	MIVWQVDRM	8	11	43	67		4985
VIF	RTWKSLVKHHI	19	11	14	22		4986
VIF	RTWNSLVKHHI	19	11	24	38		4987
VIF	TWKSLVKHHI	20	11	16	25		4988
VIF	TWNSLVKHHI	20	11	22	34		4989
VIF	EVHIPLGDARL	54	11	13	20		4990
VIF	EVHIPLGEARL	54	11	20	31		4991
VIF	HIPLGEARLVI	56	11	10	16		4992
VIF	YWGLHTGERD	71	11	22	34		4993
VIF	YWGLQTGERD	71	11	12	19		4994
VIF	GLHTGERDWH	73	11	21	33		4995
VIF	GLQTGERDWH	73	11	12	19		4996
VIF	GVSIEWRLRR	87	11	10	16		4997
VIF	QIDPDLADQLI	102	11	10	16		4998
VIF	QVDPGLADQLI	102	11	14	22		4999
VIF	GLADQLIHMH	106	11	11	17		5000
VIF	QLIHLYYFDCF	110	11	13	20		5001
VIF	QLIHMHYFDCF	110	11	14	22		5002
VIF	YYFDCFSESAI	115	11	20	31		5003
VIF	CFSDSAIRKAI	119	11	10	16		5004
VIF	CFSESAIRKAI	119	11	12	19		5005

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	CFSESAIRNAI	119	11	12	19		5006
VIF	SLQYLALTALI	149	11	27	42		5007
VIF	LIKPKKIKPPL	158	11	10	16		5008
VIF	KTKGHRGSHT	188	11	15	23		5009
VPR	ALELLEEL	19	8	10	16		5010
VPR	TLELLEEL	19	8	44	69		5011
VPR	AVRHFPRI	30	8	14	22		5012
VPR	WLHGLGQY	38	8	11	17		5013
VPR	TWAGVEAI	53	8	16	25		5014
VPR	TWEGVEAI	53	8	20	31		5015
VPR	GVEAHRI	56	8	34	53		5016
VPR	HRILQQL	60	8	42	66		5017
VPR	RILQQLLF	62	8	45	70		5018
VPR	ILQQLLFI	63	8	37	58		5019
VPR	LLFIHFRI	67	8	44	69		5020
VPR	LLFVHFRI	67	8	12	19		5021
VPR	PYNEWTLEL	14	9	30	47	0.1400	5022
VPR	WTLELLEEL	18	9	42	69		5023
VPR	AVRHFPRIW	30	9	14	22		5024
VPR	AVRHFPRPW	30	9	34	53		5025
VPR	PWLHGLGQY	37	9	11	17		5026
VPR	WLHGLGQHI	38	9	20	31		5027
VPR	IYETYGDTW	46	9	31	48	0.0580	5028
VPR	IYNTYGDTW	46	9	18	28		5029
VPR	DTWAGVEAI	52	9	16	25		5030
VPR	DTWEGVEAI	52	9	20	31		5031
VPR	TWAGVEAII	53	9	16	25		5032
VPR	TWEGVEAII	53	9	19	30		5033
VPR	GVEAHRIL	56	9	34	53		5034
VPR	AHRILQQL	59	9	39	61		5035
VPR	HRILQQLL	60	9	42	66		5036
VPR	RILQQLLFI	62	9	36	56		5037
VPR	QLLFIHFRI	66	9	44	69		5038
VPR	QLLFVHFRI	66	9	10	16		5039
VPR	RIGCQHSRI	74	9	47	73		5040
VPR	RIGCRHSRI	74	9	12	19		5041
VPR	PYNEWTLELL	14	10	30	47		5042
VPR	EWTLELLEEL	17	10	40	63		5043
VPR	ELKNEAVRHF	25	10	17	27		5044
VPR	ELKSEAVRHF	25	10	15	23		5045
VPR	AVRHFPRIWL	30	10	14	22		5046
VPR	AVRHFPRPWL	30	10	34	53		5047
VPR	HFPRIWLHSL	33	10	10	16		5048
VPR	HFPRPWLHGL	33	10	24	38		5049
VPR	PWLHGLGQHI	37	10	12	19		5050
VPR	WLHGLGQHIY	38	10	20	31		5051
VPR	HIYETYGDTW	45	10	17	27		5052
VPR	HIYNTYGDTW	45	10	14	22		5053
VPR	YIYETYGDTW	45	10	14	22		5054
VPR	DTWAGVEAII	52	10	16	25		5055

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VPR	DTWEGVEAH	52	10	19	30		5056
VPR	AHRILQQLL	59	10	39	61		5057
VPR	HRILQQLLF	60	10	41	64		5058
VPR	ILQQLLFIHF	63	10	35	55		5059
VPR	PWLHGLGQHI	37	11	12	19		5060
VPR	QYIYETYGDT	44	11	14	22		5061
VPR	TWAGVEAHRI	53	11	15	23		5062
VPR	TWEGVEAHRI	53	11	14	22		5063
VPR	AHRILQQLLF	59	11	38	59		5064
VPR	HRILQQLLFI	60	11	33	52		5065
VPR	RILQQLLFIHF	62	11	34	53		5066
VPR	HFRIGCQHSRI	71	11	44	69		5067
VPR	HFRIGCRHSRI	71	11	11	17		5068
VPR	RIGCQHSRIGI	74	11	45	70		5069
VPR	RIGCRHSRIGI	74	11	11	17		5070
VPU	KVDYRIVI	7	8	01	33		5071
VPU	LHAIVVW	26	8	10	16		5072
VPU	IVVWTIVF	30	8	15	23		5073
VPU	VVWTIVFI	31	8	15	23		5074
VPU	WTIVFIEY	34	8	12	19		5075
VPU	VFIEYRKI	37	8	12	19		5076
VPU	KILRQRKI	45	8	15	23		5077
VPU	EMGHHAPW	89	8	11	17		5078
VPU	NYELAVGAL	5	9	01	25		5079
VPU	DYKLGVGAL	10	9	02	29		5080
VPU	DYRLGVGAL	10	9	03	43		5081
VPU	HAIVVWTI	27	9	23	36		5082
VPU	AIVVWTIVF	29	9	14	22		5083
VPU	IVVWTIVFI	30	9	15	23		5084
VPU	VWTIVFIEY	33	9	12	19		5085
VPU	IVFIEYRKI	36	9	12	19		5086
VPU	KIDRLIDRI	52	9	14	22		5087
VPU	VTLLSSSKL	94	9	01	50		5088
VPU	NYELAVGALI	5	10	01	25		5089
VPU	DYKLGVGALI	10	10	02	29		5090
VPU	DYRLGVGALI	10	10	03	43		5091
VPU	AIVVWTIVFI	29	10	14	22		5092
VPU	VVWTIVFIEY	31	10	12	19		5093
VPU	ILRQRKIDRL	46	10	15	23		5094
VPU	GVEMGHHAP	91	10	01	50		5095
VPU	LVTLLSSSKL	91	10	01	50		5096
VPU	KVDYRIVIVAF	7	11	01	33		5097
VPU	KVDYRLGVGA	7	11	01	33		5098
VPU	RIDYRLGVGAL	7	11	01	33		5099
VPU	IVVWTIVFIEY	30	11	12	19		5100
VPU	EYRKILRQRKI	41	11	13	21		5101
VPU	KILRQRKIDRL	45	11	15	23		5102
VPU	ILRQRKIDRLI	46	11	13	20		5103
VPU	RIKEIRDDSDY	64	11	01	50		5104
VPU	RIKEIRDDSDY	64	11	01	50		5105

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
ENV	DPNPQEVV	91	8	13	20		5106
ENV	APAGFAIL	265	8	29	45		5107
ENV	KPVVSTQL	299	8	34	53		5108
ENV	RPVVSTQL	299	8	26	41		5109
ENV	GPGQTFYA	362	8	11	17		5110
ENV	LPCRIKQI	485	8	31	48		5111
ENV	SPLSFQTL	808	8	30	47		5112
ENV	GPDRPEGI	822	8	15	23		5113
ENV	EPDRPERI	823	8	01	33		5114
ENV	PPDRPEGI	823	8	01	33		5115
ENV	DPNPQEVVL	91	9	12	19	0.0002	5116
ENV	KPCVKLTPL	130	9	55	86	0.4100	5117
ENV	CPKVSFEPI	250	9	30	47	0.0550	5118
ENV	DPIPIHYCA	256	9	12	19		5119
ENV	EPIPIHYCA	256	9	26	41	0.0001	5120
ENV	IPIHYCAPA	259	9	36	56	0.0130	5121
ENV	IPIHYCTPA	259	9	18	28		5122
ENV	GPCKNVSTV	283	9	15	23		5123
ENV	GPCTNVSTV	283	9	11	17	0.0019	5124
ENV	KPVVSTQLL	299	9	34	53	0.0012	5125
ENV	RPVVSTQLL	299	9	26	41	0.0084	5126
ENV	DPEIVMHSF	428	9	14	22	0.0001	5127
ENV	LPCRIKQII	485	9	20	31	0.0011	5128
ENV	LPCRIKQIV	485	9	10	16		5129
ENV	APTKAKRRV	575	9	22	34	0.0082	5130
ENV	SPLSFQTLL	808	9	10	16		5131
ENV	IPRRIRQGF	950	9	10	16		5132
ENV	IPRRIRQGL	950	9	24	38		5133
ENV	IPTRIRQGL	950	9	11	17		5134
ENV	VPTDPNPQEI	88	10	25	39		5135
ENV	VPTDPNPQEV	88	10	21	33	0.0008	5136
ENV	KPVVSTQLLL	299	10	34	53		5137
ENV	RPVVSTQLLL	299	10	26	41	0.0038	5138
ENV	RPNNNTRKSI	347	10	17	27		5139
ENV	EPLGVAPTKA	570	10	21	33	0.0005	5140
ENV	APTKAKRRVV	575	10	22	34	0.1200	5141
ENV	VPVWKEATTT	53	11	22	34	0.0022	5142
ENV	VPTDPNPQEV	88	11	13	20		5143
ENV	KPCVKLTPLC	130	11	54	84	0.0004	5144
ENV	CPKVSFEPIPI	250	11	30	47		5145
ENV	DPIPIHYCAPA	256	11	10	16		5146
ENV	EPIPIHYCAPA	256	11	24	38		5147
ENV	EPIPIHYCTPA	256	11	10	16		5148
ENV	IPIHYCAPAGF	259	11	26	41		5149
ENV	IPIHYCTPAGF	259	11	10	16		5150
ENV	LPCRIKQIINM	485	11	18	28		5151
ENV	RPGGGDMRDN	547	11	38	59		5152
GAG	RPGGKKKY	22	8	35	55		5153
GAG	NPGLLETA	49	8	15	23		5154
GAG	SPRTLNAW	169	8	57	89	0.0036	5155

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HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
GAG	SPEVIPMF	186	8	55	86	0.0012	5156
GAG	TPQDLNMM	201	8	12	19		5157
GAG	TPQDLNTM	201	8	42	66	0.0001	5158
GAG	HPVHAGPI	237	8	38	59	0.0012	5159
GAG	GPIAPGQM	242	8	19	30	0.0005	5160
GAG	GPIPPGQM	242	8	17	27		5161
GAG	GPVAPGQM	242	8	10	16		5162
GAG	EPRGSDIA	251	8	56	88	0.0001	5163
GAG	PPIPVGDI	278	8	10	16		5164
GAG	PPIPVGEI	278	8	35	55	0.0001	5165
GAG	SPTSILDI	302	8	13	20		5166
GAG	SPVSILDI	302	8	40	63		5167
GAG	NPDCKSIL	351	8	11	17		5168
GAG	NPDCKTIL	351	8	46	72	0.0003	5169
GAG	GPGHKARV	379	8	36	56	0.0002	5170
GAG	GPSHKARV	379	8	19	30		5171
GAG	APRKKGCW	440	8	55	86	0.0004	5172
GAG	PPAESFGF	498	8	10	16		5173
GAG	PPEESFRF	498	8	15	23		5174
GAG	PPAESFRF	510	8	02	67		5175
GAG	PPPESFRF	510	8	01	33		5176
GAG	EPIDKELY	533	8	12	19		5177
GAG	EPIDKELY	537	8	01	25		5178
GAG	SPRTLNAWV	169	9	57	89	0.5500	5179
GAG	TPQDLNMML	201	9	12	19		5180
GAG	TPQDLNTML	201	9	42	66	0.0008	5181
GAG	HPVHAGPIA	237	9	19	30	0.0590	5182
GAG	NPPIPVGDI	277	9	10	16		5183
GAG	NPPIPVGEI	277	9	34	54	0.0002	5184
GAG	PPIPVGDIY	278	9	10	16		5185
GAG	PPIPVGEIY	278	9	35	55	0.0002	5186
GAG	GPKEPFRDY	312	9	63	98	0.0002	5187
GAG	GPAATLEEM	362	9	16	25	0.0014	5188
GAG	GPGATLEEM	362	9	18	28		5189
GAG	GPGHKARVL	379	9	35	55	0.0290	5190
GAG	GPSHKARVL	379	9	19	30		5191
GAG	RPEPTAPPA	490	9	30	47	0.0014	5192
GAG	APPAESFGF	497	9	10	16		5193
GAG	APPEESFRF	497	9	15	23	0.0046	5194
GAG	RPEPTAPPA	504	9	01	50	0.0014	5195
GAG	APPAESFRF	509	9	02	67		5196
GAG	APPPESFRF	509	9	01	33		5197
GAG	TPSQKQEPI	527	9	10	17		5198
GAG	YPLASLKSL	545	9	08	17		5199
GAG	YPLASLRSL	545	9	07	15	0.9900	5200
GAG	PPLASLKSL	546	9	04	24		5201
GAG	EPLTALRSL	547	9	01	33		5202
GAG	PPLASLKSL	547	9	01	33		5203
GAG	PPLISLKSL	547	9	01	33		5204
GAG	RPGGKKKYKL	22	10	10	16		5205

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
GAG	RPGGKKKYRL	22	10	16	25		5206
GAG	SPEVIPMFSA	186	10	41	64	0.0002	5207
GAG	SPEVIPMFTA	186	10	13	20		5208
GAG	NPPIPVGDIY	277	10	10	16		5209
GAG	NPPIPVGEIY	277	10	34	54	0.0002	5210
GAG	IPVGDIYKRW	280	10	11	17		5211
GAG	IPVGEIYKRW	280	10	34	53	0.0002	5212
GAG	GPKEPFRDYV	312	10	63	98	0.0002	5213
GAG	EPFRDYVDRF	315	10	63	98	0.0002	5214
GAG	NPDCKTILKA	351	10	28	44	0.0002	5215
GAG	NPDCKTILRA	351	10	18	28		5216
GAG	GPAATLEEMM	362	10	16	25	0.0020	5217
GAG	GPGATLEEMM	362	10	18	28		5218
GAG	GPGHKARVLA	379	10	35	55	0.0002	5219
GAG	GPSHKARVLA	379	10	19	30		5220
GAG	PPAEPTAPPA	491	10	01	50		5221
GAG	EPTAPPAESF	494	10	20	31		5222
GAG	EPTAPPEESF	494	10	15	23	0.0002	5223
GAG	EPTAPPAESF	506	10	01	50		5224
GAG	EPTAPPPESF	506	10	01	50		5225
GAG	PPESFRFEEA	511	10	01	33		5226
GAG	EPIDKELYPL	533	10	12	19	0.0019	5227
GAG	EPIDKELYPL	537	10	01	25	0.0019	5228
GAG	YPLASLKSLF	545	10	08	17		5229
GAG	YPLASLRSLF	545	10	07	15	0.0140	5230
GAG	PPLASLKSLF	546	10	04	24		5231
GAG	EPLTALRSLF	547	10	01	33		5232
GAG	PPLASLKSLF	547	10	01	33		5233
GAG	PPLISLKSLF	547	10	01	33		5234
GAG	QPSLQTGSEEL	67	11	13	20		5235
GAG	YPIVQNAQGQ	153	11	20	31		5236
GAG	YPIVQNLQGQ	153	11	29	45		5237
GAG	SPRTLNAWVK	169	11	55	86	0.0076	5238
GAG	SPEVIPMFSAL	186	11	41	64	0.0003	5239
GAG	SPEVIPMFTAL	186	11	13	20		5240
GAG	IPMFSALSEGA	190	11	45	70	0.0004	5241
GAG	IPMFTALSEGA	190	11	15	23		5242
GAG	TPQDLNMMLN	201	11	11	17		5243
GAG	IPVGDIYKRWI	280	11	10	16		5244
GAG	IPVGEIYKRWI	280	11	34	53	0.0001	5245
GAG	EPFRDYVDRFF	315	11	35	55		5246
GAG	EPFRDYVDRF	315	11	28	44	0.0001	5247
GAG	NPDCKTILKAL	351	11	28	44	0.0001	5248
GAG	NPDCKTILRAL	351	11	18	28		5249
GAG	WPSHKGRPGN	474	11	23	36		5250
GAG	WPSNKGRPGN	474	11	14	22		5251
GAG	WPSSKGRPGN	474	11	11	17		5252
GAG	PPPESFRFEEA	510	11	01	33		5253
NEF	APTAAKGV	34	8	01	33		5254
NEF	VPLRPMTF	101	8	10	16		5255

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
NEF	VPLRPMTY	101	8	46	73	0.0001	5256
NEF	RPMTYKAA	104	8	23	36		5257
NEF	RPMTYKGA	104	8	25	39		5258
NEF	TPGPGIRY	208	8	17	27		5259
NEF	TPGPGTRF	208	8	13	20		5260
NEF	GPGIRYPL	210	8	17	27		5261
NEF	GPGTRFPL	210	8	13	20		5262
NEF	VPVDPREV	230	8	11	17		5263
NEF	HPICQHGM	259	8	10	16		5264
NEF	HPMSQHGM	259	8	12	19		5265
NEF	EPAADGVGA	40	9	05	19	0.0001	5266
NEF	PPAAEGVGA	40	9	04	15		5267
NEF	FPVRPQVPL	94	9	48	75	0.7600	5268
NEF	RPQVPLRPM	98	9	47	73	1.7000	5269
NEF	RPMTYKGAF	104	9	12	19		5270
NEF	FPLTFGWCF	217	9	17	27		5271
NEF	YPLTFGWCF	217	9	24	38		5272
NEF	APTAAKGVGA	34	10	01	33		5273
NEF	EPAADGVGAV	40	10	04	15		5274
NEF	VPLRPMTYKA	101	10	20	32	0.0001	5275
NEF	TPGPGIRYPL	208	10	16	25		5276
NEF	TPGPGTRFPL	208	10	13	20		5277
NEF	GPGIRYPLTF	210	10	13	20		5278
NEF	GPGTRFPLTF	210	10	13	20		5279
NEF	APTAAKGVGA	34	11	01	33		5280
NEF	RPQVPLRPMT	98	11	10	16		5281
NEF	RPQVPLRPMT	98	11	36	56		5282
NEF	VPLRPMTYKA	101	11	19	30		5283
NEF	VPLRPMTYKG	101	11	23	37		5284
NEF	RPMTYKGAFD	104	11	12	19		5285
NEF	FPLTFGWCFK	217	11	17	27		5286
NEF	YPLTFGWCFK	217	11	20	31		5287
POL	EPGEDREL	69	8	01	17		5288
POL	GPERALSV	70	8	01	20		5289
POL	RPLVTIKI	95	8	14	22		5290
POL	RPLVTVKI	95	8	12	19		5291
POL	KPKMIGGI	130	8	60	94	0.0023	5292
POL	GPTPVNII	165	8	54	84	0.0001	5293
POL	SPIETVPV	189	8	56	88	0.0021	5294
POL	WPLTEEKI	211	8	56	88	0.0001	5295
POL	NPYNTPIF	243	8	24	38		5296
POL	NPYNTPVF	243	8	38	59	0.0008	5297
POL	TPGIRYQY	328	8	52	81	0.0001	5298
POL	PPFLWMGY	414	8	64	100	0.0001	5299
POL	EPVHGVYY	504	8	41	64	0.0001	5300
POL	DPSKDLIA	512	8	34	53		5301
POL	TPKFKLPI	578	8	17	27		5302
POL	TPKFRLPI	578	8	30	47		5303
POL	LPIQKETW	583	8	47	73	0.0001	5304
POL	TPPLVKLW	611	8	57	89	0.0001	5305

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HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	PPLVKLWY	612	8	57	89	0.0001	5306
POL	PPIVAKEI	781	8	27	42		5307
POL	PPVVAKEI	781	8	29	45	0.0001	5308
POL	NPQSQGVV	896	8	59	92	0.0001	5309
POL	DPIWKGPA	984	8	37	58		5310
POL	DPLWKGPA	984	8	15	23		5311
POL	VPRRKAKI	1013	8	51	80	0.0018	5312
POL	VPRRKVKI	1013	8	11	17		5313
POL	FPQGEAREF	8	9	10	16		5314
POL	SPTRRELQV	29	9	14	22	0.0210	5315
POL	SPTSRELQV	35	9	01	33		5316
POL	SPSSRELQV	38	9	01	50		5317
POL	VPTFNFPQI	79	9	01	17		5318
POL	LPGKWKPKM	125	9	39	61		5319
POL	LPGRWKPKM	125	9	16	25	0.0038	5320
POL	FPISPIETV	186	9	56	88	0.0016	5321
POL	VPVKLKPGM	194	9	56	88	0.0003	5322
POL	KPGMDGPKV	199	9	51	80	0.0002	5323
POL	GPKVKQWPL	205	9	51	80	0.0150	5324
POL	NPYNTPIFA	243	9	24	38		5325
POL	NPYNTPVFA	243	9	37	58	0.0002	5326
POL	SPAIFQSSM	345	9	42	66	0.4100	5327
POL	NPDIVIYQY	364	9	17	27	0.0001	5328
POL	NPEIVIYQY	364	9	23	36		5329
POL	EPPFLWMGY	413	9	63	98	0.0001	5330
POL	LPEKDSWTV	435	9	40	63	0.0001	5331
POL	YPGIKVKQL	460	9	11	17		5332
POL	YPGIKVRQL	460	9	15	23		5333
POL	IPLTEEAEL	482	9	11	17		5334
POL	VPLTEEAEL	482	9	19	30		5335
POL	TPPLVKLWY	611	9	57	89	0.0001	5336
POL	EPIVGAETF	624	9	21	33	0.0001	5337
POL	QPDKSESEL	701	9	37	58	0.0006	5338
POL	LPPIVAKEI	780	9	27	42		5339
POL	LPPVVAKEI	780	9	28	44	0.0006	5340
POL	PPIVAKEIV	781	9	26	41		5341
POL	PPVVAKEIV	781	9	28	44	0.0001	5342
POL	VPRRKAKII	1013	9	50	78	0.4800	5343
POL	VPRRKVKII	1013	9	11	17		5344
POL	SPTRRELQVW	29	10	13	20	0.0025	5345
POL	EPGEDRELSV	69	10	01	17		5346
POL	GPERALSVCL	70	10	01	20		5347
POL	LPGKWKPKMI	125	10	39	61		5348
POL	LPGRWKPKMI	125	10	15	23	0.0002	5349
POL	TPVNIIGRNL	167	10	26	41	0.0003	5350
POL	TPVNIIGRNM	167	10	24	38		5351
POL	SPIETVPVKL	189	10	53	83	0.0028	5352
POL	WPLTEEKIKA	211	10	54	84	0.0018	5353
POL	GPENPYNTPI	240	10	24	38		5354
POL	GPENPYNTPV	240	10	38	59	0.0002	5355

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	NPYNTPIFAI	243	10	24	38		5356
POL	NPYNTPVFAI	243	10	37	58	0.0034	5357
POL	VPLDKDFRKY	307	10	18	28	0.0002	5358
POL	TPGIRYQYNV	328	10	51	80	0.0004	5359
POL	LPQGWKGSPA	338	10	58	92	0.0120	5360
POL	EPFRKQNPDI	358	10	16	25	0.0002	5361
POL	NPDIVIYQYM	364	10	17	27	0.0005	5362
POL	NPEIVIYQYM	364	10	23	36		5363
POL	PPFLWMGYEL	414	10	64	100	0.0002	5364
POL	HPDKWTVQPI	424	10	53	83	0.0012	5365
POL	DPSKDLIAEI	512	10	26	41	0.0002	5366
POL	LPIQKETWEA	583	10	15	23		5367
POL	PPLVKLWYQL	612	10	53	83	0.0002	5368
POL	EPIVGAETFY	624	10	21	33	0.0002	5369
POL	QPDKSESELV	701	10	37	58	0.0002	5370
POL	LPPIVAKEIV	780	10	26	41		5371
POL	LPPVVAKEIV	780	10	27	42	0.0002	5372
POL	PPIVAKEIVA	781	10	25	39		5373
POL	PPVVAKEIVA	781	10	28	44	0.0066	5374
POL	IPAETGQETA	841	10	58	91	0.0002	5375
POL	IPYNPQSQGV	893	10	63	98	0.0023	5376
POL	DPIWKGPAKL	984	10	35	55		5377
POL	DPLWKGPAKL	984	10	15	23	0.0001	5378
POL	VPTFNFPQITL	79	11	01	17		5379
POL	FPQITLWQRPL	87	11	40	63		5380
POL	KPKMIGGIGGF	130	11	60	94	0.0004	5381
POL	TPVNIIGRNLL	167	11	26	41	0.0002	5382
POL	TPVNIIGRNML	167	11	24	38		5383
POL	FPISPIETVPV	186	11	55	86	0.0067	5384
POL	WPLTEEKIKAL	211	11	54	84	0.0001	5385
POL	GPENPYNTPIF	240	11	24	38		5386
POL	GPENPYNTPVF	240	11	38	59	0.0001	5387
POL	HPAGLKKKKS	285	11	50	78	0.0001	5388
POL	IPSINNETPGI	321	11	31	48		5389
POL	IPSTNNETPGI	321	11	11	17		5390
POL	TPGIRYQYNVL	328	11	51	80	0.0015	5391
POL	LPQGWKGSPAI	338	11	58	92	0.0002	5392
POL	EPFRKQNPDIV	358	11	14	22		5393
POL	EPPFLWMGYE	413	11	63	98	0.0001	5394
POL	HPDKWTVQPI	424	11	12	19		5395
POL	QPIQLPEKDSW	431	11	13	20		5396
POL	QPIVLPEKDSW	431	11	13	20		5397
POL	IPLTEEAELEL	482	11	11	17		5398
POL	VPLTEEAELEL	482	11	19	30		5399
POL	EPFKNLKTGK	536	11	45	70	0.0001	5400
POL	LPIQKETWEA	583	11	15	23		5401
POL	LPIQKETWET	583	11	27	42		5402
POL	TPPLVKLWYQ	611	11	53	83	0.0001	5403
POL	EPIVGAETFYV	624	11	21	33		5404
POL	LPPIVAKEIVA	780	11	25	39		5405

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HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	LPPVVAKEIVA	780	11	27	42	0.0001	5406
POL	IPAETGQETAY	841	11	58	91	0.0001	5407
POL	IPYNPQSQGVV	893	11	59	92	0.0120	5408
POL	NPQSQGVVES	896	11	53	83	0.0001	5409
POL	DPIWKGPAKLL	984	11	34	53		5410
POL	DPLWKGPAKL	984	11	14	22		5411
REV	SPEGTRQA	33	8	13	20		5412
REV	RPAEPVPL	70	8	20	31		5413
REV	VPLQLPPI	75	8	11	17		5414
REV	VPLQLPPL	75	8	36	56	0.0490	5415
REV	PPLERLTL	80	8	19	30	0.0001	5416
REV	LPPLERLTL	79	9	19	30	0.3100	5417
REV	QPQGTETGV	100	9	05	18		5418
REV	PPSPEGTRQA	30	10	12	19		5419
REV	RPAEPVPLQL	70	10	20	31		5420
REV	EPVPLQLPPI	73	10	11	17		5421
REV	EPVPLQLPPL	73	10	34	53	0.0023	5422
REV	PPPSPEGTRQA	29	11	12	19		5423
REV	VPLQLPPIERL	75	11	11	17		5424
REV	VPLQLPPLERL	75	11	34	53	0.0001	5425
TAT	HPGSQPKTA	16	9	26	41	0.0007	5426
TAT	HPGSQPRTA	16	9	10	16		5427
TAT	GPKESKKKV	90	9	13	20		5428
TAT	EPVDPNLEPW	2	10	14	22		5429
TAT	EPVDPRLEPW	2	10	13	20	0.0001	5430
VIF	HPKISSEV	48	8	13	20		5431
VIF.	HPKVSSEV	48	8	19	30		5432
VIF	HPRISSEV	48	8	13	20		5433
VIF	IPLGDARL	57	8	14	22		5434
VIF	IPLGEARL	57	8	20	31		5435
VIF	DPDLADQL	104	8	19	30		5436
VIF	DPGLADQL	104	8	19	30		5437
VIF	SPRCEYQA	135	8	21	33	0.0008	5438
VIF	IPLGDARLV	57	9	11	17		5439
VIF	IPLGEARLV	57	9	19	30		5440
VIF	DPDLADQLI	104	9	19	30	0.0002	5441
VIF	DPGLADQLI	104	9	19	30		5442
VIF	KPKKIKPPL	160	9	10	16		5443
VIF	PPLPSVKKL	167	9	21	33		5444
VIF	PPLPSVRKL	167	9	14	22		5445
VIF	HPKISSEVHI	48	10	13	20		5446
VIF	HPKVSSEVHI	48	10	19	30		5447
VIF	HPRISSEVHI	48	10	13	20	0.0330	5448
VIF	IPLGEARLVI	57	10	10	16		5449
VIF	KPPLPSVKKL	166	10	20	31		5450
VIF	DPDLADQLHHL	104	11	18	28		5451
VPR	EPYNEWTL	13	8	30	47		5452
VPR	FPRIWLHSL	34	9	10	16		5453
VPR	FPRPWLHGL	34	9	24	38		5454
VPR	GPQREPYNEW	9	10	37	58	0.0001	5455

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
VPR	EPYNEWTLEL	13	10	29	45	0.0054	5456
VPR	RPWLHGLGQY	36	10	10	16		5457
VPR	EPYNEWTLEL	13	11	29	45		5458
VPR	RPWLHGLGQH	36	11	12	19		5459
VPU	APWDVDDL	99	8	12	19		5460

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	KKLWTLYL	9	8	01	50	5461
ENV	RKSWSLYI	9	8	01	50	5462
ENV	WRWGTLFL	15	8	01	50	5463
ENV	WRWGTMLL	15	8	01	50	5464
ENV	EKLWVTVY	43	8	09	15	5465
ENV	WKEATTTL	56	8	23	36	5466
ENV	MIIEDIISL	117	8	29	45	5467
ENV	IKNCSFNI	182	8	13	20	5468
ENV	PKVSFEPI	251	8	30	47	5469
ENV	LKCNDKKF	272	8	13	20	5470
ENV	AKTIIVQL	330	8	14	22	5471
ENV	QRGPGRAF	360	8	01	33	5472
ENV	KKKKTGYI	374	8	01	50	5473
ENV	IRQAHCNI	381	8	17	27	5474
ENV	IKQIINMW	489	8	33	52	5475
ENV	IKQIVNMW	489	8	13	21	5476
ENV	QRVGQAMY	497	8	11	17	5477
ENV	FRPGGGDM	546	8	43	67	5478
ENV	WRSELYKY	557	8	54	84	5479
ENV	YKYKVVEI	562	8	13	20	5480
ENV	YKYKVVKI	562	8	29	45	5481
ENV	ARQLLSGI	627	8	38	59	5482
ENV	VRQLLSGI	627	8	10	16	5483
ENV	LKLTVWGI	652	8	13	20	5484
ENV	EKNEQDLL	749	8	17	27	5485
ENV	EKNEQELL	749	8	18	28	5486
ENV	LRIIFAVL	790	8	17	27	5487
ENV	LRIVFAVL	790	8	28	44	5488
ENV	VRQGYSPL	803	8	56	88	5489
ENV	IRLVNGFL	843	8	11	17	5490
ENV	IRLVSGFL	843	8	13	20	5491
ENV	YIIRLRDFI	865	8	13	20	5492
ENV	YIIRLRDLL	865	8	15	23	5493
ENV	IIRLRDFIL	866	8	13	20	5494
ENV	IIRLRDLLL	866	8	13	20	5495
ENV	GRRGWEAL	884	8	09	15	5496
ENV	LKGLRLGW	890	8	12	40	5497
ENV	LRGLQRGW	890	8	05	17	5498
ENV	LRLGWEGL	893	8	10	32	5499
ENV	LKYLWNLL	900	8	14	22	5500
ENV	LKYWWNLL	900	8	14	22	5501
ENV	LKNSAINL	914	8	10	16	5502
ENV	LKNSAISL	914	8	10	16	5503
ENV	LKNSAVSL	914	8	13	20	5504
ENV	PRRIRQGF	951	8	11	17	5505
ENV	PRRIRQGL	951	8	26	41	5506
ENV	GKDLWVTVY	42	9	01	33	5507
ENV	EKLWVTVYY	43	9	09	15	5508
ENV	WKEATTTLF	56	9	23	36	5509
ENV	WKNNMVEQM	109	9	35	55	5510

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	MHEDIISLW	117	9	29	45	5511
ENV	GKNEINDTY	218	9	01	20	5512
ENV	IHYCAPAGF	261	9	27	42	5513
ENV	IHYCTPAGF	261	9	10	16	5514
ENV	IKPVVSTQL	298	9	33	52	5515
ENV	IRPVVSTQL	298	9	26	41	5516
ENV	CRIKQIINM	487	9	30	47	5517
ENV	CRIKQIVNM	487	9	12	19	5518
ENV	GKAMYAPPI	501	9	23	36	5519
ENV	GRAMYAPPI	501	9	12	19	5520
ENV	MRDNWRSEL	553	9	40	63	5521
ENV	YKVVKIEPL	564	9	25	39	5522
ENV	EREKRAVGI	590	9	11	17	5523
ENV	QHLLKLTVW	649	9	13	20	5524
ENV	QHLLQLTVW	649	9	34	53	5525
ENV	QHMLQLTVW	649	9	10	16	5526
ENV	IKQLQARVL	659	9	40	63	5527
ENV	ARVLAVERY	664	9	33	52	5528
ENV	ERYLKDQQL	670	9	30	47	5529
ENV	ERYLRDQQL	670	9	18	28	5530
ENV	LKDQQLLGI	673	9	27	42	5531
ENV	LRDQQLLGI	673	9	19	30	5532
ENV	DKWASLWNW	759	9	26	41	5533
ENV	TKWLWYIKI	771	9	15	23	5534
ENV	LRNLCLFSY	857	9	16	25	5535
ENV	LRSLCLFSY	857	9	35	55	5536
ENV	YHRLRDFIL	865	9	13	20	5537
ENV	YHRLRDLLL	865	9	13	20	5538
ENV	HRLRDLLLI	866	9	11	17	5539
ENV	LKNSAVSLL	914	9	11	17	5540
ENV	IRQGLERAL	954	9	34	53	5541
ENV	KKLWTLYLAM	9	10	01	50	5542
ENV	RKSWSLYIAM	9	10	01	50	5543
ENV	WRWGTLFLGM	15	10	01	50	5544
ENV	WRWGTMLLGM	15	10	01	50	5545
ENV	GKDLWVTVYY	42	10	01	33	5546
ENV	LKPCVKLTPL	129	10	55	86	5547
ENV	VKLTPLCVTL	133	10	52	81	5548
ENV	PKVSFEPIPI	251	10	30	47	5549
ENV	IKPVVSTQLL	298	10	33	52	5550
ENV	IRPVVSTQLL	298	10	26	41	5551
ENV	MHSFNCGGEF	433	10	13	20	5552
ENV	THSFNCGGEF	433	10	22	34	5553
ENV	THSFNCRGEF	433	10	13	20	5554
ENV	CRIKQIINMW	487	10	30	47	5555
ENV	CRIKQIVNMW	487	10	12	19	5556
ENV	IRCSSNITGL	513	10	12	19	5557
ENV	MRDNWRSELY	553	10	40	63	5558
ENV	KRAVGIGAVF	593	10	11	17	5559
ENV	LRAIEAQQHL	642	10	45	70	5560

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	ARVLAVERYL	664	10	33	52	5561
ENV	ERYLKDQQLL	670	10	29	45	5562
ENV	ERYLRDQQLL	670	10	17	27	5563
ENV	LKDQQLLGIW	673	10	27	42	5564
ENV	LRDQQLLGIW	673	10	19	30	5565
ENV	EKNEQDLLAL	749	10	17	27	5566
ENV	EKNEQELLEL	749	10	13	20	5567
ENV	DKWASLWNWF	759	10	26	41	5568
ENV	TKWLWYIKIF	771	10	12	19	5569
ENV	LRIIFAVLSI	790	10	14	22	5570
ENV	LRIVFAVLSI	790	10	19	30	5571
ENV	NRVRQGYSPL	801	10	52	81	5572
ENV	VRQGYSPLSF	803	10	48	75	5573
ENV	PRGPDRPEGI	820	10	12	19	5574
ENV	IRLVSGFLAL	843	10	11	17	5575
ENV	YHRLRDLLLI	865	10	11	17	5576
ENV	LRLGWEGLKY	893	10	09	29	5577
ENV	LKYWWNLLQY	900	10	14	22	5578
ENV	IRQGLERALL	954	10	33	52	5579
ENV	WRWGTLFLGML	15	11	01	50	5580
ENV	WRWGTMLLGML	15	11	01	50	5581
ENV	YRLINCNTSAI	235	11	15	24	5582
ENV	HYCAPAGFAI	261	11	27	42	5583
ENV	IKPVVSTQLLL	298	11	33	52	5584
ENV	IRPVVSTQLLL	298	11	26	41	5585
ENV	TRPNNNTRKSI	346	11	12	19	5586
ENV	QRGPGRAFVTI	360	11	01	33	5587
ENV	MHSFNCGGEFF	433	11	13	20	5588
ENV	THSFNCGGEFF	433	11	21	33	5589
ENV	THSFNCRGEFF	433	11	13	20	5590
ENV	IRCSSNITGLL	513	11	10	16	5591
ENV	YKYKVVKIEPL	562	11	25	39	5592
ENV	EKRAVGIGAVF	592	11	10	16	5593
ENV	KRAVGIGAVFL	593	11	11	17	5594
ENV	LRAIEAQQHLL	642	11	44	69	5595
ENV	QHLLKLTVWGI	649	11	13	20	5596
ENV	QHLLQLTVWGI	649	11	34	53	5597
ENV	LKLTVWGIKQL	652	11	13	20	5598
ENV	GKLICTTAVPW	686	11	19	30	5599
ENV	GKLICTTNVPW	686	11	17	27	5600
ENV	GKLICTTTVPW	686	11	12	19	5601
ENV	TKWLWYIKIFI	771	11	12	19	5602
ENV	IKIFIMIVGGL	777	11	38	59	5603
ENV	LKGLRLGWEGL	890	11	08	27	5604
ENV	LRLGWEGLKYL	893	11	09	29	5605
ENV	LKYWWNLLQYW	900	11	14	22	5606
ENV	LHPRRIRQGL	948	11	12	19	5607
ENV	RRIRQGLERAL	952	11	16	25	5608
ENV	TRIRQGLERAL	952	11	11	17	5609
GAG	DKWEKIRL	14	8	18	28	5610

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	KKYKLKHI	28	8	10	16	5611
GAG	KKYRLKHL	28	8	16	25	5612
GAG	YKLKHIVW	30	8	13	20	5613
GAG	YRLKHLVW	30	8	17	27	5614
GAG	CRQILGQL	59	8	15	23	5615
GAG	IKDTKEAL	96	8	10	16	5616
GAG	VKDTKEAL	96	8	33	52	5617
GAG	VRDTKEAL	96	8	10	16	5618
GAG	TKEALDKI	99	8	33	52	5619
GAG	TKEALEKI	99	8	10	16	5620
GAG	GHQAAMQM	214	8	61	95	5621
GAG	KRWIILGL	287	8	55	86	5622
GAG	PKEPFRDY	313	8	63	98	5623
GAG	FRDYVDRF	317	8	64	100	5624
GAG	CKTILKAL	354	8	28	44	5625
GAG	CKTILRAL	354	8	18	28	5626
GAG	ARVLAEAM	384	8	57	89	5627
GAG	HKGRPGNF	477	8	23	37	5628
GAG	NKGRPGNF	477	8	14	23	5629
GAG	SKGRPGNF	477	8	11	18	5630
GAG	LKDKEPPL	535	8	01	25	5631
GAG	ERTENSLY	537	8	01	25	5632
GAG	EKEEKGLY	538	8	01	25	5633
GAG	GKLDAWEKI	11	9	17	27	5634
GAG	LRPGGKKKY	21	9	35	55	5635
GAG	KKKYRLKHL	27	9	13	20	5636
GAG	SRELERFAL	39	9	22	34	5637
GAG	ERFALNPGL	44	9	15	23	5638
GAG	ERFAVNPGL	44	9	15	23	5639
GAG	VKVIEEKAF	177	9	24	38	5640
GAG	VKVVEEKAF	177	9	28	44	5641
GAG	EKAFSPEVI	182	9	48	75	5642
GAG	GHQAAMQML	214	9	61	95	5643
GAG	LHPVHAGPI	236	9	22	34	5644
GAG	VHPVHAGPI	236	9	14	22	5645
GAG	MREPRGSDI	249	9	44	69	5646
GAG	YKRWIILGL	286	9	55	86	5647
GAG	VRMYSPTSI	298	9	14	22	5648
GAG	VRMYSPVSI	298	9	40	63	5649
GAG	IKQGPKEPF	309	9	20	31	5650
GAG	IRQGPKEPF	309	9	42	66	5651
GAG	FRDYVDRFF	317	9	35	55	5652
GAG	FRDYVDRFY	317	9	29	45	5653
GAG	VKNWMTDTL	337	9	16	25	5654
GAG	VKNWMTETL	337	9	36	56	5655
GAG	SHKGRPGNF	476	9	23	37	5656
GAG	HKGRPGNFL	477	9	23	37	5657
GAG	NKGRPGNFL	477	9	09	15	5658
GAG	RKEPTAPPL	492	9	01	50	5659
GAG	DKDKELYPL	536	9	01	25	5660

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	GKKKYRLKHL	25	10	12	19	5661
GAG	KKYKLKHIVW	28	10	10	16	5662
GAG	KKYRLKHLVW	28	10	16	25	5663
GAG	KHIVWASREL	33	10	21	33	5664
GAG	KHLVWASREL	33	10	36	56	5665
GAG	ERFALNPGLL	44	10	15	23	5666
GAG	ERFAVNPGLL	44	10	15	23	5667
GAG	VHQAISPRTL	164	10	27	42	5668
GAG	VHQALSPRTL	164	10	11	17	5669
GAG	VRMYSPTSIL	298	10	14	22	5670
GAG	VRMYSPVSIL	298	10	40	63	5671
GAG	VKNWMTDTLL	337	10	16	25	5672
GAG	VKNWMTETLL	337	10	36	56	5673
GAG	LKALGPAATL	358	10	16	25	5674
GAG	HKARVLAEAM	382	10	57	89	5675
GAG	CRAPRKKGCW	438	10	53	83	5676
GAG	WKCGKEGHQM	447	10	46	72	5677
GAG	ERQANFLGKI	464	10	54	84	5678
GAG	SHKGRPGNFL	476	10	23	37	5679
GAG	TRKEPTAPPL	491	10	01	50	5680
GAG	QKQEPIDKEL	530	10	12	19	5681
GAG	EKEEKGLYPL	538	10	01	25	5682
GAG	DKELYPLASL	541	10	13	21	5683
GAG	DKELYPLTSL	541	10	10	16	5684
GAG	LKSLFGNDPL	552	10	12	19	5685
GAG	ARASVLSGGEL	3	11	11	17	5686
GAG	ARASVLSGGKL	3	11	28	44	5687
GAG	GKLDAWEKIRL	11	11	16	25	5688
GAG	IRLRPGGKKKY	19	11	33	52	5689
GAG	LRPGGKKKYKL	21	11	10	16	5690
GAG	LRPGGKKKYRL	21	11	16	25	5691
GAG	KKKYRLKHLVW	27	11	13	20	5692
GAG	LKHIVWASREL	32	11	21	33	5693
GAG	LKHLVWASREL	32	11	22	34	5694
GAG	LRSLYNTVATL	77	11	13	20	5695
GAG	VKDTKEALDKI	96	11	16	25	5696
GAG	PRTLNAWVKVI	170	11	30	48	5697
GAG	EKAFSPEVIPM	182	11	48	75	5698
GAG	DRLHPVHAGPI	234	11	22	34	5699
GAG	DRVHPVHAGPI	234	11	14	22	5700
GAG	VHAGPIAPGQM	239	11	17	27	5701
GAG	VHAGPIPPGQM	239	11	17	27	5702
GAG	KRWIILGLNKI	287	11	55	86	5703
GAG	GHKARVLAEAM	381	11	35	55	5704
GAG	SHKARVLAEAM	381	11	19	30	5705
GAG	MKDCTERQANF	456	11	50	78	5706
GAG	ERQANFLGKIW	464	11	54	84	5707
GAG	QKQEPIDKELY	530	11	12	19	5708
GAG	LKDKEPPLASL	535	11	01	25	5709
GAG	ERTENSLYPPL	537	11	01	25	5710

Table XII
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	GKWSKSSI	3	8	18	28	5711
NEF	SKSSIVGW	6	8	20	31	5712
NEF	EKGGLDGL	121	8	26	41	5713
NEF	EKGGLEGL	121	8	34	53	5714
NEF	SKKRQEIL	177	8	25	39	5715
NEF	KRQDILDL	181	8	18	28	5716
NEF	KRQEILDL	181	8	32	50	5717
NEF	ARELHPEF	322	8	11	17	5718
NEF	ARELHPEY	322	8	24	38	5719
NEF	EKGGLDGLI	121	9	23	36	5720
NEF	EKGGLEGLI	121	9	27	42	5721
NEF	KKRQEILDL	179	9	25	39	5722
NEF	QKRQDILDL	179	9	12	19	5723
NEF	KRQDILDLW	181	9	18	28	5724
NEF	KRQEILDLW	181	9	32	50	5725
NEF	IRYPLTFGW	214	9	13	20	5726
NEF	TRFPLTFGW	214	9	12	19	5727
NEF	LHPICQHGM	258	9	10	16	5728
NEF	LHPMSQHGM	258	9	12	19	5729
NEF	ARELHPEFY	322	9	11	17	5730
NEF	ARELHPEYY	322	9	21	33	5731
NEF	SRDLEKHGAI	50	10	14	22	5732
NEF	VRPQVPLRPM	97	10	47	73	5733
NEF	LRPMTYKGAF	103	10	12	19	5734
NEF	SHFLKEKGGL	115	10	29	45	5735
NEF	LKEKGGLDGL	118	10	26	42	5736
NEF	LKEKGGLEGL	118	10	29	47	5737
NEF	EKGGLDGLIY	121	10	21	33	5738
NEF	EKGGLEGLIY	121	10	19	30	5739
NEF	SKKRQEILDL	177	10	25	39	5740
NEF	KKRQEILDLW	179	10	25	39	5741
NEF	QKRQDILDLW	179	10	12	19	5742
NEF	YHTQGFFPDW	193	10	14	22	5743
NEF	YHTQGYFPDW	193	10	25	39	5744
NEF	GKWSKSSIVGW	3	11	18	28	5745
NEF	LKEKGGLDGLI	118	11	23	37	5746
NEF	LKEKGGLEGLI	118	11	24	39	5747
NEF	SKKRQEILDLW	177	11	25	39	5748
NEF	KRQDILDLWVY	181	11	16	25	5749
NEF	KRQEILDLWVY	181	11	29	45	5750
NEF	TRFPLTFGWCF	214	11	10	16	5751
POL	TRRELQVW	43	8	13	20	5752
POL	GKWKPKMI	127	8	41	64	5753
POL	GRWKPKMI	127	8	16	25	5754
POL	VRQYDQIL	143	8	21	33	5755
POL	HKAIGTVL	156	8	20	31	5756
POL	KKAIGTVL	156	8	29	45	5757
POL	GRNLLTQI	173	8	21	33	5758
POL	GRNMLTQI	173	8	19	30	5759
POL	GRNMLTQL	173	8	11	17	5760

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PKVKQWPL	206	8	51	80	5761
POL	KKKDSTKW	253	8	57	89	5762
POL	NKRTQDFW	270	8	57	89	5763
POL	KKKSVTVL	291	8	50	78	5764
POL	RKYTAFTI	314	8	62	97	5765
POL	IRYQYNVL	331	8	53	83	5766
POL	WKGSPAIF	342	8	59	92	5767
POL	FRKQNPDI	360	8	16	25	5768
POL	HRAKIEEL	387	8	26	41	5769
POL	HRTKIEEL	387	8	22	34	5770
POL	LREHLLKW	394	8	17	27	5771
POL	LRQHLLRW	394	8	15	23	5772
POL	EHLLKWGF	396	8	14	22	5773
POL	QHLLRWGF	396	8	12	19	5774
POL	KHQKEPPF	409	8	62	97	5775
POL	QKEPPFLW	411	8	63	98	5776
POL	DKWTVQPI	426	8	54	84	5777
POL	VKQLCKLL	465	8	28	44	5778
POL	VRQLCKLL	465	8	19	30	5779
POL	TKALTEVI	475	8	11	17	5780
POL	SKDLIAEI	514	8	27	42	5781
POL	QKQGQDQW	522	8	16	25	5782
POL	QKQGQGQW	522	8	24	38	5783
POL	QKIATESI	565	8	14	22	5784
POL	GKTPKFKL	576	8	17	27	5785
POL	GKTPKFRL	576	8	30	47	5786
POL	QKETWEAW	586	8	15	23	5787
POL	QKETWETW	586	8	27	42	5788
POL	TKIGKAGY	642	8	10	16	5789
POL	TKLGKAGY	642	8	36	56	5790
POL	GRQKVVSL	654	8	24	38	5791
POL	QKTELHAI	667	8	12	19	5792
POL	QKTELQAI	667	8	42	66	5793
POL	IKKEKVYL	718	8	35	55	5794
POL	DKLVSAGI	741	8	16	25	5795
POL	DKLVSSGI	741	8	29	45	5796
POL	YHNNWRAM	767	8	10	16	5797
POL	YHSNWRAM	767	8	39	61	5798
POL	WRAMASDF	771	8	43	67	5799
POL	THLEGKII	818	8	35	55	5800
POL	THLEGKVI	818	8	26	41	5801
POL	VHVASGYI	829	8	53	83	5802
POL	GRWPVKTI	858	8	13	21	5803
POL	GRWPVKVI	858	8	22	35	5804
POL	NKELKKII	907	8	57	89	5805
POL	VRDQAEHL	917	8	48	75	5806
POL	VREQAEHL	917	8	13	20	5807
POL	RKGGIGGY	939	8	59	92	5808
POL	TKELQKQI	962	8	47	75	5809
POL	YRDSRDPI	979	8	35	55	5810

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	YRDSRDPL	979	8	14	22	5811
POL	WKGPAKLL	987	8	59	92	5812
POL	PRRKAKII	1014	8	50	78	5813
POL	PRRKVKII	1014	8	11	17	5814
POL	IKDYGKQM	1021	8	11	17	5815
POL	IRDYGKQM	1021	8	50	78	5816
POL	QRPLVTIKI	94	9	14	22	5817
POL	QRPLVTVKI	94	9	12	19	5818
POL	WKPKMIGGI	129	9	60	94	5819
POL	IKVRQYDQI	141	9	41	64	5820
POL	VRQYDQILI	143	9	20	31	5821
POL	VRQYDQIPI	143	9	13	20	5822
POL	GHKAIGTVL	155	9	20	31	5823
POL	GKKAIGTVL	155	9	29	45	5824
POL	EKIKALTEI	216	9	28	44	5825
POL	EKIKALVEI	216	9	15	23	5826
POL	EKEGKISKI	231	9	36	56	5827
POL	SKIGPENPY	237	9	42	66	5828
POL	SRIGPENPY	237	9	11	17	5829
POL	IKKKDSTKW	252	9	57	89	5830
POL	TKWRKLVDF	258	9	59	92	5831
POL	RKLVDFREL	261	9	63	98	5832
POL	KKKKSVTVL	290	9	50	78	5833
POL	FRKYTAFTI	313	9	61	97	5834
POL	RKQNPDIVI	361	9	14	22	5835
POL	QHRAKIEEL	386	9	26	41	5836
POL	QHRTKIEEL	386	9	22	34	5837
POL	KKHQKEPPF	408	9	60	94	5838
POL	KHQKEPPFL	409	9	62	97	5839
POL	QKEPPFLWM	411	9	63	98	5840
POL	QKLVGKLNW	447	9	62	97	5841
POL	GKLNWASQI	451	9	61	95	5842
POL	IKVKQLCKL	463	9	29	45	5843
POL	IKVRQLCKL	463	9	18	28	5844
POL	LKEPVHGVY	502	9	41	64	5845
POL	FKNLKTGKY	538	9	45	70	5846
POL	YKNLKTGKY	538	9	10	16	5847
POL	LKTGKYAKM	541	9	19	30	5848
POL	LKTGKYARM	541	9	13	20	5849
POL	AHTNDVKQL	552	9	46	72	5850
POL	QKETWEAWW	586	9	15	23	5851
POL	QKETWETWW	586	9	27	42	5852
POL	QKTELQAIY	667	9	12	19	5853
POL	KKEKVYLAW	719	9	20	32	5854
POL	KKEKVYLSW	719	9	13	21	5855
POL	RKVLFLDGI	749	9	50	78	5856
POL	DHEKYHSNW	763	9	10	16	5857
POL	EHEKYHSNW	763	9	20	31	5858
POL	EHERYHSNW	763	9	13	20	5859
POL	THLEGKIIL	818	9	31	48	5860

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	THLEGKVIL	818	9	23	36	5861
POL	HITDNGSNF	865	9	42	66	5862
POL	IKQEFGIPY	887	9	26	41	5863
POL	EHLKTAVQM	922	9	57	89	5864
POL	KRKGGIGGY	938	9	59	92	5865
POL	TKELQKQII	962	9	10	16	5866
POL	IKIQNFRVY	970	9	12	19	5867
POL	TKIQNFRVY	970	9	37	58	5868
POL	YRDSRDPIW	979	9	35	55	5869
POL	YRDSRDPLW	979	9	14	22	5870
POL	WKGPAKLLW	987	9	59	92	5871
POL	WKGEGAVVI	995	9	61	95	5872
POL	RKAKIIRDY	1016	9	41	64	5873
POL	PKMIGGIGGF	131	10	62	97	5874
POL	IKVRQYDQIL	141	10	21	33	5875
POL	KKDSTKWRKL	254	10	58	91	5876
POL	WRKLVDFREL	260	10	63	98	5877
POL	LKKKKSVTVL	289	10	49	78	5878
POL	DKDFRKYTAF	310	10	18	28	5879
POL	FRKQNPDIVI	360	10	14	22	5880
POL	RKQNPDIVIY	361	10	14	22	5881
POL	AKIEELREHL	389	10	13	20	5882
POL	TKIEELRQHL	389	10	14	22	5883
POL	LREHLLKWGF	394	10	14	22	5884
POL	LRQHLLRWGF	394	10	12	19	5885
POL	DKKHQKEPPF	407	10	60	94	5886
POL	KKHQKEPPFL	408	10	60	94	5887
POL	KHQKEPPFLW	409	10	62	97	5888
POL	DKWTVQPIQL	426	10	28	44	5889
POL	DKWTVQPIVL	426	10	12	19	5890
POL	EKDSWTVNDI	437	10	41	64	5891
POL	GKLNWASQIY	451	10	60	94	5892
POL	IKVKQLCKLL	463	10	28	44	5893
POL	IKVRQLCKLL	463	10	18	28	5894
POL	CKLLRGAKAL	469	10	25	39	5895
POL	CKLLRGTKAL	469	10	24	38	5896
POL	LRGAKALTDI	472	10	22	34	5897
POL	AKALTDIVPL	475	10	17	27	5898
POL	TKALTEVIPL	475	10	11	17	5899
POL	LKEPVHGVYY	502	10	39	61	5900
POL	QKQGQDQWTY	522	10	15	23	5901
POL	QKQGQGQWTY	522	10	24	38	5902
POL	QKIATESIVI	565	10	14	22	5903
POL	GKTPKFKLPI	576	10	17	27	5904
POL	GKTPKFRLPI	576	10	29	45	5905
POL	FKLPIQKETW	581	10	20	32	5906
POL	FRLPIQKETW	581	10	26	41	5907
POL	DRGRQKVVSL	652	10	18	28	5908
POL	QKTELQAIHL	667	10	15	23	5909
POL	QKTELQAIYL	667	10	12	19	5910

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	HHLALQDSGL	674	10	15	23	5911
POL	IKKEKVYLAW	718	10	20	31	5912
POL	IKKEKVYLSW	718	10	13	20	5913
POL	IRKVLFLDGI	748	10	49	77	5914
POL	DKAQEEHEKY	758	10	25	39	5915
POL	DKAQEEHERY	758	10	15	23	5916
POL	EKYHSNWRAM	765	10	28	44	5917
POL	ERYHSNWRAM	765	10	10	16	5918
POL	WRAMASDFNL	771	10	41	64	5919
POL	DKCQLKGEAM	793	10	44	69	5920
POL	VKAACWWAGI	878	10	31	48	5921
POL	LKTAVQMAVF	924	10	57	89	5922
POL	HINFKRKGGI	934	10	58	91	5923
POL	FKRKGGIGGY	937	10	59	92	5924
POL	QKQIIKIQNF	966	10	12	19	5925
POL	QKQITKIQNF	966	10	34	53	5926
POL	IKIQNFRVYY	970	10	12	19	5927
POL	TKIQNFRVYY	970	10	37	58	5928
POL	RRKAKIIRDY	1015	10	41	64	5929
POL	TRANSPTRREL	22	11	11	17	5930
POL	ERAHSPATREL	25	11	01	50	5931
POL	SRANSPTSRDL	25	11	01	50	5932
POL	TRANSPSSREL	34	11	01	33	5933
POL	TRANSPTTREL	36	11	01	33	5934
POL	IKIGGQLKEAL	100	11	19	30	5935
POL	GKWKPKMIGGI	127	11	41	64	5936
POL	GRWKPKMIGGI	127	11	16	25	5937
POL	PKMIGGIGGFI	131	11	62	97	5938
POL	IKVRQYDQILI	141	11	20	31	5939
POL	IKVRQYDQIPI	141	11	13	20	5940
POL	VRQYDQILIEI	143	11	20	31	5941
POL	VRQYDQIPIEI	143	11	12	19	5942
POL	VKQWPLTEEKI	208	11	52	81	5943
POL	IKALVEICTEM	218	11	15	23	5944
POL	KKKDSTKWRKL	253	11	57	89	5945
POL	FRELNKRTQDF	266	11	57	89	5946
POL	KRTQDFWEVQL	271	11	52	81	5947
POL	RKYTAFTIPSI	314	11	37	58	5948
POL	FRKQNPDIVIY	360	11	14	22	5949
POL	AKIEELREHLL	389	11	13	20	5950
POL	TKIEELRQHLL	389	11	14	22	5951
POL	DKKHQKEPPFL	407	11	60	94	5952
POL	KKHQKEPPFLW	408	11	60	94	5953
POL	KHQKEPPFLWM	409	11	62	97	5954
POL	QKEPPFLWMGY	411	11	63	98	5955
POL	LHPDKWTVQPI	423	11	53	83	5956
POL	LRGTKALTEVI	472	11	11	17	5957
POL	VKQLTEAVQKI	557	11	30	47	5958
POL	QKIATESIVIW	565	11	14	22	5959
POL	EKEPIVGAETF	622	11	16	25	5960

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	NRETKLGKAGY	639	11	28	44	5961
POL	DKSESELVNQI	703	11	18	28	5962
POL	DKSESELVSQI	703	11	19	30	5963
POL	MHGQVDCSPGI	802	11	52	81	5964
POL	LKTAVQMAVFI	924	11	56	88	5965
POL	ERIIDIIASDI	950	11	12	19	5966
POL	ERIIDIIATDI	950	11	29	45	5967
POL	ERIVDIIATDI	950	11	11	17	5968
POL	TKELQKQIIKI	962	11	10	16	5969
POL	TKELQKQITKI	962	11	31	49	5970
POL	IKVVPRRKAKI	1010	11	51	80	5971
POL	IKVVPRRKVKI	1010	11	11	17	5972
POL	PRRKAKIIRDY	1014	11	41	64	5973
POL	AKIIRDYGKQM	1018	11	42	66	5974
REV	VRIIKILY	18	8	18	28	5975
REV	RKNRRRRW	42	8	21	33	5976
REV	RRNRRRRW	42	8	40	63	5977
REV	WRARQRQI	49	8	36	56	5978
REV	WRERQRQI	49	8	11	17	5979
REV	ERILSTCL	61	8	11	17	5980
REV	ARKNRRRRW	41	9	18	28	5981
REV	ARRNRRRRW	41	9	39	61	5982
REV	ARQRQIISI	51	9	10	16	5983
REV	GRPAEPVPL	69	9	20	31	5984
REV	GRSAEPVPL	69	9	12	19	5985
REV	GRSGDSDEEL	3	10	17	27	5986
REV	IKILYQSNPY	21	10	25	39	5987
REV	RRWRARQRQI	47	10	34	53	5988
REV	RRWRERQRQI	47	10	11	17	5989
REV	GRSGDSDEELL	3	11	16	25	5990
REV	RRRWRARQRQI	46	11	34	53	5991
REV	RRRWRERQRQI	46	11	11	17	5992
REV	WRARQRQIISI	49	11	10	16	5993
REV	GRPAEPVPLQL	69	11	20	31	5994
REV	GRSAEPVPLQL	69	11	12	19	5995
TAT	KKGLGISY	43	8	15	23	5996
TAT	NKGLGISY	43	8	14	22	5997
TAT	TKGLGISY	43	8	19	30	5998
VIF	DRMKIRTW	14	8	12	19	5999
VIF	DRMRINTW	14	8	10	16	6000
VIF	DRMRIRTW	14	8	32	50	6001
VIF	ARLVITTY	64	8	11	17	6002
VIF	LHTGERDW	74	8	22	34	6003
VIF	GHGVSIEW	85	8	31	48	6004
VIF	GHNKVGSL	143	8	47	73	6005
VIF	NKVGSLQY	145	8	47	75	6006
VIF	PKKIKPPL	161	8	19	30	6007
VIF	KKLTEDRW	176	8	13	21	6008
VIF	GHRGSHTM	191	8	25	39	6009
VIF	NRWQVLIVW	3	9	10	16	6010

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	NRWQVMIVW	3	9	42	66	6011
VIF	MKIRTWNSL	16	9	12	19	6012
VIF	MRIRTWKSL	16	9	15	23	6013
VIF	MRIRTWNSL	16	9	15	23	6014
VIF	WKSLVKHHM	21	9	18	28	6015
VIF	WKSLVKYHM	21	9	10	16	6016
VIF	PKISSEVHI	49	9	15	23	6017
VIF	PKVSSEVHI	49	9	20	31	6018
VIF	PRISSEVHI	49	9	15	23	6019
VIF	ARLVITTYW	64	9	11	17	6020
VIF	WHLGHGVSI	82	9	23	36	6021
VIF	WHLGQGVSI	82	9	26	41	6022
VIF	IHLYYFDCF	112	9	16	25	6023
VIF	IHMHYFDCF	112	9	15	23	6024
VIF	NKVGSLQYL	145	9	47	75	6025
VIF	VKKLTEDRW	175	9	13	20	6026
VIF	WKSLVKHHMY	21	10	18	28	6027
VIF	AKGWFYRHHY	35	10	10	16	6028
VIF	VHIPLGDARL	55	10	13	20	6029
VIF	VHIPLGEARL	55	10	20	31	6030
VIF	LHTGERDWHL	74	10	21	33	6031
VIF	GHGVSIEWRL	85	10	15	23	6032
VIF	GHNKVGSLQY	143	10	47	73	6033
VIF	IKPKKIKPPL	159	10	10	16	6034
VIF	TKGHRGSHTM	189	10	18	29	6035
VIF	DRMKIRTWNSL	14	11	12	19	6036
VIF	DRMRIRTWKSL	14	11	15	23	6037
VIF	DRMRIRTWNSL	14	11	15	23	6038
VIF	WKSLVKHHMYI	21	11	11	17	6039
VIF	RHPKVSSEVHI	47	11	16	25	6040
VIF	PKISSEVHIPL	49	11	14	22	6041
VIF	PKVSSEVHIPL	49	11	19	30	6042
VIF	PRISSEVHIPL	49	11	13	20	6043
VIF	ARLVITTYWGL	64	11	11	17	6044
VIF	WHLGHGVSIEW	82	11	23	36	6045
VIF	WHLGQGVSIEW	82	11	26	41	6046
VIF	GHNKVGSLQYL	143	11	47	73	6047
VIF	NKVGSLQYLAL	145	11	46	73	6048
VPR	QREPYNEW	11	8	38	59	6049
VPR	VRHFPRIW	31	8	14	22	6050
VPR	VRHFPRPW	31	8	34	53	6051
VPR	RHFPRIWL	32	8	14	22	6052
VPR	RHFPRPWL	32	8	34	53	6053
VPR	PRIWLHSL	35	8	10	16	6054
VPR	PRPWLHGL	35	8	24	38	6055
VPR	LHGLGQHI	39	8	20	31	6056
VPR	IRILQQLL	61	8	45	70	6057
VPR	CRHSRIGI	77	8	11	17	6058
VPR	QHSRIGII	78	8	16	25	6059
VPR	LKNEAVRHF	26	9	18	28	6060

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	LKQEAVRHF	26	9	11	17	6061
VPR	LKSEAVRHF	26	9	15	23	6062
VPR	VRHFPRIWL	31	9	14	22	6063
VPR	VRHFPRPWL	31	9	34	53	6064
VPR	LHGLGQHIY	39	9	20	31	6065
VPR	IRILQQLLF	61	9	44	69	6066
VPR	QREPYNEWTL	11	10	30	47	6067
VPR	IRILQQLLFI	61	10	36	56	6068
VPR	FRIGCQHSRI	73	10	44	69	6069
VPR	FRIGCRHSRI	73	10	12	19	6070
VPR	RHFPRIWLHSL	32	11	10	16	6071
VPR	RHFPRPWLHGL	32	11	24	38	6072
VPR	PRPWLHGLGQY	35	11	10	16	6073
VPR	QHIYETYGDTW	44	11	17	27	6074
VPR	QHIYNTYGDTW	44	11	13	20	6075
VPU	QRKIDRLI	49	8	21	33	6076
VPU	AKVDYRIVI	6	9	01	33	6077
VPU	RKILRQRKI	44	9	13	21	6078
VPU	LRQRKIDRL	47	9	17	27	6079
VPU	YRKILRQRKI	42	10	13	21	6080
VPU	#KKLLKQKKI	43	10	01	50	6081
VPU	LRQRKIDRLI	47	10	15	24	6082
VPU	RKIDRLIDRI	51	10	12	19	6083
VPU	QRKIDRLIDRI	49	11	12	19	6084

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NTSPRSRV	376	8	01	33	6085
ENV	NTSPRSRVAY	376	10	01	33	6086
ENV	TAGNSSRAAY	376	10	01	33	6087
ENV	TSNSSNSSTPI	160	11	01	33	6088
ENV	GTAGNSSRAAY	375	11	01	33	6089
ENV	HTEGNITL	478	8	01	50	6090
ENV	NANITIPCRI	478	10	01	50	6091
ENV	STRTHREKRAV	586	11	01	50	6092
ENV	DSSNSTGNY	218	9	01	20	6093
ENV	STNGTETF	537	8	01	17	6094
ENV	NTETNKTETF	537	10	01	17	6095
ENV	NTTGNTTETF	537	10	01	17	6096
ENV	GSENGTETF	538	9	02	18	6097
ENV	NTRKSIRI	351	8	10	16	6098
ENV	SSLKGLRL	886	8	10	16	6099
ENV	SSLKGLRLGW	886	10	10	16	6100
ENV	CTPAGFAI	264	8	10	16	6101
ENV	QSSGGDPEI	423	9	10	16	6102
ENV	QSSGGDPEIV	423	10	10	16	6103
ENV	WSQELKNSAV	910	10	10	16	6104
ENV	FAILKCNDKKF	269	11	10	16	6105
ENV	RAVGIGAVF	594	9	11	17	6106
ENV	RAVGIGAVFL	594	10	11	17	6107
ENV	AARTVELL	876	8	11	17	6108
ENV	GTDRVIEV	932	8	11	17	6109
ENV	LALDKWASL	756	9	11	17	6110
ENV	IAARTVELL	874	9	11	17	6111
ENV	VSLLNATAI	919	9	11	17	6112
ENV	YATGDIIGDI	368	10	11	17	6113
ENV	TTNVPWNSSW	691	10	11	17	6114
ENV	LALDKWASLW	756	10	11	17	6115
ENV	ISNWLWYIKI	770	10	11	17	6116
ENV	RSIRLVNGFL	841	10	11	17	6117
ENV	CTTNVPWNSSW	690	11	11	17	6118
ENV	ISNWLWYIKIF	770	11	11	17	6119
ENV	SAVSLLNATAI	917	11	11	17	6120
ENV	VSLLNATAIAV	919	11	11	17	6121
ENV	RAVGIGAV	594	8	12	19	6122
ENV	EAQQHLLKL	646	9	12	19	6123
ENV	EAQQHLLKLTV	646	11	12	19	6124
ENV	RAMYAPPI	502	8	12	19	6125
ENV	GALFLGFL	601	8	12	19	6126
ENV	IAARTVEL	874	8	12	19	6127
ENV	PTRIRQGL	951	8	12	19	6128
ENV	ATGDIIGDI	369	9	12	19	6129
ENV	RSIRLVNGF	841	9	12	19	6130
ENV	MTWMEWEREI	721	10	12	19	6131
ENV	RAILHIPRRI	945	10	12	19	6132
ENV	PTDPNPQEVVL	89	11	12	19	6133
ENV	TSVITQACPKV	242	11	12	19	6134

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	GTGPCKNVSTV	281	11	12	19	6135
ENV	TTHSFNCRGEF	432	11	12	19	6136
ENV	CSGKLICTTTV	684	11	12	19	6137
ENV	ITKWLWYIKIF	770	11	12	19	6138
ENV	FSYHRLRDLLL	863	11	12	19	6139
ENV	LAEEEVVI	312	8	13	20	6140
ENV	GAMFLGFL	601	8	13	20	6141
ENV	RSIRLVSGF	841	9	13	20	6142
ENV	PTDPNPQEVV	89	10	13	20	6143
ENV	SAITQACPKV	243	10	13	20	6144
ENV	GSLAEEEVVI	310	10	13	20	6145
ENV	SSGGDPEIVM	424	10	13	20	6146
ENV	RSIRLVSGFL	841	10	13	20	6147
ENV	FSYHRLRDFI	863	10	13	20	6148
ENV	TSAITQACPKV	242	11	13	20	6149
ENV	FSYHRLRDFIL	863	11	13	20	6150
ENV	NAKTIIVQL	329	9	14	22	6151
ENV	QAMYAPPI	502	8	14	22	6152
ENV	ISNWLWYI	770	8	14	22	6153
ENV	GSLAEEEVV	310	9	14	22	6154
ENV	ITNWLWYIKI	770	10	14	22	6155
ENV	FSYHRLRDLL	863	10	14	22	6156
ENV	IAVAEGTDRV	927	10	14	22	6157
ENV	ITNWLWYIKIF	770	11	14	22	6158
ENV	IAVAEGTDRVI	927	11	14	22	6159
ENV	ITKWLWYIKI	770	10	15	23	6160
ENV	ITLPCRIKQII	483	11	15	23	6161
ENV	IAVAEGTDRII	927	11	15	23	6162
ENV	GSLAEEEV	310	8	16	25	6163
ENV	SSGGDLEI	424	8	16	25	6164
ENV	ITKWLWYI	770	8	16	25	6165
ENV	VAEGTDRV	929	8	16	25	6166
ENV	HSFNCRGEF	434	9	16	25	6167
ENV	VSGFLALAW	846	9	16	25	6168
ENV	VAEGTDRVI	929	9	16	25	6169
ENV	HSFNCRGEFF	434	10	16	25	6170
ENV	IAVAEGTDRI	927	10	16	25	6171
ENV	TTHSFNCGGEF	432	11	16	25	6172
ENV	HSFNCRGEFFY	434	11	16	25	6173
ENV	GTGPCKNV	281	8	17	27	6174
ENV	DAKAYDTEV	70	9	17	27	6175
ENV	ASLWNWFDI	762	9	17	27	6176
ENV	KAYDTEVHNV	72	10	17	27	6177
ENV	VAPTKAKRRV	574	10	17	27	6178
ENV	WASLWNWFDI	761	10	17	27	6179
ENV	ASDAKAYDTEV	68	11	17	27	6180
ENV	KAYDTEVHNVW	72	11	17	27	6181
ENV	VAPTKAKRRVV	574	11	17	27	6182
ENV	CSGKLICTTNV	684	11	17	27	6183
ENV	SSGGDPEIV	424	9	18	28	6184

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	FSYHRLRDF	863	9	18	28	6185
ENV	VAEGTDRII	929	9	18	28	6186
ENV	DTEVHNVW	75	8	19	30	6187
ENV	SSNITGLL	516	8	19	30	6188
ENV	ITNWLWYI	770	8	19	30	6189
ENV	VAEGTDRI	929	8	19	30	6190
ENV	CSSNITGLL	515	9	19	30	6191
ENV	SSNITGLLL	516	9	19	30	6192
ENV	CSSNITGLLL	515	10	19	30	6193
ENV	CSGKLICTTAV	684	11	19	30	6194
ENV	LALAWDDLRSL	850	11	19	30	6195
ENV	LAWDDLRSL	852	9	20	31	6196
ENV	LAWDDLRSLCL	852	11	20	31	6197
ENV	CSSNITGL	515	8	21	33	6198
ENV	PTDPNPQEV	89	9	21	33	6199
ENV	ETFRPGGGDM	544	10	21	33	6200
ENV	PTKAKRRV	576	8	22	34	6201
ENV	GAVFLGFL	601	8	22	34	6202
ENV	PTKAKRRVV	576	9	22	34	6203
ENV	KAMYAPPI	502	8	23	36	6204
ENV	FSYHRLRDL	863	9	23	36	6205
ENV	SSGGDPEI	424	8	24	38	6206
ENV	LALAWDDL	850	8	25	39	6207
ENV	PTDPNPQEI	89	9	25	39	6208
ENV	ITLPCRIKQI	483	10	25	39	6209
ENV	LSGIVQQQNNL	631	11	25	39	6210
ENV	CTHGIRPV	294	8	26	41	6211
ENV	QSNLLRAI	638	8	26	41	6212
ENV	CTHGIRPVV	294	9	26	41	6213
ENV	ITLTVQARQL	621	10	27	42	6214
ENV	ITLTVQARQLL	621	11	27	42	6215
ENV	VSFEPIPIHY	253	10	28	44	6216
ENV	YSPLSFQTL	807	9	29	46	6217
ENV	CAPAGFAI	264	8	29	45	6218
ENV	CAPAGFAIL	264	9	29	45	6219
ENV	ITQACPKVSF	245	10	29	45	6220
ENV	VSFEPIPI	253	8	30	47	6221
ENV	WASLWNWF	761	8	30	47	6222
ENV	QACPKVSFEPI	248	11	30	47	6223
ENV	FAVLSIVNRV	794	10	31	48	6224
ENV	RSLCLFSYHRL	858	11	31	48	6225
ENV	CTHGIKPVV	294	9	32	50	6226
ENV	LSGIVQQQSNL	631	11	32	50	6227
ENV	CTHGIKPV	294	8	33	52	6228
ENV	QARVLAVERY	663	10	33	52	6229
ENV	QARVLAVERYL	663	11	33	52	6230
ENV	EAQQHLLQLTV	646	11	34	54	6231
ENV	VTENFNMW	102	8	34	53	6232
ENV	AAGSTMGAASI	611	11	34	53	6233
ENV	LSIVNRVRQGY	797	11	34	53	6234

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	EAQQHLLQL	646	9	35	56	6235
ENV	RSLCLFSY	858	8	35	55	6236
ENV	HSFNCGGEFF	434	10	35	55	6237
ENV	HSFNCGGEFFY	434	11	35	55	6238
ENV	AASITLTV	618	8	36	56	6239
ENV	HSFNCGGEF	434	9	36	56	6240
ENV	GAASITLTV	617	9	36	56	6241
ENV	LTVQARQLL	623	9	36	56	6242
ENV	ITQACPKV	245	8	37	58	6243
ENV	LTVQARQL	623	8	38	59	6244
ENV	QARQLLSGI	626	9	38	59	6245
ENV	QARQLLSGIV	626	10	38	59	6246
ENV	STMGAASI	614	8	39	61	6247
ENV	GSTMGAASI	613	9	39	61	6248
ENV	STMGAASITL	614	10	39	61	6249
ENV	GSTMGAASITL	613	11	39	61	6250
ENV	QACPKVSF	248	8	40	63	6251
ENV	CASDAKAY	67	8	42	66	6252
ENV	RAIEAQQHLL	643	10	44	69	6253
ENV	RAIEAQQHL	643	9	45	70	6254
ENV	ISLWDQSL	122	8	48	75	6255
ENV	QSLKPCVKL	127	9	48	75	6256
ENV	RSELYKYKVV	558	10	49	77	6257
ENV	RSELYKYKV	558	9	50	78	6258
ENV	STVQCTHGI	289	9	51	80	6259
ENV	VSTVQCTHGI	288	10	51	80	6260
ENV	LTPLCVTL	135	8	54	84	6261
ENV	VTVYYGVPV	47	9	55	86	6262
ENV	VTVYYGVPVW	47	10	55	86	6263
ENV	STQLLLNGSL	303	10	57	89	6264
ENV	VSTQLLLNGSL	302	11	57	89	6265
ENV	LTVWGIKQL	654	9	59	92	6266
GAG	TAPPPESF	508	8	01	33	6267
GAG	ETIDKDLY	537	8	01	25	6268
GAG	PTAPPPESF	507	9	01	33	6269
GAG	TAPPPESFRF	508	10	01	33	6270
GAG	ETIDKDLYPL	537	10	01	25	6271
GAG	RTENSLYPPL	538	10	01	25	6272
GAG	AAAIMMQKSNF	405	11	01	25	6273
GAG	SATIMMQRGNF	405	11	01	25	6274
GAG	PTAPPPESFRF	507	11	01	33	6275
GAG	GAAAATDSNI	123	10	01	50	6276
GAG	AADKGVSQNY	130	10	01	50	6277
GAG	AAGTGNSSQV	130	10	01	50	6278
GAG	GANSIPVGDI	276	10	01	50	6279
GAG	SAQQDLKGGY	393	10	01	50	6280
GAG	TAQQDLKGGY	393	10	01	50	6281
GAG	GANSIPVGDIY	276	11	01	50	6282
GAG	ASAQQDLKGGY	392	11	01	50	6283
GAG	ATAQQDLKGGY	392	11	01	50	6284

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	PAEPTAPPAEI	492	11	01	50	6285
GAG	TAPPAESF	508	8	02	67	6286
GAG	PTAPPAESF	507	9	02	67	6287
GAG	TAPPAESFRF	508	10	02	67	6288
GAG	PTAPPAESFRF	507	11	02	67	6289
GAG	GTRPGNYV	480	8	02	100	6290
GAG	AADKGKVSQNY	129	11	02	18	6291
GAG	EADGKVSQNY	129	10	04	36	6292
GAG	AAIMMQKSNF	406	10	06	15	6293
GAG	TTPSQKQEPI	522	10	09	45	6294
GAG	GASLEEMM	364	8	10	16	6295
GAG	DTKEALEKI	98	9	10	16	6296
GAG	TAPPAESFGF	496	10	10	16	6297
GAG	QALSPRTLNAW	166	11	10	16	6298
GAG	PTAPPAESFGF	495	11	10	16	6299
GAG	ATIMMQRGNF	406	10	11	28	6300
GAG	PSQKQEPI	528	8	11	18	6301
GAG	SSKGRPGNF	476	9	11	18	6302
GAG	TTSTLQEQIAW	260	11	11	17	6303
GAG	QALSPRTL	166	8	11	17	6304
GAG	ASQEVKNW	333	8	11	17	6305
GAG	ASVLSGGEL	5	9	11	17	6306
GAG	QASQEVKNW	332	9	11	17	6307
GAG	ASQEVKNWM	333	9	11	17	6308
GAG	NANPDCKSI	349	9	11	17	6309
GAG	RASVLSGGEL	4	10	11	17	6310
GAG	QASQEVKNWM	332	10	11	17	6311
GAG	NANPDCKSIL	349	10	11	17	6312
GAG	PSSKGRPGNF	475	10	11	17	6313
GAG	QTGSEELRSL	71	10	12	19	6314
GAG	GSEELKSL	73	8	12	19	6315
GAG	GTEELRSL	73	8	12	19	6316
GAG	ATPQDLNM	200	8	12	19	6317
GAG	LTSLRSLF	549	8	12	19	6318
GAG	GSEELRSLY	73	9	12	19	6319
GAG	GATPQDLNM	199	9	12	19	6320
GAG	ATPQDLNMM	200	9	12	19	6321
GAG	STLQEQIAW	262	9	12	19	6322
GAG	RAEQASQEV	329	9	12	19	6323
GAG	KSLFGNDPL	553	9	12	19	6324
GAG	ATLYCVHQKI	85	10	12	19	6325
GAG	GATPQDLNMM	199	10	12	19	6326
GAG	ATPQDLNMML	200	10	12	19	6327
GAG	TSTLQEQIAW	261	10	12	19	6328
GAG	STLQEQIAWM	262	10	12	19	6329
GAG	VATLYCVHQKI	84	11	12	19	6330
GAG	GATPQDLNMML	199	11	12	19	6331
GAG	TSTLQEQIAWM	261	11	12	19	6332
GAG	TSNPPIPVGEI	272	11	12	19	6333
GAG	LTSLKSLF	549	8	13	20	6334

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	YSPTSILDI	301	9	13	20	6335
GAG	PSLQTGSEEL	68	10	13	20	6336
GAG	NSSQVSQNY	144	9	14	31	6337
GAG	NSSQVSQNYPI	144	11	14	31	6338
GAG	TSEGCRQIL	55	9	14	22	6339
GAG	ETSEGCRQIL	54	10	14	22	6340
GAG	AAEWDRVHPV	230	10	14	22	6341
GAG	PSNKGRPGNF	475	10	14	22	6342
GAG	TAPPEESFRF	496	10	14	22	6343
GAG	EAAEWDRVHPV	229	11	14	22	6344
GAG	PTAPPEESFRF	495	11	14	22	6345
GAG	SSQVSQNY	145	8	15	31	6346
GAG	SSQVSQNYPI	145	10	15	31	6347
GAG	SSQVSQNYPIV	145	11	15	31	6348
GAG	RSLYNTVATL	78	10	15	24	6349
GAG	RSLYNTVATLY	78	11	15	24	6350
GAG	EAAEWDRV	229	8	15	23	6351
GAG	ATQDVKNW	333	8	15	23	6352
GAG	TAPPEESF	496	8	15	23	6353
GAG	LASLKSLF	549	8	15	23	6354
GAG	RAEQATQDV	329	9	15	23	6355
GAG	QATQDVKNW	332	9	15	23	6356
GAG	ATQDVKNWM	333	9	15	23	6357
GAG	PTAPPEESF	495	9	15	23	6358
GAG	ATLYCVHQRI	85	10	15	23	6359
GAG	QATQDVKNWM	332	10	15	23	6360
GAG	VATLYCVHQRI	84	11	15	23	6361
GAG	FAVNPGLL	46	8	16	25	6362
GAG	TSEGCRQI	55	8	16	25	6363
GAG	GSEELRSL	73	8	16	25	6364
GAG	TSNPPIPV	272	8	16	25	6365
GAG	PAATLEEM	363	8	16	25	6366
GAG	AATLEEMM	364	8	16	25	6367
GAG	LSGGKLDAW	8	9	16	25	6368
GAG	ETSEGCRQI	54	9	16	25	6369
GAG	MTSNPPIPV	271	9	16	25	6370
GAG	KALGPAATL	359	9	16	25	6371
GAG	PAATLEEMM	363	9	16	25	6372
GAG	DAWEKIRL	14	8	17	27	6373
GAG	LSPRTLNAW	168	9	17	27	6374
GAG	ASRELERFAV	38	10	17	27	6375
GAG	LSPRTLNAWV	168	10	17	27	6376
GAG	HAGPIPPGQM	240	10	17	27	6377
GAG	WASRELERFAV	37	11	17	27	6378
GAG	ATQEVKNW	333	8	18	28	6379
GAG	QATQEVKNW	332	9	18	28	6380
GAG	ATQEVKNWM	333	9	18	28	6381
GAG	HAGPIAPGQM	240	10	18	28	6382
GAG	QATQEVKNWM	332	10	18	28	6383
GAG	PSHKARVL	380	8	19	30	6384

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	TAPPAESF	496	8	20	31	6385
GAG	MTNNPPIPV	271	9	20	31	6386
GAG	PTAPPAESF	495	9	20	31	6387
GAG	FALNPGLL	46	8	22	34	6388
GAG	ASRELERFAL	38	10	22	34	6389
GAG	ETINEEAAEW	224	10	22	34	6390
GAG	WASRELERFAL	37	11	22	34	6391
GAG	PSHKGRPGNF	475	10	23	36	6392
GAG	PSHKGRPGNFL	475	11	23	36	6393
GAG	AAMQMLKETI	217	10	26	41	6394
GAG	QAAMQMLKETI	216	11	26	41	6395
GAG	TTSTLQEQIGW	260	11	27	43	6396
GAG	STLQEQIGW	262	9	27	42	6397
GAG	RAEQATQEV	329	9	27	42	6398
GAG	TSTLQEQIGW	261	10	27	42	6399
GAG	STLQEQIGWM	262	10	27	42	6400
GAG	TSTLQEQIGWM	261	11	27	42	6401
GAG	VSQNYPIVQNL	149	11	28	48	6402
GAG	ASVLSGGKL	5	9	28	44	6403
GAG	RASVLSGGKL	4	10	28	44	6404
GAG	QAISPRTL	166	8	29	45	6405
GAG	GATLEEMM	364	8	29	45	6406
GAG	QAISPRTLNAW	166	11	29	45	6407
GAG	RTLNAWVKVI	171	10	30	47	6408
GAG	RTLNAWVKVV	171	10	31	48	6409
GAG	DTINEEAAEW	224	10	31	48	6410
GAG	DTKEALDKI	98	9	32	50	6411
GAG	AAMQMLKDTI	217	10	33	52	6412
GAG	QAAMQMLKDTI	216	11	33	52	6413
GAG	AAEWDRLHPV	230	10	34	53	6414
GAG	EAAEWDRLHPV	229	11	34	53	6415
GAG	LAEAMSQV	387	8	36	57	6416
GAG	ISPRTLNAW	168	9	36	56	6417
GAG	ISPRTLNAWV	168	10	36	56	6418
GAG	EAAEWDRL	229	8	39	61	6419
GAG	YSPVSILDI	301	9	40	63	6420
GAG	NTVATLYCV	82	9	41	64	6421
GAG	ATPQDLNTM	200	9	42	66	6422
GAG	GATPQDLNTM	199	10	42	66	6423
GAG	ATPQDLNTML	200	10	42	66	6424
GAG	GATPQDLNTML	199	11	42	66	6425
GAG	TTSTLQEQI	260	9	45	71	6426
GAG	NANPDCKTI	349	9	45	70	6427
GAG	GTTSTLQEQI	259	10	45	70	6428
GAG	NANPDCKTIL	349	10	45	70	6429
GAG	ASRELERF	38	8	46	72	6430
GAG	WASRELERF	37	9	46	72	6431
GAG	TSTLQEQI	261	8	47	73	6432
GAG	NTVGGHQAAM	210	10	47	73	6433
GAG	GSDIAGTTSTL	254	11	47	73	6434

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	VSQNYPIV	149	8	48	83	6435
GAG	IAGTTSTL	257	8	48	75	6436
GAG	KAFSPEVI	183	8	50	78	6437
GAG	KAFSPEVIPM	183	10	50	78	6438
GAG	KAFSPEVIPMF	183	11	50	78	6439
GAG	RAPRKKGCW	439	9	53	83	6440
GAG	FSPEVIPM	185	8	54	84	6441
GAG	FSPEVIPMF	185	9	54	84	6442
GAG	CTERQANF	459	8	55	87	6443
GAG	CTERQANFL	459	9	55	87	6444
GAG	QANFLGKI	466	8	57	89	6445
GAG	KARVLAEAM	383	9	57	89	6446
GAG	QANFLGKIW	466	9	57	89	6447
GAG	LSEGATPQDL	196	10	58	91	6448
GAG	RTLNAWVKV	171	9	61	95	6449
NEF	QAEPAAAGV	34	9	01	33	6450
NEF	QTEPAAVGV	32	9	01	17	6451
NEF	RAEPAADGV	32	9	01	17	6452
NEF	RTEPAAVGV	32	9	01	17	6453
NEF	QAEPAAEGV	33	9	01	17	6454
NEF	QAPTAAKGV	33	9	01	17	6455
NEF	RAQAEPAAAGV	32	11	01	17	6456
NEF	GAFDLSFF	110	8	10	16	6457
NEF	GAFDLSFFL	110	9	10	16	6458
NEF	MARELHPEY	321	9	10	16	6459
NEF	MARELHPEYY	321	10	10	16	6460
NEF	AADGVGAV	42	8	11	18	6461
NEF	PAADGVGAV	41	9	11	17	6462
NEF	VSRDLEKHGAI	49	11	11	17	6463
NEF	ATNADCAW	71	8	12	22	6464
NEF	AATNADCAW	70	9	12	22	6465
NEF	ATNADCAWL	71	9	12	22	6466
NEF	AATNADCAWL	70	10	12	22	6467
NEF	PAAEGVGAV	41	9	12	19	6468
NEF	MTYKGAFDL	106	9	12	19	6469
NEF	NTQGYFPDW	194	9	12	19	6470
NEF	TAATNADCAW	69	10	12	19	6471
NEF	GTRFPLTFGW	213	10	12	19	6472
NEF	NTAATNADCAW	68	11	12	19	6473
NEF	TAATNADCAWL	69	11	12	19	6474
NEF	GTRFPLTF	213	8	13	20	6475
NEF	YTPGPGTRF	207	9	13	20	6476
NEF	YTPGPGTRFPL	207	11	13	20	6477
NEF	HTQGFFPDW	194	9	14	22	6478
NEF	EAQEEEEV	82	8	16	25	6479
NEF	EAQEEEEVGF	82	10	16	25	6480
NEF	YTPGPGIRYPL	207	11	16	25	6481
NEF	AAEGVGAV	42	8	17	28	6482
NEF	YTPGPGIRY	207	9	17	27	6483
NEF	WSKSSIVGW	5	9	20	31	6484

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	YSKKRQEI	176	8	22	34	6485
NEF	YSKKRQEIL	176	9	22	34	6486
NEF	LSFFLKEKGGL	114	11	22	34	6487
NEF	YSKKRQEILDL	176	11	22	34	6488
NEF	HTQGYFPDW	194	9	25	39	6489
NEF	LSHFLKEKGGL	114	11	27	42	6490
NEF	LTFGWCFKLV	221	10	35	55	6491
NEF	LTFGWCFKL	221	9	39	61	6492
POL	NSPTSREL	34	8	01	33	6493
POL	PTSRELQV	36	8	01	33	6494
POL	GTLNCPQI	80	8	01	33	6495
POL	PTFNFPQI	80	8	01	33	6496
POL	STNSPTSREL	32	10	01	33	6497
POL	NSPTSRELQV	34	10	01	33	6498
POL	RANSPSSREL	35	10	01	33	6499
POL	GTLNCPQITL	80	10	01	33	6500
POL	PTFNFPQITL	80	10	01	33	6501
POL	NSTNSPTSREL	31	11	01	33	6502
POL	GTLNCPQITLW	80	11	01	33	6503
POL	PTFNFPQITLW	80	11	01	33	6504
POL	NSPSSREL	37	8	01	50	6505
POL	NSPTTREL	39	8	01	50	6506
POL	PSSRELQV	39	8	01	50	6507
POL	NSPSSRELQV	37	10	01	50	6508
POL	RANSPTTREL	37	10	01	50	6509
POL	NSPTTRELQV	39	10	01	50	6510
POL	GADRQGIV	70	8	01	20	6511
POL	GSGRAVPI	70	8	01	20	6512
POL	GADRQGIVSF	70	10	01	20	6513
POL	GSGRAVPICL	70	10	01	20	6514
POL	GTTLNFPQI	79	9	01	17	6515
POL	GAISLSLPQI	79	10	01	17	6516
POL	GTTLNFPQITF	79	11	01	17	6517
POL	PSLSFPQI	79	8	02	33	6518
POL	PSLSFPQITL	79	10	02	33	6519
POL	PSLSFPQITLW	79	11	02	33	6520
POL	SSFSFPQI	82	8	03	30	6521
POL	SSFSFPQITL	82	10	03	30	6522
POL	SSFSFPQITLW	82	11	03	30	6523
POL	VSFSFPQITLW	78	11	07	15	6524
POL	VSFSFPQI	78	8	08	17	6525
POL	VSFSFPQITL	78	10	08	17	6526
POL	ETWWTDYW	591	8	10	16	6527
POL	RANSPTSREL	26	10	10	16	6528
POL	ETWETWWTDY	588	10	10	16	6529
POL	ETWETWWTEY	588	10	10	16	6530
POL	QTKELQKQH	961	10	10	16	6531
POL	LAFPQGEAREF	6	11	10	16	6532
POL	RSAHTNDVKQL	550	11	10	16	6533
POL	EAVQKIATESI	562	11	10	16	6534

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	ETWETWWTDYW	588	11	10	16	6535
POL	RTAHTNDV	550	8	11	17	6536
POL	WAGIQQEF	884	8	11	17	6537
POL	VTVKIGGQL	98	9	11	17	6538
POL	STNNETPGI	323	9	11	17	6539
POL	GTKALTEVI	474	9	11	17	6540
POL	GSNFTSTTV	870	9	11	17	6541
POL	GADDTVLEEM	114	10	11	17	6542
POL	ISRIGPENPY	236	10	11	17	6543
POL	PSTNNETPGI	322	10	11	17	6544
POL	TAHTNDVKQL	551	10	11	17	6545
POL	WAGIQQEFGI	884	10	11	17	6546
POL	STNNETPGIRY	323	11	11	17	6547
POL	ESWTVNDIQKL	439	11	11	17	6548
POL	GTKALTEVIPL	474	11	11	17	6549
POL	ESWTVNDI	439	8	12	19	6550
POL	KTELQAIY	668	8	12	19	6551
POL	KTELQAIYL	668	9	12	19	6552
POL	NSPTRRELQVW	28	11	12	19	6553
POL	TTNQKTELHAI	664	11	12	19	6554
POL	KTELQAIYLAL	668	11	12	19	6555
POL	GAVVIQDNSEI	999	11	12	19	6556
POL	KTGKYARM	542	8	13	21	6557
POL	WTVQPIVL	428	8	13	20	6558
POL	PTRRELQVW	30	9	13	20	6559
POL	DTVLEDINL	117	9	13	20	6560
POL	NSPTRRELQV	28	10	13	20	6561
POL	LAGRWPVKTI	856	10	13	20	6562
POL	RAKIEELREHL	388	11	13	20	6563
POL	IATESIVI	567	8	14	22	6564
POL	IATESIVIW	567	9	14	22	6565
POL	NSPTSREL	28	8	14	22	6566
POL	PTRRELQV	30	8	14	22	6567
POL	FSFPQITLW	85	9	14	22	6568
POL	DTVLEEINL	117	9	14	22	6569
POL	WTDYWQATW	594	9	14	22	6570
POL	SAGERIVDI	947	9	14	22	6571
POL	ASDIQTKEL	957	9	14	22	6572
POL	WTDYWQATWI	594	10	14	22	6573
POL	TSTTVKAACW	874	10	14	22	6574
POL	YSAGERIVDI	946	10	14	22	6575
POL	SAGERIVDII	947	10	14	22	6576
POL	IASDIQTKEL	956	10	14	22	6577
POL	RTKIEELRQHL	388	11	14	22	6578
POL	FTSTTVKAACW	873	11	14	22	6579
POL	TSTTVKAACWW	874	11	14	22	6580
POL	YSAGERIVDII	946	11	14	22	6581
POL	KALVEICTEM	219	10	15	24	6582
POL	FSFPQITL	85	8	15	23	6583
POL	LTQLGCTL	177	8	15	23	6584

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	RSAHTNDV	550	8	15	23	6585
POL	VSAGIRKV	744	8	15	23	6586
POL	SAGIRKVL	745	8	15	23	6587
POL	TTVKAACW	876	8	15	23	6588
POL	KTELQAIHL	668	9	15	23	6589
POL	VSAGIRKVL	744	9	15	23	6590
POL	SAGIRKVLF	745	9	15	23	6591
POL	STTVKAACW	875	9	15	23	6592
POL	TTVKAACWW	876	9	15	23	6593
POL	GADDTVLEDI	114	10	15	23	6594
POL	LTQLGCTLNF	177	10	15	23	6595
POL	LTEEKIKALV	213	10	15	23	6596
POL	VSAGIRKVLF	744	10	15	23	6597
POL	SAGIRKVLFL	745	10	15	23	6598
POL	STTVKAACWW	875	10	15	23	6599
POL	KTELQAIHLAL	668	11	15	23	6600
POL	VSAGIRKVLFL	744	11	15	23	6601
POL	KAQEEHERY	759	9	16	25	6602
POL	YSAGERIV	946	8	16	25	6603
POL	KALTEVIPL	476	9	16	25	6604
POL	RANSPTRREL	26	10	16	25	6605
POL	SAHTNDVKQL	551	10	16	25	6606
POL	NSPTRREL	28	8	17	27	6607
POL	VTIKIGGQL	98	9	17	27	6608
POL	KTPKFKLPI	577	9	17	27	6609
POL	GAKALTDIVPL	474	11	17	27	6610
POL	FSVPLDKDF	305	9	18	28	6611
POL	YAGIKVKQL	460	9	18	28	6612
POL	GADDTVLEEI	114	10	18	28	6613
POL	ITLWQRPLVTV	90	11	18	28	6614
POL	KTGKYAKM	542	8	19	30	6615
POL	GTKALTEV	474	8	19	30	6616
POL	ATESIVIW	568	8	19	30	6617
POL	GAHTNDVKQL	551	10	19	30	6618
POL	KSESELVNQI	704	10	19	30	6619
POL	KSESELVSQI	704	10	19	30	6620
POL	ITLWQRPLVTI	90	11	19	30	6621
POL	LTDTTNQKTEL	661	11	19	30	6622
POL	KSESELVNQII	704	11	19	30	6623
POL	KSESELVSQII	704	11	19	30	6624
POL	VSQHEQL	710	8	20	31	6625
POL	VSQHEQLI	710	9	20	31	6626
POL	MASDFNLPPIV	774	11	20	31	6627
POL	ESELVSQI	706	8	21	33	6628
POL	WAGIKQEF	884	8	21	33	6629
POL	KALTDIVPL	476	9	21	33	6630
POL	ESELVSQII	706	9	21	33	6631
POL	ASDFNLPPIV	775	10	21	33	6632
POL	WAGIKQEFGI	884	10	21	33	6633
POL	LAWVPAHKGI	725	10	22	34	6634

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	MASDFNLPPI	774	10	22	34	6635
POL	LAGRWPVKVI	856	10	22	34	6636
POL	ASDFNLPPI	775	9	23	36	6637
POL	CTHLEGKVIL	817	10	23	36	6638
POL	CTHLEGKVILV	817	11	23	36	6639
POL	GAKALTDIV	474	9	24	38	6640
POL	WTEYWQATW	594	9	24	38	6641
POL	WTEYWQATWI	594	10	24	38	6642
POL	PTPVNIIGRNM	166	11	24	38	6643
POL	GAKALTDI	474	8	25	39	6644
POL	DSGSEVNI	680	8	25	39	6645
POL	DSGSEVNIV	680	9	25	39	6646
POL	ASDFNLPPV	775	9	25	39	6647
POL	LALQDSGSEV	676	10	25	39	6648
POL	SSGIRKVLFL	745	10	25	39	6649
POL	MASDFNLPPV	774	10	25	39	6650
POL	ASDFNLPPVV	775	10	25	39	6651
POL	LTETTNQKTEL	661	11	25	39	6652
POL	VSSGIRKVLFL	744	11	25	39	6653
POL	MASDFNLPPVV	774	11	25	39	6654
POL	ASQIYAGIKV	456	10	26	41	6655
POL	VSSGIRKV	744	8	26	41	6656
POL	SSGIRKVL	745	8	26	41	6657
POL	CTHLEGKV	817	8	26	41	6658
POL	PSKDLIAEI	513	9	26	41	6659
POL	DTTNQKTEL	663	9	26	41	6660
POL	VSSGIRKVL	744	9	26	41	6661
POL	SSGIRKVLF	745	9	26	41	6662
POL	CTHLEGKVI	817	9	26	41	6663
POL	GSNFTSAAV	870	9	26	41	6664
POL	VSSGIRKVLF	744	10	26	41	6665
POL	ETGQETAYFL	844	10	26	41	6666
POL	PTPVNIIGRNL	166	11	26	41	6667
POL	WASQIYAGIKV	455	11	26	41	6668
POL	ETGQETAYFLL	844	11	26	41	6669
POL	ASQIYAGI	456	8	27	43	6670
POL	KAQEEHEKY	759	9	27	43	6671
POL	ASQIYPGIKV	456	10	27	43	6672
POL	LALQDSGL	676	8	27	42	6673
POL	ESELVNQI	706	8	27	42	6674
POL	TAYFLLKL	849	8	27	42	6675
POL	WASQIYAGI	455	9	27	42	6676
POL	ESELVNQII	706	9	27	42	6677
POL	ETAYFLLKL	848	9	27	42	6678
POL	CTEMEKEGKI	225	10	27	42	6679
POL	LALQDSGLEV	676	10	27	42	6680
POL	TSAAVKAACW	874	10	27	42	6681
POL	WASQIYPGIKV	455	11	27	42	6682
POL	FTSAAVKAACW	873	11	27	42	6683
POL	TSAAVKAACWW	874	11	27	42	6684

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WTVQPIQL	428	8	28	44	6685
POL	DSGLEVNI	680	8	28	44	6686
POL	AAVKAACW	876	8	28	44	6687
POL	DSGLEVNIV	680	9	28	44	6688
POL	SAAVKAACW	875	9	28	44	6689
POL	AAVKAACWW	876	9	28	44	6690
POL	VTDRGRQKVV	650	10	28	44	6691
POL	SAAVKAACWW	875	10	28	44	6692
POL	ASQIYPGI	456	8	29	46	6693
POL	WASQIYPGI	455	9	29	45	6694
POL	KTPKFRLPI	577	9	29	45	6695
POL	ETTNQKTEL	663	9	29	45	6696
POL	AANRETKL	637	8	30	47	6697
POL	GAANRETKL	636	9	30	47	6698
POL	VTDRGRQKV	650	9	30	47	6699
POL	LAGRWPVKV	856	9	30	47	6700
POL	KAACWWAGI	879	9	31	49	6701
POL	ETAYFILKL	848	9	31	48	6702
POL	PSINNETPGI	322	10	31	48	6703
POL	CTHLEGKIIL	817	10	31	48	6704
POL	ETGQETAYFI	844	10	31	48	6705
POL	CTHLEGKIILV	817	11	31	48	6706
POL	ETGQETAYFIL	844	11	31	48	6707
POL	TAYFILKL	849	8	32	50	6708
POL	AACWWAGI	880	8	32	50	6709
POL	HSNWRAMASDF	768	11	32	50	6710
POL	SSMTKILEPF	351	10	33	52	6711
POL	QSSMTKILEPF	350	11	33	52	6712
POL	LTEAVQKI	560	8	34	53	6713
POL	CTHLEGKI	817	8	35	55	6714
POL	ETKLGKAGY	641	9	35	55	6715
POL	CTHLEGKII	817	9	35	55	6716
POL	ATDIQTKEL	957	9	35	55	6717
POL	ETKLGKAGYV	641	10	35	55	6718
POL	IATDIQTKEL	956	10	35	55	6719
POL	ITKIQNFRV	969	9	36	57	6720
POL	ITKIQNFRVY	969	10	36	57	6721
POL	ITKIQNFRVYY	969	11	36	57	6722
POL	PAIFQSSMTKI	346	11	36	56	6723
POL	QAQPDKSESEL	699	11	36	56	6724
POL	TAFTIPSI	317	8	37	58	6725
POL	YTAFTIPSI	316	9	37	58	6726
POL	LTEEAELEL	484	9	37	58	6727
POL	LSWVPAHKGI	725	10	37	58	6728
POL	GAVVIQDNSDI	999	11	37	58	6729
POL	QSSMTKIL	350	8	38	59	6730
POL	KAKIIRDY	1017	8	41	64	6731
POL	RAMASDFNL	772	9	41	64	6732
POL	SAGERIIDI	947	9	41	64	6733
POL	LTQIGCTLNF	177	10	41	64	6734

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	YSAGERIIDI	946	10	41	64	6735
POL	SAGERIIDII	947	10	41	64	6736
POL	YSAGERIIDII	946	11	41	64	6737
POL	LTQIGCTL	177	8	42	66	6738
POL	PAIFQSSM	346	8	42	66	6739
POL	YSAGERII	946	8	42	66	6740
POL	ISKIGPENPY	236	10	42	66	6741
POL	GSPAIFQSSM	344	10	42	66	6742
POL	WTYQIYQEPF	529	10	42	66	6743
POL	TTNQKTELQAI	664	11	42	66	6744
POL	DSWTVNDI	439	8	43	67	6745
POL	ASCDKCQL	790	8	43	67	6746
POL	VASCDKCQL	789	9	43	67	6747
POL	DSWTVNDIQKL	439	11	43	67	6748
POL	MTKILEPF	353	8	44	69	6749
POL	QTKELQKQI	961	9	46	72	6750
POL	ITLWQRPL	90	8	47	73	6751
POL	ITLWQRPLV	90	9	47	73	6752
POL	KAIGTVLV	157	8	48	75	6753
POL	HTNDVKQL	553	8	49	77	6754
POL	PAGLKKKKSV	286	10	50	78	6755
POL	QATWIPEWEFV	599	11	51	81	6756
POL	KSVTVLDV	293	8	51	80	6757
POL	HTDNGSNF	866	8	51	80	6758
POL	ATWIPEWEFV	600	10	51	80	6759
POL	ETVPVKLKPGM	192	11	51	80	6760
POL	ETPGIRYQYNV	327	11	51	80	6761
POL	QATWIPEWEF	599	10	52	83	6762
POL	ETPGIRYQY	327	9	52	81	6763
POL	ATWIPEWEF	600	9	52	81	6764
POL	VASGYIEAEV	831	10	52	81	6765
POL	VASGYIEAEVI	831	11	52	81	6766
POL	ASGYIEAEV	832	9	53	83	6767
POL	QSQGVVESM	898	9	53	83	6768
POL	GTVLVGPTPV	160	10	53	83	6769
POL	RTQDFWEVQL	272	10	53	83	6770
POL	VAVHVASGYI	827	10	53	83	6771
POL	ASGYIEAEVI	832	10	53	83	6772
POL	ESMNKELKKI	904	10	53	83	6773
POL	ISPIETVPVKL	188	11	53	83	6774
POL	ESMNKELKKII	904	11	53	83	6775
POL	QATWIPEW	599	8	54	86	6776
POL	RTQDFWEV	272	8	55	86	6777
POL	DAYFSVPL	302	8	55	86	6778
POL	TTNQKTEL	664	8	55	86	6779
POL	ISPIETVPV	188	9	56	88	6780
POL	LTEEKIKAL	213	9	56	88	6781
POL	VTVLDVGDAY	295	10	56	88	6782
POL	KTAVQMAVFI	925	10	56	88	6783
POL	VTVLDVGDAYF	295	11	56	88	6784

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PAETGQETAYF	842	11	56	88	6785
POL	LAENREIL	492	8	57	89	6786
POL	NTPPLVKL	610	8	57	89	6787
POL	CSPGIWQL	808	8	57	89	6788
POL	KTAVQMAV	925	8	57	89	6789
POL	NTPPLVKLW	610	9	57	89	6790
POL	ETGQETAYF	844	9	57	89	6791
POL	KTAVQMAVF	925	9	57	89	6792
POL	NTPPLVKLWY	610	10	57	89	6793
POL	FAIKKKDSTKW	250	11	57	89	6794
POL	QAEHLKTAVQM	920	11	57	89	6795
POL	STKWRKLVDF	257	10	58	91	6796
POL	VTDSQYALGI	688	10	58	91	6797
POL	PAETGQETAY	842	10	58	91	6798
POL	DSTKWRKLVDF	256	11	58	91	6799
POL	VTDSQYALGII	688	11	58	91	6800
POL	DSTKWRKL	256	8	59	92	6801
POL	STKWRKLV	257	8	59	92	6802
POL	VTDSQYAL	688	8	59	92	6803
POL	DSQYALGI	690	8	59	92	6804
POL	ETGQETAY	844	8	59	92	6805
POL	DSTKWRKLV	256	9	59	92	6806
POL	DSQYALGII	690	9	59	92	6807
POL	VAVIIVASGY	827	9	59	92	6808
POL	QAEHLKTAV	920	9	59	92	6809
POL	TAVQMAVFI	926	9	59	92	6810
POL	MAVFIHNF	930	8	60	94	6811
POL	CTLNFPISPI	182	10	60	94	6812
POL	TAVQMAVF	926	8	61	95	6813
POL	DTGADDTVL	112	9	61	95	6814
POL	WTVNDIQKLV	441	10	61	95	6815
POL	WTVNDIQKL	441	9	62	97	6816
POL	DTGADDTV	112	8	63	98	6817
REV	RARQRQHSI	50	10	10	16	6818
REV	GTQGVGSPQI	97	10	11	18	6819
REV	RSAEPVPL	70	8	12	19	6820
REV	SAEPVPLQL	71	9	12	19	6821
REV	RSAEPVPLQL	70	10	12	19	6822
REV	RSGDSDEELL	4	10	16	25	6823
REV	QARKNRRRRW	40	10	16	25	6824
REV	RSGDSDEEL	4	9	17	27	6825
REV	GTSGTQGV	94	8	21	33	6826
REV	PAEPVPLQL	71	9	21	33	6827
REV	QARRNRRRRW	40	10	38	59	6828
TAT	PTGPKESKKKV	88	11	12	19	6829
VIF	KSLVKYHM	22	8	10	16	6830
VIF	FSDSAIRKAI	120	10	10	16	6831
VIF	YSTQIDPDL	99	9	11	17	6832
VIF	YSTQVDPGL	99	9	11	17	6833
VIF	STQVDPGL	100	8	11	17	6834

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	KSLVKHHMYI	22	10	11	17	6835
VIF	VSIEWRLRRY	88	10	11	17	6836
VIF	FSESAIRKAIL	120	11	11	17	6837
VIF	GSLQYLALKAL	148	11	11	17	6838
VIF	STQIDPDL	100	8	12	19	6839
VIF	ESAIRNAI	122	8	12	19	6840
VIF	SAIRNAIL	123	8	12	19	6841
VIF	QTGERDWHL	75	9	12	19	6842
VIF	ESAIRNAIL	122	9	12	19	6843
VIF	KTKPPLPSV	164	9	12	19	6844
VIF	FSESAIRKAI	120	10	12	19	6845
VIF	FSESAIRNAI	120	10	12	19	6846
VIF	FSESAIRNAIL	120	11	12	19	6847
VIF	GSLQYLALAAL	148	11	12	19	6848
VIF	LADQLIHMHY	107	10	13	20	6849
VIF	ESRHPKVSSEV	45	11	13	20	6850
VIF	LADQLIHMHYF	107	11	13	20	6851
VIF	PSVKKLTEDRW	173	11	13	20	6852
VIF	NSLVKHHMYV	22	10	14	22	6853
VIF	LADQLIHLYY	107	10	14	22	6854
VIF	RTWKSLVKHHM	19	11	14	22	6855
VIF	LADQLIHLYYF	107	11	14	22	6856
VIF	LADQLIHLY	107	9	15	23	6857
VIF	KTKGHRGSHTM	188	11	15	23	6858
VIF	ESAIRKAIL	122	9	16	25	6859
VIF	LADQLIHM	107	8	17	27	6860
VIF	ESAIRKAI	122	8	17	27	6861
VIF	KSLVKHHM	22	8	18	28	6862
VIF	KSLVKHHMY	22	9	18	28	6863
VIF	DSAIRKAIL	122	9	19	30	6864
VIF	DSAIRKAI	122	8	20	31	6865
VIF	HTGERDWHL	75	9	21	33	6866
VIF	NSLVKHHMY	22	9	24	38	6867
VIF	RTWNSLVKHHM	19	11	24	38	6868
VIF	LADQLIHL	107	8	25	39	6869
VIF	NSLVKHHM	22	8	27	42	6870
VIF	ISSEVHIPL	51	9	27	42	6871
VIF	VSSEVHIPL	51	9	27	42	6872
VIF	GSLQYLALTAL	148	11	31	48	6873
VIF	SAIRKAIL	123	8	35	55	6874
VIF	QAGHNKVGSL	141	10	38	59	6875
VIF	SSEVHIPL	52	8	55	86	6876
VIF	GSLQYLAL	148	8	58	91	6877
VPR	WALELLEEL	18	9	09	15	6878
VPR	ETYGDTWTGV	48	10	11	17	6879
VPR	EAVRHFPRI	29	9	14	22	6880
VPR	EAVRHFPRIW	29	10	14	22	6881
VPR	EAVRHFPRIWL	29	11	14	22	6882
VPR	KSEAVRHF	27	8	15	23	6883
VPR	WAGVEAIIRI	54	10	15	23	6884

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	WAGVEAHRIL	54	11	15	23	6885
VPR	WAGVEAH	54	8	16	25	6886
VPR	DTWAGVEAI	52	9	16	25	6887
VPR	ETYGDTWAGV	48	10	16	25	6888
VPR	NTYGDTWEGV	48	10	16	25	6889
VPR	DTWAGVEAH	52	10	16	25	6890
VPR	DTWEGVEAH	52	10	19	30	6891
VPR	DTWEGVEAI	52	9	20	31	6892
VPR	EAHRILQQL	58	10	33	52	6893
VPR	EAHRILQQLL	58	11	33	52	6894
VPR	EAVRHFPRPW	29	10	34	53	6895
VPR	EAVRHFPRPWL	29	11	34	53	6896
VPR	WTLELLEEL	18	9	42	69	6897
VPU	LAKVDYRI	5	8	01	25	6898
VPU	LAKVDYRL	5	8	01	25	6899
VPU	LAKVDYRIV	5	9	01	25	6900
VPU	LAKVDYRIVI	5	10	01	25	6901
VPU	LAKVDYRLGV	5	10	01	25	6902
VPU	LAKVDYRIVIV	5	11	01	25	6903
VPU	VTLLSSSKL	94	9	01	50	6904
VPU	LAIVALVV	13	8	12	20	6905
VPU	WTIVFIEY	34	8	12	19	6906
VPU	ESEGDQEEL	75	9	13	20	6907
VPU	ESEGDTEEL	75	9	13	20	6908
VPU	IAIVVWTIV	28	9	20	31	6909
VPU	IAIVVWTI	28	8	23	36	6910

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	GIGPGQTF	360	8	01	33	6911
ENV	SIGSGQAF	360	8	01	33	6912
ENV	KLREIRQF	405	8	01	25	6913
ENV	EPDRPERI	823	8	01	33	6914
ENV	PPDRPEGI	823	8	01	33	6915
ENV	GIGPGQTFY	360	9	01	33	6916
ENV	SIGSGQAFY	360	9	01	33	6917
ENV	SIGSGQAFYV	360	10	01	33	6918
ENV	KQLYATVY	34	8	01	50	6919
ENV	QLYATVYAGV	34	10	01	50	6920
ENV	KQLYATVYSGV	34	11	01	50	6921
ENV	TIGAMFLGF	599	9	03	27	6922
ENV	MLGAMFLGF	599	9	04	36	6923
ENV	SLRGLQRGW	889	9	05	18	6924
ENV	RLGWEGLKYLW	894	11	07	23	6925
ENV	RLGWEGLKY	894	9	09	29	6926
ENV	GLRLGWEGLKY	892	11	09	29	6927
ENV	LILGLVII	21	8	09	15	6928
ENV	IPRRIRQGF	950	9	10	16	6929
ENV	ALFYKLDV	202	8	10	16	6930
ENV	IIMLQLTVW	650	8	10	16	6931
ENV	DITNWLWY	769	8	10	16	6932
ENV	DIRQAIICNV	380	9	10	16	6933
ENV	LPCRIKQIV	485	9	10	16	6934
ENV	MLQLTVWGI	651	9	10	16	6935
ENV	DITNWLWYI	769	9	10	16	6936
ENV	SQELKNSAV	911	9	10	16	6937
ENV	PIIYCTPAGF	260	10	10	16	6938
ENV	TLPCRIKQIV	484	10	10	16	6939
ENV	IPIIYCTPAGF	259	11	10	16	6940
ENV	RVGQAMYAPPI	498	11	10	16	6941
ENV	WMEWEREIDNY	723	11	10	16	6942
ENV	ALDKWASLWNW	757	11	10	16	6943
ENV	SLKGLRLGW	889	9	11	39	6944
ENV	GIGAVFLGF	598	9	11	18	6945
ENV	KLWVTVYY	44	8	11	17	6946
ENV	AVGIGAVF	595	8	11	17	6947
ENV	KLWVTVYYGV	44	10	11	17	6948
ENV	AVGIGAVFLGF	595	11	11	17	6949
ENV	RIGPGQTF	357	8	11	17	6950
ENV	NITLPCRI	482	8	11	17	6951
ENV	WQRVGQAM	496	8	11	17	6952
ENV	QIRCSSNI	512	8	11	17	6953
ENV	ALFYRLDVV	202	9	11	17	6954
ENV	GPCTNVSTV	283	9	11	17	6955
ENV	RIGPGQTFY	357	9	11	17	6956
ENV	WQRVGQAMY	496	9	11	17	6957
ENV	GQIRCSSNI	511	9	11	17	6958
ENV	ALDKWASLW	757	9	11	17	6959
ENV	AVSLLNATAI	918	10	11	17	6960

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NITLPCRIKQI	482	11	11	17	6961
ENV	VVEREKRAVGI	588	11	11	17	6962
ENV	LLALDKWASLW	755	11	11	17	6963
ENV	NMWKNDMV	107	8	12	19	6964
ENV	ALFYRLDV	202	8	12	19	6965
ENV	RIKQIVNM	488	8	12	19	6966
ENV	KLICTTTV	687	8	12	19	6967
ENV	WMEWEREI	723	8	12	19	6968
ENV	ILKCNDKKF	271	9	12	19	6969
ENV	RIKQIVNMW	488	9	12	19	6970
ENV	LICTTTVPW	688	9	12	19	6971
ENV	GQELKNSAI	911	9	12	19	6972
ENV	AILHIPRRI	946	9	12	19	6973
ENV	AILKCNDKKF	270	10	12	19	6974
ENV	KLICTTTVPW	687	10	12	19	6975
ENV	NMTWMEWEREI	720	11	12	19	6976
ENV	IVGGLIGLRII	783	11	12	19	6977
ENV	ELYKYKVVEI	560	10	13	21	6978
ENV	DPNPQEVV	91	8	13	20	6979
ENV	HLLKLTVW	650	8	13	20	6980
ENV	NVPWNSSW	693	8	13	20	6981
ENV	EIWDNMTW	716	8	13	20	6982
ENV	SIRLVNGF	842	8	13	20	6983
ENV	SIRLVSGF	842	8	13	20	6984
ENV	RLRDLLLI	867	8	13	20	6985
ENV	ILHIPRRI	947	8	13	20	6986
ENV	EIKNCSFNI	181	9	13	20	6987
ENV	AITQACPKV	244	9	13	20	6988
ENV	SLAEEEVVI	311	9	13	20	6989
ENV	QQHLLKLTV	648	9	13	20	6990
ENV	LLKLTVWGI	651	9	13	20	6991
ENV	AQQHLLKLTV	647	10	13	20	6992
ENV	QQHLLKLTVW	648	10	13	20	6993
ENV	HLLKLTVWGI	650	10	13	20	6994
ENV	EQELLELDKW	752	10	13	20	6995
ENV	VPTDPNPQEVV	88	11	13	20	6996
ENV	VMHSFNCGGEF	432	11	13	20	6997
ENV	TITLPCRIKQI	482	11	13	20	6998
ENV	AQQHLLKLTVW	647	11	13	20	6999
ENV	SLAEEEVV	311	8	14	22	7000
ENV	TITLPCRI	482	8	14	22	7001
ENV	SLLNATAI	920	8	14	22	7002
ENV	DPEIVMHSF	428	9	14	22	7003
ENV	GQAMYAPPI	501	9	14	22	7004
ENV	RIIFAVLSI	791	9	14	22	7005
ENV	AVAEGTDRV	928	9	14	22	7006
ENV	EQDLLALDKW	752	10	14	22	7007
ENV	RIIFAVLSIV	791	10	14	22	7008
ENV	SLLNATAIAV	920	10	14	22	7009
ENV	AVAEGTDRVI	928	10	14	22	7010

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	VITQACPKVSF	244	11	14	22	7011
ENV	GLRHFAVLSI	789	11	14	22	7012
ENV	AIAVAEGTDRV	926	11	14	22	7013
ENV	RLINCNTSAI	236	10	15	24	7014
ENV	GLIGLRH	786	8	15	23	7015
ENV	HFAVLSI	792	8	15	23	7016
ENV	GPDRPEGI	822	8	15	23	7017
ENV	LINCNTSAI	237	9	15	23	7018
ENV	VITQACPKV	244	9	15	23	7019
ENV	GPCKNVSTV	283	9	15	23	7020
ENV	DIRQAHCNI	380	9	15	23	7021
ENV	GLIGLRHF	786	9	15	23	7022
ENV	HFAVLSIV	792	9	15	23	7023
ENV	LLNATAIAV	921	9	15	23	7024
ENV	SVITQACPKV	243	10	15	23	7025
ENV	TLPCRIKQH	484	10	15	23	7026
ENV	NMWQEVGKAM	494	10	15	23	7027
ENV	AVAEGTDRH	928	10	15	23	7028
ENV	NMWQEVGKAMY	494	11	15	23	7029
ENV	GLIGLRHFAV	786	11	15	23	7030
ENV	LIGLRHF	787	8	16	25	7031
ENV	VVQREKRAV	588	9	16	25	7032
ENV	AVAEGTDRI	928	9	16	25	7033
ENV	RVVQREKRAV	587	10	16	25	7034
ENV	LIGLRHFAV	787	10	16	25	7035
ENV	LVSGFLALAW	845	10	16	25	7036
ENV	DLRNLCLFSY	856	10	16	25	7037
ENV	LLNGSLAEEEV	307	11	16	25	7038
ENV	ELDKWASLWNW	757	11	16	25	7039
ENV	RLVSGFLALAW	844	11	16	25	7040
ENV	AIAVAEGTDRI	926	11	16	25	7041
ENV	VQREKRAV	589	8	17	27	7042
ENV	HNMWQEV	492	8	17	27	7043
ENV	KLICTTNV	687	8	17	27	7044
ENV	SLWNWFDI	763	8	17	27	7045
ENV	DLRNLCLF	856	8	17	27	7046
ENV	QHNMWQEV	491	9	17	27	7047
ENV	LICTTNVPW	688	9	17	27	7048
ENV	RPNNNTRKSI	347	10	17	27	7049
ENV	KQHNMWQEV	490	10	17	27	7050
ENV	EIFRPGGGDM	544	10	17	27	7051
ENV	KLICTTNVPW	687	10	17	27	7052
ENV	RIVFAVLSIV	791	10	17	27	7053
ENV	GVAPTKAKRRV	573	11	17	27	7054
ENV	WQEVGKAM	496	8	18	28	7055
ENV	GLRHFAV	789	8	18	28	7056
ENV	WQEVGKAMY	496	9	18	28	7057
ENV	ELDKWASLW	757	9	18	28	7058
ENV	IVFAVLSIV	792	9	18	28	7059
ENV	YLRDQQLLGI	672	10	18	28	7060

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	LPCRIKQIINM	485	11	18	28	7061
ENV	EVGKAMYAPPI	498	11	18	28	7062
ENV	YLRDQQLLGIW	672	11	18	28	7063
ENV	LLELDKWASLW	755	11	18	28	7064
ENV	CLFSYHRLRDF	861	11	18	28	7065
ENV	KLICTTAV	687	8	19	30	7066
ENV	LICTTAVPW	688	9	19	30	7067
ENV	RIVFAVLSI	791	9	19	30	7068
ENV	KLICTTAVPW	687	10	19	30	7069
ENV	GLRIVFAVLSI	789	11	19	30	7070
ENV	ELLELDKW	754	8	20	31	7071
ENV	IVFAVLSI	792	8	20	31	7072
ENV	LPCRIKQII	485	9	20	31	7073
ENV	NMVEQMHEDI	112	10	20	31	7074
ENV	NMVEQMHEDII	112	11	20	31	7075
ENV	DLLALDKW	754	8	21	33	7076
ENV	DLEITTHSF	428	9	21	33	7077
ENV	VPTDPNPQEV	88	10	21	33	7078
ENV	LIGLRIVFAV	787	10	21	33	7079
ENV	CVPTDPNPQEV	87	11	21	33	7080
ENV	GLIGLRIVFAV	786	11	21	33	7081
ENV	APTKAKRRV	575	9	22	34	7082
ENV	APTKAKRRVV	575	10	22	34	7083
ENV	IVELLGRRGW	879	10	22	34	7084
ENV	PVWKEATTTLF	54	11	22	34	7085
ENV	EQMHEDIISLW	115	11	22	34	7086
ENV	TVQCTHGIRPV	290	11	22	34	7087
ENV	RIVELLGRRGW	878	11	22	34	7088
ENV	ELLGRRGW	881	8	23	37	7089
ENV	MVEQMHEDI	113	9	23	36	7090
ENV	VVKIEPLGV	566	9	23	36	7091
ENV	MVEQMHEDII	113	10	23	36	7092
ENV	KVVKIEPLGV	565	10	23	36	7093
ENV	EQMHEDII	115	8	24	38	7094
ENV	VVEREKRAV	588	9	25	39	7095
ENV	VPTDPNPQEI	88	10	25	39	7096
ENV	VQCTHGIRPV	292	10	25	39	7097
ENV	RVVEREKRAV	587	10	25	39	7098
ENV	QQQNNLLRAI	636	10	25	39	7099
ENV	CVPTDPNPQEI	87	11	25	39	7100
ENV	VQCTHGIRPVV	292	11	25	39	7101
ENV	VQQQNNLLRAI	635	11	25	39	7102
ENV	TLPCRIKQI	484	9	26	41	7103
ENV	QQNNLLRAI	637	9	26	41	7104
ENV	QQSNLLRAI	637	9	26	41	7105
ENV	QQQSNLLRAI	636	10	26	41	7106
ENV	IPIHYCAPAGF	259	11	26	41	7107
ENV	VQQQSNLLRAI	635	11	26	41	7108
ENV	PIHYCAPAGF	260	10	27	42	7109
ENV	YLKDQQLLGI	672	10	27	42	7110

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	YLKDQQLLGIW	672	11	27	42	7111
ENV	KVSFEPIPIHY	252	11	28	44	7112
ENV	TVQCTHGIKPV	290	11	28	44	7113
ENV	ELYKYKVVKI	560	10	29	46	7114
ENV	LIGLRIVF	787	8	29	45	7115
ENV	GLRIVFAV	789	8	29	45	7116
ENV	GLIGLRIVF	786	9	29	45	7117
ENV	QMHEDIISLW	116	10	29	45	7118
ENV	RIKQIINM	488	8	30	47	7119
ENV	TQACPKVSF	247	9	30	47	7120
ENV	CPKVSFEPI	250	9	30	47	7121
ENV	KVSFEPIPI	252	9	30	47	7122
ENV	RIKQIINMW	488	9	30	47	7123
ENV	NMWKNNMVEQM	107	11	30	47	7124
ENV	CPKVSFEPIPI	250	11	30	47	7125
ENV	IVGGLIGLRIV	783	11	30	47	7126
ENV	LPCRIKQI	485	8	31	48	7127
ENV	AVLSIVNRV	795	9	31	48	7128
ENV	VQCTHGIKPVV	292	11	31	48	7129
ENV	KIFIMIVGGLI	778	11	31	48	7130
ENV	GLIGLRIV	786	8	32	50	7131
ENV	VQCTHGIKPV	292	10	32	50	7132
ENV	LQARVLAV	662	8	33	52	7133
ENV	RVLAVERY	665	8	33	52	7134
ENV	QLQARVLAV	661	9	33	52	7135
ENV	KQLQARVLAV	660	10	33	52	7136
ENV	LQARVLAVERY	662	11	33	52	7137
ENV	NLWVTVYYGV	44	10	34	54	7138
ENV	NVTENFNM	101	8	34	53	7139
ENV	NMWKNNMV	107	8	34	53	7140
ENV	HLLQLTVW	650	8	34	53	7141
ENV	NVTENFNMW	101	9	34	53	7142
ENV	QQHLLQLTV	648	9	34	53	7143
ENV	LLQLTVWGI	651	9	34	53	7144
ENV	AQQHLLQLTV	647	10	34	53	7145
ENV	QQHLLQLTVW	648	10	34	53	7146
ENV	HLLQLTVWGI	650	10	34	53	7147
ENV	AQQHLLQLTVW	647	11	34	53	7148
ENV	NLWVTVYY	44	8	35	56	7149
ENV	IMIVGGLI	781	8	35	56	7150
ENV	FIMIVGGLI	780	9	35	55	7151
ENV	DLRSLCLFSY	856	10	35	55	7152
ENV	VQARQLLSGI	625	10	36	56	7153
ENV	SIVNRVRQGY	798	10	36	56	7154
ENV	TMGAASITLTV	615	11	36	56	7155
ENV	TVQARQLLSGI	624	11	36	56	7156
ENV	VQARQLLSGIV	625	11	36	56	7157
ENV	MIVGGLIGLRI	782	11	36	56	7158
ENV	DMRDNWRSELY	552	11	37	58	7159
ENV	VLSIVNRV	796	8	38	59	7160

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	DLRSLCLF	856	8	38	59	7161
ENV	IVNRVRQGY	799	9	38	59	7162
ENV	RPGGGDMRDNW	547	11	38	59	7163
ENV	YIKIFIMIV	776	9	39	61	7164
ENV	GIKQLQARV	658	9	40	63	7165
ENV	TLFCASDAKAY	64	11	40	63	7166
ENV	IVGGLIGLRI	783	10	42	66	7167
ENV	YIKIFIMI	776	8	43	67	7168
ENV	WLWYIKIFIM	773	10	43	67	7169
ENV	WLWYIKIFIMI	773	11	43	67	7170
ENV	LQLTVWGI	652	8	44	69	7171
ENV	SLWDQSLKPCV	123	11	47	75	7172
ENV	RVRQGYSPLSF	802	11	47	73	7173
ENV	RQGYSPLSF	804	9	48	75	7174
ENV	GIWGCSGKLI	680	10	48	75	7175
ENV	RQLLSGIV	628	8	49	77	7176
ENV	NVWATHACV	80	9	49	77	7177
ENV	WLWYIKIFI	773	9	49	77	7178
ENV	DQSLKPCV	126	8	50	78	7179
ENV	WLWYIKIF	773	8	50	78	7180
ENV	TVQCTHGI	290	8	51	80	7181
ENV	DQQLLGIW	675	8	51	80	7182
ENV	NVSTVQCTHGI	287	11	51	80	7183
ENV	KPCVKLTPLCV	130	11	54	84	7184
ENV	TVYYGVPV	48	8	55	86	7185
ENV	TVYYGVPVW	48	9	55	86	7186
ENV	CVKLTPLCV	132	9	55	86	7187
ENV	FLGAAGSTM	608	9	55	86	7188
ENV	WVTVYYGVPV	46	10	55	86	7189
ENV	WVTVYYGVPVW	46	11	55	86	7190
ENV	ELYKYKVV	560	8	56	89	7191
ENV	WVTVYYGV	46	8	58	91	7192
GAG	PPPESFRF	510	8	01	33	7193
GAG	EPIDKELY	537	8	01	25	7194
GAG	APPPESFRF	509	9	01	33	7195
GAG	KQEPIDKELY	535	10	01	25	7196
GAG	KQETIDKDLY	535	10	01	25	7197
GAG	EPLTALRSLF	547	10	01	33	7198
GAG	PPLASLKSLF	547	10	01	33	7199
GAG	PPLISLKSLF	547	10	01	33	7200
GAG	EPTAPPAESF	506	10	01	50	7201
GAG	EPTAPPPESF	506	10	01	50	7202
GAG	PPAESFRF	510	8	02	67	7203
GAG	APPAESFRF	509	9	02	67	7204
GAG	PPLASLKSLF	546	10	04	24	7205
GAG	YPLASLRSLF	545	10	07	15	7206
GAG	YPLASLKSLF	545	10	08	17	7207
GAG	NIMMQRGNF	407	9	10	17	7208
GAG	TPSQKQEPI	527	9	10	17	7209
GAG	NPPIPVGDI	277	9	10	16	7210

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	NPPIPVGDIY	277	10	10	16	7211
GAG	QIGWMTSNPPI	267	11	10	16	7212
GAG	KLDKWEKI	12	8	10	16	7213
GAG	GPVAPGQM	242	8	10	16	7214
GAG	PPIPVGDI	278	8	10	16	7215
GAG	PPAESFGF	498	8	10	16	7216
GAG	PPIPVGDIY	278	9	10	16	7217
GAG	APPAESFGF	497	9	10	16	7218
GAG	ALSPRTLNAW	167	10	10	16	7219
GAG	ALSPRTLNAWV	167	11	10	16	7220
GAG	IPVGDIYKRWI	280	11	10	16	7221
GAG	VQNANPDCKSI	347	11	10	16	7222
GAG	PIPVGDIY	279	8	11	17	7223
GAG	SQEVKNWM	334	8	11	17	7224
GAG	IMMQKSNF	408	8	11	17	7225
GAG	PQDLNMMLNI	202	10	11	17	7226
GAG	IPVGDIYKRW	280	10	11	17	7227
GAG	EQASQEVKNW	331	10	11	17	7228
GAG	TPQDLNMMLNI	201	11	11	17	7229
GAG	PQDLNMMLNIV	202	11	11	17	7230
GAG	IVGGHQAAMQM	211	11	11	17	7231
GAG	TLRAEQATQDV	327	11	11	17	7232
GAG	EQASQEVKNWM	331	11	11	17	7233
GAG	WPSSKGRPGNF	474	11	11	17	7234
GAG	EPIDKELY	533	8	12	19	7235
GAG	KQEPIDKELY	531	10	12	19	7236
GAG	TPQDLNMM	201	8	12	19	7237
GAG	DLNMMLNI	204	8	12	19	7238
GAG	TLQEQIAW	263	8	12	19	7239
GAG	TLYCVHQKI	86	9	12	19	7240
GAG	DLNMMLNIV	204	9	12	19	7241
GAG	IVGGHQAAM	211	9	12	19	7242
GAG	TLQEQIAWM	263	9	12	19	7243
GAG	PLTSLKSLF	548	9	12	19	7244
GAG	PLTSLRSLF	548	9	12	19	7245
GAG	NIVGGHQAAM	210	10	12	19	7246
GAG	TLRAEQASQEV	327	11	12	19	7247
GAG	TIMMQRGNF	407	9	13	22	7248
GAG	SPTSILDI	302	8	13	20	7249
GAG	RMYSPTSILDI	299	11	13	20	7250
GAG	LQEQIAWM	264	8	14	22	7251
GAG	RMYSPTSI	299	8	14	22	7252
GAG	VQNAQGQMV	156	9	14	22	7253
GAG	IVQNAQGQMV	155	10	14	22	7254
GAG	RVHPVHAGPI	235	10	14	22	7255
GAG	IVRMYSPTSI	297	10	14	22	7256
GAG	PIVQNAQGQMV	154	11	14	22	7257
GAG	KIVRMYSPTSI	296	11	14	22	7258
GAG	WPSNKGRPGNF	474	11	14	22	7259
GAG	KVSQNYPI	148	8	15	27	7260

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	KVSQNYPIV	148	9	15	27	7261
GAG	TQDVKNWM	334	8	15	23	7262
GAG	PPEESFRF	498	8	15	23	7263
GAG	ELRSLYNTV	76	9	15	23	7264
GAG	TLYCVHQRI	86	9	15	23	7265
GAG	APPEESFRF	497	9	15	23	7266
GAG	PLASLKSLF	548	9	15	23	7267
GAG	VLSGGKLDAW	7	10	15	23	7268
GAG	SLFNTVATLY	79	10	15	23	7269
GAG	LQGQMVHQAI	159	10	15	23	7270
GAG	EQATQDVKNW	331	10	15	23	7271
GAG	EPTAPPEESF	494	10	15	23	7272
GAG	SVLSGGKLDAW	6	11	15	23	7273
GAG	NLQGQMVHQAI	158	11	15	23	7274
GAG	EQATQDVKNWM	331	11	15	23	7275
GAG	WMTSNPPI	270	8	16	25	7276
GAG	GPAATLEEM	362	9	16	25	7277
GAG	WMTSNPPIPV	270	10	16	25	7278
GAG	GPAATLEEMM	362	10	16	25	7279
GAG	LLETSEGCRQI	52	11	16	25	7280
GAG	ALGPAATLEEM	360	11	16	25	7281
GAG	GPIPPGQM	242	8	17	27	7282
GAG	DIYKRWII	284	8	17	27	7283
GAG	PVGDIYKRWI	281	10	17	27	7284
GAG	PVGDIYKRWII	281	11	17	27	7285
GAG	ALGPGATLEEM	360	11	17	27	7286
GAG	QIGWMTNNPPI	267	11	18	29	7287
GAG	KLDAWEKI	12	8	18	28	7288
GAG	TQEVKNWM	334	8	18	28	7289
GAG	PVGDIYKRW	281	9	18	28	7290
GAG	GPGATLEEM	362	9	18	28	7291
GAG	EQATQEVKNW	331	10	18	28	7292
GAG	GPGATLEEMM	362	10	18	28	7293
GAG	EQATQEVKNWM	331	11	18	28	7294
GAG	GPIAPGQM	242	8	19	30	7295
GAG	GPSHKARV	379	8	19	30	7296
GAG	DIKQGPKEPF	308	10	19	30	7297
GAG	IVWASRELERF	35	11	19	30	7298
GAG	GVGGPSHKARV	376	11	19	30	7299
GAG	WMTNNPPI	270	8	20	31	7300
GAG	WMTNNPPIPV	270	10	20	31	7301
GAG	EPTAPPAESF	494	10	20	31	7302
GAG	YPIVQNAQGQM	153	11	20	31	7303
GAG	VIEEKAFSPEV	179	11	20	31	7304
GAG	VQNAQGQM	156	8	21	33	7305
GAG	KQGPKEPF	310	8	21	33	7306
GAG	IVQNAQGQM	155	9	21	33	7307
GAG	PIVQNAQGQM	154	10	21	33	7308
GAG	KQGPKEPFRDY	310	11	21	33	7309
GAG	SQVSQNYPI	146	9	22	44	7310

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	SQVSQNYPIV	146	10	22	44	7311
GAG	WMTDTLLV	340	8	22	34	7312
GAG	SLYNTVATLY	79	10	22	34	7313
GAG	RLHPVHAGPI	235	10	22	34	7314
GAG	WPSHKGRPGNF	474	11	23	36	7315
GAG	KVIEEKAF	178	8	24	38	7316
GAG	WVKVIEEKAF	176	10	24	38	7317
GAG	TLRAEQATQEV	327	11	24	38	7318
GAG	LVWASRELERF	35	11	25	39	7319
GAG	MQMLKETI	219	8	26	41	7320
GAG	AMQMLKETI	218	9	26	41	7321
GAG	QVSQNYPI	148	8	27	48	7322
GAG	QVSQNYPIV	148	9	27	48	7323
GAG	TLQEQIGW	263	8	27	42	7324
GAG	IMMQRGNF	408	8	27	42	7325
GAG	TLQEQIGWM	263	9	27	42	7326
GAG	GQMVHQAI	161	8	28	44	7327
GAG	KVVEEKAF	178	8	28	44	7328
GAG	WVKVVEEKAF	176	10	28	44	7329
GAG	VVEEKAFSPEV	179	11	28	44	7330
GAG	EPFRDYVDRFY	315	11	28	44	7331
GAG	VQNLQGQM	156	8	29	45	7332
GAG	LQEQIGWM	264	8	29	45	7333
GAG	IVQNLQGQM	155	9	29	45	7334
GAG	VQNLQGQMV	156	9	29	45	7335
GAG	PIVQNLQGQM	154	10	29	45	7336
GAG	IVQNLQGQMV	155	10	29	45	7337
GAG	AISPRTLNAW	167	10	29	45	7338
GAG	YPIVQNLQGQM	153	11	29	45	7339
GAG	PIVQNLQGQMV	154	11	29	45	7340
GAG	AISPRTLNAWV	167	11	29	45	7341
GAG	TLNAWVKVI	172	9	30	47	7342
GAG	TLNAWVKVV	172	9	31	48	7343
GAG	MQMLKDTI	219	8	33	52	7344
GAG	AMQMLKDTI	218	9	33	52	7345
GAG	VLAEAMSQV	386	9	33	52	7346
GAG	RVLAEAMSQV	385	10	33	52	7347
GAG	NPPIPVGEI	277	9	34	54	7348
GAG	NPPIPVGEIY	277	10	34	54	7349
GAG	RLRPGGKKKY	20	10	34	53	7350
GAG	IPVGEIYKRW	280	10	34	53	7351
GAG	PIPVGEIYKRW	279	11	34	53	7352
GAG	IPVGEIYKRWI	280	11	34	53	7353
GAG	RPGGKKKY	22	8	35	55	7354
GAG	PPIPVGEI	278	8	35	55	7355
GAG	PIPVGEIY	279	8	35	55	7356
GAG	PPIPVGEIY	278	9	35	55	7357
GAG	EPFRDYVDRFF	315	11	35	55	7358
GAG	GPGHKARV	379	8	36	56	7359
GAG	GVGGPGHKARV	376	11	36	56	7360

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	WMTETLLV	340	8	37	58	7361
GAG	HPVHAGPI	237	8	38	59	7362
GAG	RMYSPVSILDI	299	11	38	59	7363
GAG	EIYKRWII	284	8	39	61	7364
GAG	PVGEIYKRWII	281	11	39	61	7365
GAG	KIVRMYSPVSI	296	11	39	61	7366
GAG	RMYSPVSI	299	8	40	63	7367
GAG	SPVSILDI	302	8	40	63	7368
GAG	PVGEIYKRW	281	9	40	63	7369
GAG	PVGEIYKRWI	281	10	40	63	7370
GAG	IVRMYSPVSI	297	10	40	63	7371
GAG	TVATLYCV	83	8	41	64	7372
GAG	KIVRMYSPV	296	9	41	64	7373
GAG	DIRQGPKEPF	308	10	41	64	7374
GAG	PQDLNTMLNTV	202	11	41	64	7375
GAG	TPQDLNTM	201	8	42	66	7376
GAG	IVRMYSPV	297	8	42	66	7377
GAG	RQGPKEPF	310	8	42	66	7378
GAG	DLNTMLNTV	204	9	42	66	7379
GAG	RQGPKEPFRDY	310	11	42	66	7380
GAG	QMREPRGSDI	248	10	44	69	7381
GAG	GQMREPRGSDI	247	11	44	69	7382
GAG	VQNANPDCKTI	347	11	45	70	7383
GAG	TVGGHQAAM	211	9	47	73	7384
GAG	TVGGHQAAMQM	211	11	47	73	7385
GAG	TINEEAAEW	225	9	53	83	7386
GAG	SPEVIPMF	186	8	55	86	7387
GAG	APRKKGCW	440	8	55	86	7388
GAG	SPRTLNAWVKV	169	11	55	86	7389
GAG	RQANFLGKI	465	9	56	88	7390
GAG	RQANFLGKIW	465	10	56	88	7391
GAG	HLGLNKIVRM	290	11	56	88	7392
GAG	SPRTLNAW	169	8	57	89	7393
GAG	HLGLNKI	290	8	57	89	7394
GAG	SPRTLNAWV	169	9	57	89	7395
GAG	WHLGLNKI	289	9	57	89	7396
GAG	HLGLNKIV	290	9	57	89	7397
GAG	WHLGLNKIV	289	10	57	89	7398
GAG	ILGLNKIVRM	291	10	57	89	7399
GAG	ILGLNKIVRMY	291	11	57	89	7400
GAG	ILGLNKIV	291	8	58	91	7401
GAG	EMMTACQGV	369	9	59	92	7402
GAG	GLNKIVRM	293	8	60	94	7403
GAG	MMTACQGV	370	8	60	94	7404
GAG	GLNKIVRMY	293	9	60	94	7405
GAG	TLNAWVKV	172	8	61	95	7406
GAG	GPKEPFRDY	312	9	63	98	7407
GAG	GPKEPFRDYV	312	10	63	98	7408
GAG	EPFRDYVDRF	315	10	63	98	7409
NEF	APTAAKGV	34	8	01	33	7410

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	APTAAKGVGAV	34	11	01	33	7411
NEF	KQAEPAAEGV	32	10	01	17	7412
NEF	RQAPTAAKGV	32	10	01	17	7413
NEF	AQAEPAAAGV	33	10	01	17	7414
NEF	EPAADGVGAV	40	10	04	15	7415
NEF	VPLRPMTF	101	8	10	16	7416
NEF	HPICQHGM	259	8	10	16	7417
NEF	QVPLRPMTF	100	9	10	16	7418
NEF	PQVPLRPMTF	99	10	10	16	7419
NEF	LLHPICQHGM	257	10	10	16	7420
NEF	HMARELHPEY	320	10	10	16	7421
NEF	RPQVPLRPMTF	98	11	10	16	7422
NEF	CLLHPMSQHGM	256	11	10	16	7423
NEF	HMARELHPEYY	320	11	10	16	7424
NEF	WQNYTPGPGV	204	10	11	17	7425
NEF	VPVDPREV	230	8	11	17	7426
NEF	LVPVDPREV	229	9	11	17	7427
NEF	KLVPVDPREV	228	10	11	17	7428
NEF	PMTYKGAF	105	8	12	19	7429
NEF	HPMSQHGM	259	8	12	19	7430
NEF	RPMTYKGAF	104	9	12	19	7431
NEF	LLHPMSQHGM	257	10	12	19	7432
NEF	PLRPMTYKGAF	102	11	12	19	7433
NEF	SQKRQDILDLW	177	11	12	19	7434
NEF	WVYHTQGF	191	8	13	20	7435
NEF	TPGPGTRF	208	8	13	20	7436
NEF	GIRYPLTF	213	8	13	20	7437
NEF	WVYHTQGFF	191	9	13	20	7438
NEF	DLWVYHTQGF	188	10	13	20	7439
NEF	GPGIRYPLTF	210	10	13	20	7440
NEF	GPGTRFPLTF	210	10	13	20	7441
NEF	GIRYPLTFGW	213	10	13	20	7442
NEF	DLWVYHTQGFF	188	11	13	20	7443
NEF	DLEKHGAI	57	8	14	22	7444
NEF	WLEAQEEEEV	79	10	15	24	7445
NEF	AQEEEEVGF	83	9	17	27	7446
NEF	AQEEEEVGFPV	83	11	17	27	7447
NEF	TPGPGIRY	208	8	17	27	7448
NEF	FPLTFGWCF	217	9	17	27	7449
NEF	TQGFFPDWQNY	195	11	17	27	7450
NEF	WQNYTPGPGI	204	10	18	29	7451
NEF	LIYSKKRQEI	174	10	18	28	7452
NEF	GLIYSKKRQEI	173	11	18	28	7453
NEF	DILDLWVY	185	8	20	31	7454
NEF	RQDILDLWV	182	9	20	31	7455
NEF	RQDILDLWVY	182	10	20	31	7456
NEF	WVYHTQGY	191	8	21	33	7457
NEF	WVYHTQGYF	191	9	21	33	7458
NEF	DLWVYHTQGY	188	10	21	33	7459
NEF	DLWVYHTQGYF	188	11	21	33	7460

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	TQGFFPDW	195	8	22	34	7461
NEF	YPLTFGWCF	217	9	24	38	7462
NEF	RQDILDLW	182	8	25	39	7463
NEF	RQEILDLWVY	182	10	32	50	7464
NEF	EILDLWVY	185	8	33	52	7465
NEF	RQEILDLWV	182	9	35	55	7466
NEF	PLTFGWCFKLV	219	11	35	55	7467
NEF	RPQVPLRPMTY	98	11	36	56	7468
NEF	TQGYFPDWQNY	195	11	36	56	7469
NEF	RQEILDLW	182	8	37	58	7470
NEF	TQGYFPDW	195	8	37	58	7471
NEF	EVGFPVRPQV	91	10	40	63	7472
NEF	PLTFGWCF	219	8	43	67	7473
NEF	PQVPLRPMTY	99	10	45	70	7474
NEF	VPLRPMTY	101	8	46	73	7475
NEF	QVPLRPMTY	100	9	46	72	7476
NEF	RPQVPLRPM	98	9	47	73	7477
NEF	PVRPQVPLRPM	95	11	47	73	7478
NEF	PQVPLRPM	99	8	56	88	7479
POL	SPTSRELQV	35	9	01	33	7480
POL	AISLSLPQI	80	9	01	33	7481
POL	SPSSRELQV	38	9	01	50	7482
POL	GPERALSV	70	8	01	20	7483
POL	VPTFNFPQI	79	9	01	17	7484
POL	EPGEDRELSV	69	10	01	17	7485
POL	GQRQGTVSLSF	69	11	01	17	7486
POL	PQGEAREF	9	8	10	16	7487
POL	FPQGEAREF	8	9	10	16	7488
POL	LIEICGHKAI	150	10	10	16	7489
POL	AVQKIATESI	563	10	10	16	7490
POL	MLTQLGCTLNF	176	11	10	16	7491
POL	AVQKIATESIV	563	11	10	16	7492
POL	AVKAACWWAGI	877	11	10	16	7493
POL	IQTKELQKQII	960	11	10	16	7494
POL	RIGPENPY	238	8	11	17	7495
POL	YQLETEPI	619	8	11	17	7496
POL	AQEDHEKY	760	8	11	17	7497
POL	GIQQEFGI	886	8	11	17	7498
POL	KVVPRRKV	1011	8	11	17	7499
POL	VPRRKVKI	1013	8	11	17	7500
POL	VVPRRKVKI	1012	9	11	17	7501
POL	VPRRKVKII	1013	9	11	17	7502
POL	IIKDYGKQM	1020	9	11	17	7503
POL	GIQQEFGIPY	886	10	11	17	7504
POL	KVVPRRKVKI	1011	10	11	17	7505
POL	VVPRRKVKII	1012	10	11	17	7506
POL	KIIKDYGKQM	1019	10	11	17	7507
POL	KISRIGPENPY	235	11	11	17	7508
POL	IPSTNNETPGI	321	11	11	17	7509
POL	KLWYQLETEPI	616	11	11	17	7510

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KVVPRRKVKII	1011	11	11	17	7511
POL	KQIIKIQNF	967	9	12	19	7512
POL	IIKIQNFRV	969	9	12	19	7513
POL	IIKIQNFRVY	969	10	12	19	7514
POL	KQIIKIQNFRV	967	11	12	19	7515
POL	IIKIQNFRVYY	969	11	12	19	7516
POL	RPLVTVKI	95	8	12	19	7517
POL	EINLPGKW	122	8	12	19	7518
POL	QIIKIQNF	968	8	12	19	7519
POL	VIQDNSEI	1003	8	12	19	7520
POL	RQIILLRWGF	395	9	12	19	7521
POL	NQKTELIIAI	666	9	12	19	7522
POL	IIDIIASDI	952	9	12	19	7523
POL	IVDIIATDI	952	9	12	19	7524
POL	VVIQDNSEI	1002	9	12	19	7525
POL	IQDNSEIKV	1004	9	12	19	7526
POL	WQRPLVTVKI	93	10	12	19	7527
POL	RQYDQIPIEI	144	10	12	19	7528
POL	GQDQWTYQIY	525	10	12	19	7529
POL	RMRGAIITNDV	548	10	12	19	7530
POL	NQKTELQAIY	666	10	12	19	7531
POL	RIIDIIASDI	951	10	12	19	7532
POL	RIVDIIATDI	951	10	12	19	7533
POL	QIIKIQNFRV	968	10	12	19	7534
POL	AVVIQDNSEI	1000	10	12	19	7535
POL	VIQDNSEIKV	1003	10	12	19	7536
POL	IQDNSEIKVV	1004	10	12	19	7537
POL	VLEEINLPGKW	119	11	12	19	7538
POL	ELRQIILLRWGF	393	11	12	19	7539
POL	IIPDKWTVQPIV	424	11	12	19	7540
POL	IQKQGQDQWTY	521	11	12	19	7541
POL	LQKQIIKIQNF	965	11	12	19	7542
POL	QIIKIQNFRVY	968	11	12	19	7543
POL	VVIQDNSEIKV	1002	11	12	19	7544
POL	VIQDNSEIKVV	1003	11	12	19	7545
POL	ELQKQIIKI	964	9	13	21	7546
POL	NLKTGKYARM	540	10	13	21	7547
POL	DINLPGKW	122	8	13	20	7548
POL	RQYDQIPI	144	8	13	20	7549
POL	QLPEKDSW	434	8	13	20	7550
POL	VLPEKDSW	434	8	13	20	7551
POL	LQKQIIKI	965	8	13	20	7552
POL	IQLPEKDSW	433	9	13	20	7553
POL	IVLPEKDSW	433	9	13	20	7554
POL	IQKQGQDQW	521	9	13	20	7555
POL	GQDQWTYQI	525	9	13	20	7556
POL	SPTRRELQVW	29	10	13	20	7557
POL	KVRQYDQIPI	142	10	13	20	7558
POL	LIEICGKKAI	150	10	13	20	7559
POL	PIQLPEKDSW	432	10	13	20	7560

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PIVLPEKDSW	432	10	13	20	7561
POL	QLPEKDSWTV	434	10	13	20	7562
POL	VLPEKDSWTV	434	10	13	20	7563
POL	EIQKQGQDQW	520	10	13	20	7564
POL	EQAEHLKTAV	919	10	13	20	7565
POL	VLEDINLPGKW	119	11	13	20	7566
POL	ILIEICGKKAI	149	11	13	20	7567
POL	QPIQLPEKDSW	431	11	13	20	7568
POL	QPIVLPEKDSW	431	11	13	20	7569
POL	IQLPEKDSWTV	433	11	13	20	7570
POL	IVLPEKDSWTV	433	11	13	20	7571
POL	KQGQDQWTYQI	523	11	13	20	7572
POL	LIKKEKVYLSW	717	11	13	20	7573
POL	KLAGRWPVKTI	855	11	13	20	7574
POL	RPLVTIKI	95	8	14	22	7575
POL	KQNPDIVI	362	8	14	22	7576
POL	KIATESIV	566	8	14	22	7577
POL	YQLEKDPI	619	8	14	22	7578
POL	SPTRRELQV	29	9	14	22	7579
POL	KQNPDIVIY	362	9	14	22	7580
POL	VQKIATESI	564	9	14	22	7581
POL	KIATESIVI	566	9	14	22	7582
POL	WQRPLVTIKI	93	10	14	22	7583
POL	VQKIATESIV	564	10	14	22	7584
POL	KIATESIVIW	566	10	14	22	7585
POL	THTDNGSNF	864	10	14	22	7586
POL	EPFRKQNPDIV	358	11	14	22	7587
POL	KQNPDIVIYQY	362	11	14	22	7588
POL	ELREHLLKWGF	393	11	14	22	7589
POL	VQKIATESIVI	564	11	14	22	7590
POL	KLWYQLEKDPI	616	11	14	22	7591
POL	LVEICTEM	221	8	15	24	7592
POL	KIKALVEI	217	8	15	23	7593
POL	TQLGCTLNF	178	9	15	23	7594
POL	ALVEICTEM	220	9	15	23	7595
POL	ELRQHLLRW	393	9	15	23	7596
POL	IQKQGQGQW	521	9	15	23	7597
POL	KQGQDQWTY	523	9	15	23	7598
POL	IQKETWEAW	585	9	15	23	7599
POL	LVSAGIRKV	743	9	15	23	7600
POL	LPGRWKPKMI	125	10	15	23	7601
POL	EIQKQGQGQW	520	10	15	23	7602
POL	PIQKETWEAW	584	10	15	23	7603
POL	IQKETWEAWW	585	10	15	23	7604
POL	QVDKLVSAGI	739	10	15	23	7605
POL	KLVSAGIRKV	742	10	15	23	7606
POL	TQLGCTLNFPI	178	11	15	23	7607
POL	PLTEEKIKALV	212	11	15	23	7608
POL	IQKQGQGQWTY	521	11	15	23	7609
POL	LPIQKETWEAW	583	11	15	23	7610

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PIQKETWEAWW	584	11	15	23	7611
POL	HLALQDSGLEV	675	11	15	23	7612
POL	EQVDKLVSAGI	738	11	15	23	7613
POL	LVSAGIRKVLF	743	11	15	23	7614
POL	QLGCTLNF	179	8	16	25	7615
POL	QLEKEPIV	620	8	16	25	7616
POL	AQEEHERY	760	8	16	25	7617
POL	LPGRWKPKM	125	9	16	25	7618
POL	YQLEKEPIV	619	9	16	25	7619
POL	IQQEFGIPY	887	9	16	25	7620
POL	QLGCTLNFPI	179	10	16	25	7621
POL	EPFRKQNPDI	358	10	16	25	7622
POL	TPKFKLPI	578	8	17	27	7623
POL	NPDIVIYQY	364	9	17	27	7624
POL	ELREHLLKW	393	9	17	27	7625
POL	NPDIVIYQYM	364	10	17	27	7626
POL	MLTQIGCTLNF	176	11	17	27	7627
POL	NLKTGKYAKM	540	10	18	29	7628
POL	SVPLDKDF	306	8	18	28	7629
POL	DIVIYQYM	366	8	18	28	7630
POL	TLWQRPLVTV	91	10	18	28	7631
POL	IIGRNMLTQI	171	10	18	28	7632
POL	VPLDKDFRKY	307	10	18	28	7633
POL	NIIGRNMLTQI	170	11	18	28	7634
POL	SVPLDKDFRKY	306	11	18	28	7635
POL	LLRGTKALTEV	471	11	18	28	7636
POL	ELVNQIIEQLI	708	11	18	28	7637
POL	AMASDFNLPPI	773	11	18	28	7638
POL	PLWKGPAKLLW	985	11	18	28	7639
POL	PLDKDFRKY	308	9	19	30	7640
POL	WQRPLVTV	93	8	19	30	7641
POL	EICGHKAI	152	8	19	30	7642
POL	LVNQIIEQLI	709	10	19	30	7643
POL	LVSQIIEQLI	709	10	19	30	7644
POL	EICGHKAIGTV	152	11	19	30	7645
POL	ELVSQIIEQLI	708	11	19	30	7646
POL	QQEFGIPY	888	8	20	32	7647
POL	RQYDQILI	144	8	20	31	7648
POL	SQIIEQLI	711	8	20	31	7649
POL	KLPIQKETW	582	9	20	31	7650
POL	KVRQYDQILI	142	10	20	31	7651
POL	RQYDQILIEI	144	10	20	31	7652
POL	DLEIGQHRTKI	381	11	20	31	7653
POL	LIKKEKVYLAW	717	11	20	31	7654
POL	TVKAACWWAGI	877	11	20	31	7655
POL	KVIHTDNGSNF	863	11	21	33	7656
POL	WQRPLVTI	93	8	21	33	7657
POL	EIGQHRTKI	383	9	21	33	7658
POL	EPIVGAETF	624	9	21	33	7659
POL	TLWQRPLVTI	91	10	21	33	7660

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	IIGRNLLTQI	171	10	21	33	7661
POL	EPIVGAETFY	624	10	21	33	7662
POL	NIIGRNLLTQI	170	11	21	33	7663
POL	LLTQIGCTLNF	176	11	21	33	7664
POL	EPIVGAETFYV	624	11	21	33	7665
POL	DQWTYQIY	527	8	22	34	7666
POL	GIKQEFGI	886	8	22	34	7667
POL	GIKQEFGIPY	886	10	22	34	7668
POL	LLRGAKALTDI	471	11	22	34	7669
POL	YLAWVPAHKGI	724	11	22	34	7670
POL	KLAGRWPVKVI	855	11	22	34	7671
POL	NPEIVIYQY	364	9	23	36	7672
POL	HLEGKVILV	819	9	23	36	7673
POL	KVILVAVHV	823	9	23	36	7674
POL	NPEIVIYQYM	364	10	23	36	7675
POL	EICGKKAIGTV	152	11	23	36	7676
POL	HLEGKVILVAV	819	11	23	36	7677
POL	EICGKKAI	152	8	24	38	7678
POL	NPYNTPIF	243	8	24	38	7679
POL	EIVIYQYM	366	8	24	38	7680
POL	NQIIEQLI	711	8	24	38	7681
POL	VILVAVHV	824	8	24	38	7682
POL	TVKAACWW	877	8	24	38	7683
POL	PVNIIGRNM	168	9	24	38	7684
POL	TPVNIIGRNM	167	10	24	38	7685
POL	GPENPYNTPI	240	10	24	38	7686
POL	NPYNTPIFAI	243	10	24	38	7687
POL	GQGQWTYQIY	525	10	24	38	7688
POL	VIHTDNGSNF	864	10	24	38	7689
POL	GPENPYNTPIF	240	11	24	38	7690
POL	LQDSGSEV	678	8	25	39	7691
POL	LLKLAGRW	853	8	25	39	7692
POL	KQGQGQWTY	523	9	25	39	7693
POL	GQGQWTYQI	525	9	25	39	7694
POL	ALQDSGSEV	677	9	25	39	7695
POL	FLLKLAGRW	852	9	25	39	7696
POL	LQDSGSEVNI	678	10	25	39	7697
POL	LLKLAGRWPV	853	10	25	39	7698
POL	KQGQGQWTYQI	523	11	25	39	7699
POL	ALQDSGSEVNI	677	11	25	39	7700
POL	LQDSGSEVNIV	678	11	25	39	7701
POL	AMASDFNLPPV	773	11	25	39	7702
POL	FLLKLAGRWPV	852	11	25	39	7703
POL	QLDCTHLEGKV	814	11	26	41	7704
POL	PIVAKEIV	782	8	26	41	7705
POL	EIGQHRAKI	383	9	26	41	7706
POL	RLPIQKETW	582	9	26	41	7707
POL	LVSSGIRKV	743	9	26	41	7708
POL	PPIVAKEIV	781	9	26	41	7709
POL	DPSKDLIAEI	512	10	26	41	7710

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KLVSSGIRKV	742	10	26	41	7711
POL	NLPPIVAKEI	779	10	26	41	7712
POL	LPPIVAKEIV	780	10	26	41	7713
POL	DLEIGQHRAKI	381	11	26	41	7714
POL	LVSSGIRKVLF	743	11	26	41	7715
POL	NLPPIVAKEIV	779	11	26	41	7716
POL	QIYAGIKV	458	8	27	43	7717
POL	QIYPGIKV	458	8	27	43	7718
POL	LQDSGLEV	678	8	27	42	7719
POL	AQEEHEKY	760	8	27	42	7720
POL	PPIVAKEI	781	8	27	42	7721
POL	SQIYAGIKV	457	9	27	42	7722
POL	SQIYPGIKV	457	9	27	42	7723
POL	IQKETWETW	585	9	27	42	7724
POL	ALQDSGLEV	677	9	27	42	7725
POL	LPPIVAKEI	780	9	27	42	7726
POL	PIQKETWETW	584	10	27	42	7727
POL	IQKETWETWW	585	10	27	42	7728
POL	LQDSGLEVNI	678	10	27	42	7729
POL	NLPPVVAKEI	779	10	27	42	7730
POL	LPPVVAKEIV	780	10	27	42	7731
POL	LPIQKETWETW	583	11	27	42	7732
POL	PIQKETWETWW	584	11	27	42	7733
POL	YVTDRGRQKVV	649	11	27	42	7734
POL	ALQDSGLEVNI	677	11	27	42	7735
POL	LQDSGLEVNIV	678	11	27	42	7736
POL	NLPPVVAKEIV	779	11	27	42	7737
POL	KQEFGIPY	888	8	28	44	7738
POL	KIKALTEI	217	8	28	44	7739
POL	PIVGAETF	625	8	28	44	7740
POL	IVGAETFY	626	8	28	44	7741
POL	QLIKKEKV	716	8	28	44	7742
POL	PVVAKEIV	782	8	28	44	7743
POL	PIVGAETFY	625	9	28	44	7744
POL	IVGAETFYV	626	9	28	44	7745
POL	EQLIKKEKV	715	9	28	44	7746
POL	QLIKKEKVY	716	9	28	44	7747
POL	LPPVVAKEI	780	9	28	44	7748
POL	PPVVAKEIV	781	9	28	44	7749
POL	PIVGAETFYV	625	10	28	44	7750
POL	EQLIKKEKVY	715	10	28	44	7751
POL	HEQLIKKEKV	713	11	28	44	7752
POL	PPVVAKEI	781	8	29	45	7753
POL	HDHATDI	952	9	29	45	7754
POL	YVTDRGRQKV	649	10	29	45	7755
POL	QVDKLVSSGI	739	10	29	45	7756
POL	RHDHATDI	951	10	29	45	7757
POL	EQVDKLVSSGI	738	11	29	45	7758
POL	TPKFRLPI	578	8	30	47	7759
POL	HLVAVHV	824	8	30	47	7760

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KIILVAVIIV	823	9	30	47	7761
POL	KLAGRWPVKV	855	10	30	47	7762
POL	GQWTYQIY	527	8	31	48	7763
POL	YQLEKEPI	619	8	31	48	7764
POL	GQETAYFI	846	8	31	48	7765
POL	IILEGKIILV	819	9	31	48	7766
POL	IPSINNETPGI	321	11	31	48	7767
POL	GVYYDPSKDLI	508	11	31	48	7768
POL	KLWYQLEKEPI	616	11	31	48	7769
POL	IILEGKIILVAV	819	11	31	48	7770
POL	KQLTEAVQKI	558	10	32	51	7771
POL	AVKAACWW	877	8	32	50	7772
POL	SINNETPGI	323	9	32	50	7773
POL	FILKLAGRW	852	9	32	50	7774
POL	EMEKEGKISKI	229	11	32	50	7775
POL	SINNETPGIRY	323	11	32	50	7776
POL	FILKLAGRWPV	852	11	32	50	7777
POL	QLDCTIILEGKI	814	11	33	52	7778
POL	DVKQLTEAV	556	9	33	52	7779
POL	ELQKQITKI	964	9	34	54	7780
POL	KQITKIQNF	967	9	34	54	7781
POL	KQITKIQNFRV	967	11	34	54	7782
POL	ILKLAGRW	853	8	34	53	7783
POL	QLTEAVQKI	559	9	34	53	7784
POL	ILKLAGRWPV	853	10	34	53	7785
POL	LQKQITKIQNF	965	11	34	53	7786
POL	RVYYRDSRDPI	976	11	34	53	7787
POL	LIKKEKVY	717	8	35	55	7788
POL	QITKIQNF	968	8	35	55	7789
POL	NLPGKWKPKM	124	10	35	55	7790
POL	QITKIQNFRV	968	10	35	55	7791
POL	NLPGKWKPKMI	124	11	35	55	7792
POL	QITKIQNFRVY	968	11	35	55	7793
POL	PIWKGPAKLLW	985	11	35	55	7794
POL	KLGKAGYV	643	8	36	56	7795
POL	LQKQITKI	965	8	36	56	7796
POL	AIFQSSMTKI	347	10	36	56	7797
POL	AQPDKSESELV	700	11	36	56	7798
POL	VIQDNSDI	1003	8	37	58	7799
POL	VVIQDNSDI	1002	9	37	58	7800
POL	NPYNTPVFAI	243	10	37	58	7801
POL	QPDKSESELV	701	10	37	58	7802
POL	AVVIQDNSDI	1000	10	37	58	7803
POL	VIQDNSDIKV	1003	10	37	58	7804
POL	YLSWVPAIIKGI	724	11	37	58	7805
POL	VVIQDNSDIKV	1002	11	37	58	7806
POL	VIQDNSDIKVV	1003	11	37	58	7807
POL	NPYNTPVF	243	8	38	59	7808
POL	FQSSMTKI	349	8	38	59	7809
POL	IQDNSDIKV	1004	9	38	59	7810

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	GPENPYNTPV	240	10	38	59	7811
POL	IQDNSDIKVV	1004	10	38	59	7812
POL	GPENPYNTPVF	240	11	38	59	7813
POL	ILKEPVIIGVYY	498	11	38	59	7814
POL	LPGKWKPKM	125	9	39	61	7815
POL	LPGKWKPKMI	125	10	39	61	7816
POL	LPEKDSWTV	435	9	40	63	7817
POL	ILKEPVIIGVY	498	10	40	63	7818
POL	EILKEPVIIGVY	497	11	40	63	7819
POL	KVRQYDQI	142	8	41	64	7820
POL	QIGCTLNF	179	8	41	64	7821
POL	EPVIIGVYY	504	8	41	64	7822
POL	TQIGCTLNF	178	9	41	64	7823
POL	ILKEPVIIGV	498	9	41	64	7824
POL	FIKVRQYDQI	140	10	41	64	7825
POL	QIGCTLNFPI	179	10	41	64	7826
POL	EILKEPVIIGV	497	10	41	64	7827
POL	TQIGCTLNFPI	178	11	41	64	7828
POL	KISKIGPENPY	235	11	41	64	7829
POL	SIVIWGKTPKF	571	11	41	64	7830
POL	EMEKEGKI	229	8	42	66	7831
POL	SPAIFQSSM	345	9	42	66	7832
POL	NQKTELQAI	666	9	42	66	7833
POL	IVIYQYMDDLY	367	11	42	66	7834
POL	YQIYQEPF	531	8	43	67	7835
POL	SMTKILEPF	352	9	43	67	7836
POL	QMAGDDCV	1027	8	44	69	7837
POL	KQMAGDDCV	1026	9	44	69	7838
POL	IQTKELQKQI	960	10	44	69	7839
POL	DIQTKELQKQI	959	11	44	69	7840
POL	EPFKNLKTGKY	536	11	45	70	7841
POL	DQAEHLKTAV	919	10	46	72	7842
POL	LPIQKETW	583	8	47	73	7843
POL	VIWGKTPKF	573	9	47	73	7844
POL	QITLWQRPLV	89	10	47	73	7845
POL	IVIWGKTPKF	572	10	47	73	7846
POL	PQITLWQRPLV	88	11	47	73	7847
POL	KLKPGMDGPKV	197	11	47	73	7848
POL	LVAVIIVASGYI	826	11	47	73	7849
POL	TLWQRPLV	91	8	49	77	7850
POL	GLKKKKSVTV	288	10	49	77	7851
POL	GIRKVLFLDGI	747	11	49	77	7852
POL	KVLFLDGI	750	8	50	78	7853
POL	VPRRKAKII	1013	9	50	78	7854
POL	IIRDYGKQM	1020	9	50	78	7855
POL	VVPRRKAKII	1012	10	50	78	7856
POL	KIIRDYGKQM	1019	10	50	78	7857
POL	HPAGLKKKKSV	285	11	50	78	7858
POL	KVVPRRKAKII	1011	11	50	78	7859
POL	KIGPENPY	238	8	51	80	7860

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	VPRRKAKI	1013	8	51	80	7861
POL	KPGMDGPKV	199	9	51	80	7862
POL	VVPRRKAKI	1012	9	51	80	7863
POL	GMDGPKVKQW	201	10	51	80	7864
POL	TPGIRYQYNV	328	10	51	80	7865
POL	VIYQYMDDLY	368	10	51	80	7866
POL	KVVPRRKAKI	1011	10	51	80	7867
POL	VLVGPTPVNII	162	11	51	80	7868
POL	VIYQYMDDLYV	368	11	51	80	7869
POL	WIPEWEFV	602	8	52	84	7870
POL	IQNFRVYY	972	8	52	84	7871
POL	GLKKKKSV	288	8	52	81	7872
POL	TPGIRYQY	328	8	52	81	7873
POL	GIRYQYNV	330	8	52	81	7874
POL	KIQNFRVY	971	8	52	81	7875
POL	KIQNFRVYY	971	9	52	81	7876
POL	LVGPTPVNII	163	10	52	81	7877
POL	WQATWIPEWEF	598	11	52	81	7878
POL	IIVASGYIEAEV	830	11	52	81	7879
POL	VLVGPTPV	162	8	53	83	7880
POL	CQLKGEAM	795	8	53	83	7881
POL	SQGVVESM	899	8	53	83	7882
POL	TVLVGPTPV	161	9	53	83	7883
POL	AVHVASGYI	828	9	53	83	7884
POL	SMNKELKKI	905	9	53	83	7885
POL	VLVGPTPVNI	162	10	53	83	7886
POL	HPDKWTVQPI	424	10	53	83	7887
POL	ELELAENREI	489	10	53	83	7888
POL	LVAVHVASGY	826	10	53	83	7889
POL	PQSQGVVESM	897	10	53	83	7890
POL	SMNKELKKII	905	10	53	83	7891
POL	GIGGFIKVRQY	136	11	53	83	7892
POL	TVLVGPTPVNI	161	11	53	83	7893
POL	VLDVGDAYFSV	297	11	53	83	7894
POL	QLKGEAMHGQV	796	11	53	83	7895
POL	ILVAVHVASGY	825	11	53	83	7896
POL	NPQSQGVVESM	896	11	53	83	7897
POL	FVNTPPLV	608	8	54	86	7898
POL	FVNTPPLVKLW	608	11	54	86	7899
POL	GPTPVNII	165	8	54	84	7900
POL	LVGPTPVNI	163	9	54	84	7901
POL	DVGDAYFSV	299	9	54	84	7902
POL	WQATWIPEW	598	9	54	84	7903
POL	TVPVKLKPGM	193	10	54	84	7904
POL	FPISPIETVPV	186	11	55	86	7905
POL	TQDFWEVQLGI	273	11	55	86	7906
POL	SPIETVPV	189	8	56	88	7907
POL	PVKLKPGM	195	8	56	88	7908
POL	WPLTEEKI	211	8	56	88	7909
POL	FPISPIETV	186	9	56	88	7910

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	VPVKLKPGM	194	9	56	88	7911
POL	PISPIETVPV	187	10	56	88	7912
POL	KQWPLTEEKI	209	10	56	88	7913
POL	SVTVLDVGDAY	294	11	56	88	7914
POL	PISPIETV	187	8	57	89	7915
POL	ELAENREI	491	8	57	89	7916
POL	TPPLVKLW	611	8	57	89	7917
POL	PPLVKLWY	612	8	57	89	7918
POL	QVDCSPGI	805	8	57	89	7919
POL	HLKTAVQM	923	8	57	89	7920
POL	ELNKRTQDF	268	9	57	89	7921
POL	TVLDVGDAY	296	9	57	89	7922
POL	TPPLVKLWY	611	9	57	89	7923
POL	GQVDCSPGI	804	9	57	89	7924
POL	QVDCSPGIW	805	9	57	89	7925
POL	ELKKIIGQV	909	9	57	89	7926
POL	AIKKKDSTKW	251	10	57	89	7927
POL	ELNKRTQDFW	268	10	57	89	7928
POL	TVLDVGDAYF	296	10	57	89	7929
POL	GQVDCSPGIW	804	10	57	89	7930
POL	HLKTAVQMAV	923	10	57	89	7931
POL	HLKTAVQMAVF	923	11	57	89	7932
POL	GIGGYSAGERI	942	11	57	89	7933
POL	LPQGWKGSPAI	338	11	58	92	7934
POL	YVGSDLEI	377	8	58	91	7935
POL	DLYVGSDLEI	375	10	58	91	7936
POL	IVTDSQYALGI	687	11	58	91	7937
POL	IPAETGQETAY	841	11	58	91	7938
POL	FIHNFKRKGGI	933	11	58	91	7939
POL	SQYALGII	691	8	59	92	7940
POL	GIGGNEQV	733	8	59	92	7941
POL	AVHVASGY	828	8	59	92	7942
POL	KLAGRWPV	855	8	59	92	7943
POL	NPQSQGVV	896	8	59	92	7944
POL	PQGWKGSPAI	339	10	59	92	7945
POL	EVNIVTDSQY	684	10	59	92	7946
POL	PQGWKGSPAIF	339	11	59	92	7947
POL	IPYNPQSQGVV	893	11	59	92	7948
POL	KLLWKGEGAVV	992	11	59	92	7949
POL	LLWKGEGAVVI	993	11	59	92	7950
POL	KPKMIGGI	130	8	60	94	7951
POL	VLDVGDAY	297	8	60	94	7952
POL	AVQMAVFI	927	8	60	94	7953
POL	VLDVGDAYF	297	9	60	94	7954
POL	ELHPDKWTV	422	9	60	94	7955
POL	KLNWASQIY	452	9	60	94	7956
POL	QMAVFIHNF	929	9	60	94	7957
POL	VQMAVFIHNF	928	10	60	94	7958
POL	KLLWKGEGAV	992	10	60	94	7959
POL	KPKMIGGIGGF	130	11	60	94	7960

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WMGYELHPDKW	418	11	60	94	7961
POL	LVGKLNWASQI	449	11	60	94	7962
POL	AVQMAVFIHNF	927	11	60	94	7963
POL	TLNFPISPI	183	9	61	97	7964
POL	YQYMDDLY	370	8	61	95	7965
POL	KLNWASQI	452	8	61	95	7966
POL	YQYMDDLYV	370	9	61	95	7967
POL	TVNDIQKLV	442	9	61	95	7968
POL	LLWKGEGAVV	993	10	61	95	7969
POL	ALLDTGADDTV	109	11	61	95	7970
POL	MIGGIGGF	133	8	62	97	7971
POL	KLVGKLNW	448	8	62	97	7972
POL	NIVTDSQY	686	8	62	97	7973
POL	KMIGGIGGF	132	9	62	97	7974
POL	MIGGIGGFI	133	9	62	97	7975
POL	HQKEPPFLW	410	9	62	97	7976
POL	LLWKGEGAV	993	9	62	97	7977
POL	KMIGGIGGFI	132	10	62	97	7978
POL	HQKEPPFLWM	410	10	62	97	7979
POL	IQKLVGKLNW	446	10	62	97	7980
POL	MIGGIGGFIKV	133	11	62	97	7981
POL	DIQKLVGKLNW	445	11	62	97	7982
POL	WVPAHKGI	727	8	63	98	7983
POL	EPPFLWMGY	413	9	63	98	7984
POL	LLDTGADDTV	110	10	63	98	7985
POL	YQYNVLPQGW	333	10	63	98	7986
POL	IPYNPQSQGV	893	10	63	98	7987
POL	GIPYNPQSQGV	892	11	63	98	7988
POL	GIGGFIKV	136	8	64	100	7989
POL	PPFLWMGY	414	8	64	100	7990
REV	PQGTETGV	101	8	05	18	7991
REV	SQGTETGV	101	8	05	18	7992
REV	QPQGTETGV	100	9	05	18	7993
REV	CLGRPAEPV	67	9	10	16	7994
REV	TQGVGSPQI	98	9	11	18	7995
REV	LLKTVRLI	12	8	11	17	7996
REV	RQRQIHSI	52	8	11	17	7997
REV	VPLQLPPI	75	8	11	17	7998
REV	PVPLQLPPI	74	9	11	17	7999
REV	EPVPLQLPPI	73	10	11	17	8000
REV	AVRIIKILY	17	9	13	20	8001
REV	RQARKNRRRRW	39	11	16	25	8002
REV	IIKILYQSNPY	20	11	18	28	8003
REV	KILYQSNPY	22	9	26	41	8004
REV	ILYQSNPY	23	8	27	42	8005
REV	RQARRNRRRRW	39	11	38	59	8006
TAT	GPKESKKKV	90	9	13	20	8007
TAT	EPVDPRLEPW	2	10	13	20	8008
TAT	FLNKGLGI	41	8	14	22	8009
TAT	PVDPRLEPW	3	9	14	22	8010

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
TAT	EPVDPNLEPW	2	10	14	22	8011
TAT	FLNKGLGISY	41	10	14	22	8012
TAT	PVDPNLEPW	3	9	20	31	8013
VIF	ALIKPKKI	157	8	10	16	8014
VIF	PLGEARLVI	58	9	10	16	8015
VIF	QVDRMRINTW	12	10	10	16	8016
VIF	HPLGDARLV	56	10	10	16	8017
VIF	IPLGEARLVI	57	10	10	16	8018
VIF	WQVDRMRINTW	11	11	10	16	8019
VIF	HPLGEARLVI	56	11	10	16	8020
VIF	GVSIEWRLRRY	87	11	10	16	8021
VIF	QIDPDLADQLI	102	11	10	16	8022
VIF	PLGDARLV	58	8	11	17	8023
VIF	IPLGDARLV	57	9	11	17	8024
VIF	SIEWRLRRY	89	9	11	17	8025
VIF	GLADQLIHMHY	106	11	11	17	8026
VIF	RLVITTYW	65	8	12	19	8027
VIF	LQTGERDW	74	8	12	19	8028
VIF	KIRTWNSLV	17	9	12	19	8029
VIF	GLQTGERDW	73	9	12	19	8030
VIF	IVWQVDRMKI	9	10	12	19	8031
VIF	QVDRMKIRTW	12	10	12	19	8032
VIF	WQVDRMKIRTW	11	11	12	19	8033
VIF	RMKIRTWNSLV	15	11	12	19	8034
VIF	WQVDRMKI	11	8	13	20	8035
VIF	HPKISSEV	48	8	13	20	8036
VIF	HPRISSEV	48	8	13	20	8037
VIF	DQLIHMHY	109	8	13	20	8038
VIF	DQLIHMHYF	109	9	13	20	8039
VIF	HPKISSEVHI	48	10	13	20	8040
VIF	HPRISSEVHI	48	10	13	20	8041
VIF	SVKKLTEDRW	174	10	13	20	8042
VIF	QLIHLYYFDCF	110	11	13	20	8043
VIF	DQLIHLYY	109	8	14	22	8044
VIF	QLIHLYYF	110	8	14	22	8045
VIF	QLIHMHYF	110	8	14	22	8046
VIF	IVSPRCEY	133	8	14	22	8047
VIF	DQLIHLYYF	109	9	14	22	8048
VIF	QVDPGLADQLI	102	11	14	22	8049
VIF	QLIHMHYFDCF	110	11	14	22	8050
VIF	KISSEVHI	50	8	15	23	8051
VIF	RISSEVHI	50	8	15	23	8052
VIF	HMHYFDCF	113	8	15	23	8053
VIF	RIRTWKSLV	17	9	15	23	8054
VIF	RIRTWNSLV	17	9	15	23	8055
VIF	GLADQLIHM	106	9	15	23	8056
VIF	LIHMHYFDCF	111	10	15	23	8057
VIF	RMRIRTWKSLV	15	11	15	23	8058
VIF	RMRIRTWNSLV	15	11	15	23	8059
VIF	HLYYFDCF	113	8	16	25	8060

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	LHILYYFDCF	111	10	16	25	8061
VIF	LVKHHMYI	24	8	19	30	8062
VIF	HPKVSSEV	48	8	19	30	8063
VIF	PLGEARLV	58	8	19	30	8064
VIF	SLVKHHMYI	23	9	19	30	8065
VIF	IPLGEARLV	57	9	19	30	8066
VIF	DPDLADQLI	104	9	19	30	8067
VIF	DPGLADQLI	104	9	19	30	8068
VIF	KIKPPLPSV	164	9	19	30	8069
VIF	HPKVSSEVHI	48	10	19	30	8070
VIF	HIPLGEARLV	56	10	19	30	8071
VIF	KVSSEVHI	50	8	20	31	8072
VIF	LVKHHMYV	24	8	21	33	8073
VIF	SLVKHHMYV	23	9	21	33	8074
VIF	GLHTGERDW	73	9	22	34	8075
VIF	HLGHGVSI	83	8	25	39	8076
VIF	HLGHGVSIEW	83	10	25	39	8077
VIF	HLGQGVSI	83	8	26	41	8078
VIF	GQGVSIEW	85	8	26	41	8079
VIF	HLGQGVSIEW	83	10	26	41	8080
VIF	SLQYLALTALI	149	11	27	42	8081
VIF	YLALTALI	152	8	28	44	8082
VIF	LQYLALTALI	150	10	28	44	8083
VIF	QVDRMRIRTW	12	10	31	48	8084
VIF	WQVDRMRIRTW	11	11	31	48	8085
VIF	YQAGHNKV	140	8	38	59	8086
VIF	QVMIVWQV	6	8	43	67	8087
VIF	WQVMIVWQV	5	9	43	67	8088
VIF	QVMIVWQVDRM	6	11	43	67	8089
VIF	MIVWQVDRMRI	8	11	43	67	8090
VIF	SLVKHHMY	23	8	44	69	8091
VIF	VMIVWQVDRM	7	10	44	69	8092
VIF	MIVWQVDRM	8	9	46	72	8093
VIF	IVWQVDRMRI	9	10	47	73	8094
VIF	WQVDRMRI	11	8	48	75	8095
VIF	IVWQVDRM	9	8	59	92	8096
VPR	RPWLHGLGQY	36	10	10	16	8097
VPR	QQLLFVHF	65	8	10	16	8098
VPR	LQQLLFVHF	64	9	10	16	8099
VPR	QLLFVHFRI	66	9	10	16	8100
VPR	QQLLFVHFRI	65	10	10	16	8101
VPR	LQQLLFVHFRI	64	11	10	16	8102
VPR	KQEAVRHF	27	8	11	17	8103
VPR	WLHGLGQY	38	8	11	17	8104
VPR	RIGCRHSRIGI	74	11	11	17	8105
VPR	RPWLHGLGQHI	36	11	12	19	8106
VPR	LLFVHFRI	67	8	12	19	8107
VPR	RIGCRHSRI	74	9	12	19	8108
VPR	GQHIYNTY	43	8	13	20	8109
VPR	AVRHFPRI	30	8	14	22	8110

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	GQYIYETY	43	8	14	22	8111
VPR	AVRHFPRIW	30	9	14	22	8112
VPR	HIYNTYGDTW	45	10	14	22	8113
VPR	YIYETYGDTW	45	10	14	22	8114
VPR	ELKSEAVRHF	25	10	15	23	8115
VPR	CQHSRIGII	77	9	16	25	8116
VPR	LLEELKSEAV	22	10	16	25	8117
VPR	ELLEELKNEAV	21	11	16	25	8118
VPR	ELLEELKSEAV	21	11	16	25	8119
VPR	GQHIYETY	43	8	17	27	8120
VPR	LLEELKNEAV	22	10	17	27	8121
VPR	ELKNEAVRHF	25	10	17	27	8122
VPR	HIYETYGDTW	45	10	17	27	8123
VPR	WLHGLGQHI	38	9	20	31	8124
VPR	WLHGLGQHIY	38	10	20	31	8125
VPR	IIRILQQLLFI	60	11	33	52	8126
VPR	GVEAIIRI	56	8	34	53	8127
VPR	AVRHFPRPW	30	9	34	53	8128
VPR	RILQQLLFIHF	62	11	34	53	8129
VPR	ILQQLLFIHF	63	10	35	55	8130
VPR	RILQQLLFI	62	9	36	56	8131
VPR	ILQQLLFI	63	8	37	58	8132
VPR	PQREPYNEW	10	9	37	58	8133
VPR	GPQREPYNEW	9	10	37	58	8134
VPR	AIIRILQQLLF	59	11	38	59	8135
VPR	DQGPQREPY	7	9	41	64	8136
VPR	IIRILQQLLF	60	10	41	64	8137
VPR	QQLLFIHF	65	8	44	69	8138
VPR	LLFIHFRI	67	8	44	69	8139
VPR	LQQLLFIHF	64	9	44	69	8140
VPR	QLLFIHFRI	66	9	44	69	8141
VPR	QQLLFIHFRI	65	10	44	69	8142
VPR	LQQLLFIHFRI	64	11	44	69	8143
VPR	RILQQLLF	62	8	45	70	8144
VPR	CQHSRIGI	77	8	45	70	8145
VPR	RIGCQHSRIGI	74	11	45	70	8146
VPR	RIGCQHSRI	74	9	47	73	8147
VPU	KVDYRIVI	7	8	01	33	8148
VPU	KVDYRLGV	7	8	01	33	8149
VPU	RIDYRLGV	7	8	01	33	8150
VPU	KVDYRIVIV	7	9	01	33	8151
VPU	KVDYRIVIVAF	7	11	01	33	8152
VPU	GVEMGHHAPW	91	10	01	50	8153
VPU	RIKEIRDDSDY	64	11	01	50	8154
VPU	RIREIRDDSDY	64	11	01	50	8155
VPU	LIIAIVVW	26	8	10	16	8156
VPU	DQEELSALV	79	9	11	18	8157
VPU	ILAIVALVV	12	9	11	17	8158
VPU	EMGHHAPW	89	8	11	17	8159
VPU	ILAIVALV	12	8	12	19	8160

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPU	IVFIEYRKI	36	9	12	19	8161
VPU	VVWTIVFIEY	31	10	12	19	8162
VPU	IVVWTIVFIEY	30	11	12	19	8163
VPU	ILRQRKIDRLI	46	11	13	20	8164
VPU	AIVVWTIVF	29	9	14	22	8165
VPU	KIDRLIDRI	52	9	14	22	8166
VPU	AIVVWTIVFI	29	10	14	22	8167
VPU	IVVWTIVF	30	8	15	23	8168
VPU	VVWTIVFI	31	8	15	23	8169
VPU	KILRQRKI	45	8	15	23	8170
VPU	IVVWTIVFI	30	9	15	23	8171
VPU	RQRKIDRLI	48	9	17	27	8172
VPU	IIAIVVWTIV	27	10	20	31	8173
VPU	IIAIVVWTI	27	9	23	36	8174
VPU	AIVVWTIV	29	8	29	45	8175

Table XV
HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
ENV	IGSGQAFY	361	8	01	25		8176
ENV	GKDLWVTVY	42	9	01	33		8177
ENV	GKDLWVTVYY	42	10	01	33		8178
ENV	NTSPRSRVAY	376	10	01	33		8179
ENV	GTAGNSSRAA	375	11	01	33		8180
ENV	DSSNSTGNY	218	9	01	20		8181
ENV	TNSSYTNDTY	458	10	01	17		8182
ENV	WFDITNWLW	767	10	10	16		8183
ENV	WMEWEREIDN	723	11	10	16		8184
ENV	EWEREIDNY	725	9	11	17		8185
ENV	NMWQEVGKA	494	11	15	23		8186
ENV	HSFNCRGEFFY	434	11	16	25		8187
ENV	WQEVGKAMY	496	9	18	28		8188
ENV	VSFEPIPIHY	253	10	28	44		8189
ENV	KVSFEPIPIHY	252	11	28	44		8190
ENV	SFEPIPIHY	254	9	31	48		8191
ENV	LQARVLAVER	662	11	33	52		8192
ENV	LSIVNRVRQGY	797	11	34	53		8193
ENV	RSLCLFSY	858	8	35	55		8194
ENV	LRSLCLFSY	857	9	35	55		8195
ENV	HSFNCGGEFFY	434	11	35	55		8196
ENV	DMRDNWRSEL	552	11	37	58		8197
ENV	MRDNWRSELY	553	10	40	63	0.0010	8198
ENV	CASDAKAY	67	8	42	66		8199
ENV	FCASDAKAY	66	9	42	66		8200
ENV	WRSELYKY	557	8	54	84		8201
GAG	ETIDKDLY	537	8	01	25		8202
GAG	EKEEKGLY	538	8	01	25		8203
GAG	KQEPIDKELY	535	10	01	25		8204
GAG	KQETIDKDLY	535	10	01	25		8205
GAG	AADKGVSQNY	130	10	01	50		8206
GAG	ASAQQDLKGG	392	11	01	50		8207
GAG	ATAQQDLKGG	392	11	01	50		8208
GAG	AADKGKVSQN	129	11	02	18		8209
GAG	EADGKVSQNY	129	10	04	36		8210
GAG	GNSSQVSQNY	140	10	12	23		8211
GAG	KQEPIDKELY	531	10	12	19		8212
GAG	SEELRSLY	74	8	12	19		8213
GAG	GSEELRSLY	73	9	12	19		8214
GAG	TGSEELRSLY	72	10	12	19		8215
GAG	NSSQVSQNY	144	9	14	31		8216
GAG	SSQVSQNY	145	8	15	31		8217
GAG	RSLYNTVATL	78	11	15	24		8218
GAG	FRDYVDRFY	317	9	29	45	0.0900	8219
GAG	PKEPFRDY	313	8	63	98		8220
NEF	HMARELHPEY	320	10	10	16		8221
NEF	HMARELHPEY	320	11	10	16		8222
NEF	ARELHPEFY	322	9	11	17		8223
NEF	YTPGPGIRY	207	9	17	27		8224
NEF	RQDILDLWVY	182	10	20	31		8225

Table XV
HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
NEF	ARELIIPEYY	322	9	21	33		8226
NEF	ARELIIPEY	322	8	24	38		8227
NEF	RQEILDLWVY	182	10	32	50		8228
POL	TWETWWTDY	589	9	10	16		8229
POL	TWETWWTEY	589	9	10	16		8230
POL	ETWETWWTD	588	10	10	16		8231
POL	ETWETWWTE	588	10	10	16		8232
POL	AQEDHEKY	760	8	11	17		8233
POL	ISRIGPENPY	236	10	11	17		8234
POL	KISRIGPENPY	235	11	11	17		8235
POL	STNNETPGIRY	323	11	11	17		8236
POL	KTELQAIY	668	8	12	19		8237
POL	GQDQWTYQIY	525	10	12	19		8238
POL	DKAQEEHERY	758	10	15	23		8239
POL	AQEEHERY	760	8	16	25		8240
POL	NPDIVIYQY	364	9	17	27	0.0011	8241
POL	PLDKDFRKY	308	9	19	30		8242
POL	QQEFGIPY	888	8	20	32		8243
POL	NPEIVIYQY	364	9	23	36		8244
POL	DKAQEEHEKY	758	10	25	39		8245
POL	AQEEHEKY	760	8	27	42		8246
POL	KQEFGIPY	888	8	28	44		8247
POL	NRETKLGKAG	639	11	28	44		8248
POL	ETKLGKAGY	641	9	35	55	0.0010	8249
POL	ITKIQNFRVY	969	10	36	57	0.0010	8250
POL	ITKIQNFRVYY	969	11	36	57	0.0110	8251
POL	LKEPVHGVYY	502	10	39	61	0.0010	8252
POL	LKEPVHGVY	502	9	41	64	0.0007	8253
POL	RKAKIIRDY	1016	9	41	64		8254
POL	KISKIGPENPY	235	11	41	64		8255
POL	ISKIGPENPY	236	10	42	66	0.0130	8256
POL	NNETPGIRY	325	9	51	80	0.0007	8257
POL	NNETPGIRYQY	325	11	51	80	0.0004	8258
POL	ETPGIRYQY	327	9	52	81	0.0052	8259
POL	LVAVHVASGY	826	10	53	83	0.0390	8260
POL	VTVLDVGDAY	295	10	56	88	0.2800	8261
POL	NTPPLVKLWY	610	10	57	89	0.0041	8262
POL	PAETGQETAY	842	10	58	91	0.0130	8263
POL	IPAETGQETAY	841	11	58	91		8264
POL	ETGQETAY	844	8	59	92		8265
POL	VLDVGDAY	297	8	60	94		8266
POL	QKEPPFLWMG	411	11	63	98	0.0004	8267
VIF	GVSIEWRLRR	87	11	10	16		8268
VIF	SIEWRLRRY	89	9	11	17		8269
VIF	VSIEWRLRRY	88	10	11	17		8270
VIF	GLADQLIHMH	106	11	11	17		8271
VIF	LADQLIHMHY	107	10	13	20		8272
VIF	IVSPRCEY	133	8	14	22		8273
VIF	LADQLIHLYY	107	10	14	22		8274
VIF	LADQLIHLY	107	9	15	23		8275

Table XV

HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
VIF	KSLVKHHMY	22	9	18	28		8276
VIF	WKSLVKHHM	21	10	18	28		8277
VIF	NSLVKHHMY	22	9	24	38		8278
VIF	WNSLVKHHM	21	10	24	38		8279
VPR	PEDQGPQREPY	5	11	37	58		8280
VPU	WTIVFIEY	34	8	12	19		8281

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	GIGPGQTF	360	8	01	33		8282
ENV	SIGSGQAF	360	8	01	33		8283
ENV	IGPGQTFY	361	8	01	25		8284
ENV	IGSGQAFY	361	8	01	25		8285
ENV	GTAGNSSR	375	8	01	33		8286
ENV	TAGNSSRA	376	8	01	33		8287
ENV	KLREIRQF	405	8	01	25		8288
ENV	ADNLWVTVY	42	9	01	33		8289
ENV	GIGPGQTFY	360	9	01	33		8290
ENV	SIGSGQAFY	360	9	01	33		8291
ENV	IGPGQTFYA	361	9	01	25		8292
ENV	GTAGNSSRA	375	9	01	33		8293
ENV	NTSPRSRVA	376	9	01	33		8294
ENV	TAGNSSRAA	376	9	01	33		8295
ENV	ADNLWVTVYY	42	10	01	33		8296
ENV	EGKNEINDTY	217	10	01	33		8297
ENV	GIGPGQTFYA	360	10	01	33		8298
ENV	GTAGNSSRAA	375	10	01	33		8299
ENV	NTSPRSRVAY	376	10	01	33		8300
ENV	TAGNSSRAAY	376	10	01	33		8301
ENV	FGLGALFLGF	597	10	01	33		8302
ENV	VGLGAVFLGF	597	10	01	33		8303
ENV	GTAGNSSRAA	375	11	01	33		8304
ENV	KLREIRQFENK	405	11	01	25		8305
ENV	QLYATVYA	34	8	01	50		8306
ENV	HNHITPH	584	8	01	50		8307
ENV	VISTRTHR	584	8	01	50		8308
ENV	STRTHREK	586	8	01	50		8309
ENV	NANITIPCR	478	9	01	50		8310
ENV	HNHITPHR	584	9	01	50		8311
ENV	ISTRTHREK	585	9	01	50		8312
ENV	NHITPHREK	586	9	01	50		8313
ENV	STRTHREKR	586	9	01	50		8314
ENV	VISTRTHREK	584	10	01	50		8315
ENV	ISTRTHREKR	585	10	01	50		8316
ENV	NHITPHREKR	586	10	01	50		8317
ENV	STRTHREKRA	586	10	01	50		8318
ENV	HTEGNITLQCR	478	11	01	50		8319
ENV	NANITIPCRIK	478	11	01	50		8320
ENV	HNHITPHREK	584	11	01	50		8321
ENV	VISTRTHREKR	584	11	01	50		8322
ENV	ISTRTHREKRA	585	11	01	50		8323
ENV	NHITPHREKRA	586	11	01	50		8324
ENV	VTSTGNSA	161	8	01	20		8325
ENV	DSSNSTGNY	218	9	01	20		8326
ENV	STNGTETF	537	8	01	17		8327
ENV	STNGTETFR	537	9	01	17		8328
ENV	NDTENNTEIF	537	10	01	17		8329
ENV	NTETNKTETF	537	10	01	17		8330
ENV	NTTGNTTETF	537	10	01	17		8331

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	NDTENNTEIFR	537	11	01	17		8332
ENV	NTETNKTETF	537	11	01	17		8333
ENV	NTTGNTTETF	537	11	01	17		8334
ENV	NGSENGTETF	537	10	02	33		8335
ENV	NGSENGTETF	537	11	02	33		8336
ENV	GSENGTETF	538	9	02	18		8337
ENV	GSENGTETFR	538	10	02	18		8338
ENV	TIGAMFLGF	599	9	03	27		8339
ENV	NDTITLPCR	477	9	03	20		8340
ENV	NDTITLPCRIK	477	11	03	20		8341
ENV	MLGAMFLGF	599	9	04	36		8342
ENV	RGWEALKY	895	8	06	19		8343
ENV	KGLRLGWEGL	891	11	08	27		8344
ENV	LGWEGLKY	895	8	09	29		8345
ENV	RLGWEGLKY	894	9	09	29		8346
ENV	GLRLGWEGLK	892	11	09	29		8347
ENV	LGRRGWEALK	883	10	09	15		8348
ENV	LLGRRGWEAL	882	11	09	15		8349
ENV	EIIGDIRQA	372	9	09	15		8350
ENV	LILGLVIICSA	21	11	09	15		8351
ENV	TGEIIGDIRQA	370	11	09	15		8352
ENV	RLGWEGLK	894	8	10	32		8353
ENV	GLRLGWEGLK	892	10	10	32		8354
ENV	LGRRGWEA	883	8	10	16		8355
ENV	LLGRRGWEA	882	9	10	16		8356
ENV	DIIGDIRQAH	372	10	10	16		8357
ENV	ELLGRRGWEA	881	10	10	16		8358
ENV	TGDIIGDIRQA	370	11	10	16		8359
ENV	GLVIICSA	28	8	10	16		8360
ENV	RVGQAMYA	498	8	10	16		8361
ENV	PLGVAPTR	571	8	10	16		8362
ENV	LGVAPTRA	572	8	10	16		8363
ENV	DITNWLWY	769	8	10	16		8364
ENV	RDFILIAA	869	8	10	16		8365
ENV	DFILIAAR	870	8	10	16		8366
ENV	DTIAIAVA	923	8	10	16		8367
ENV	LGLVIICSA	27	9	10	16		8368
ENV	STITQACPK	243	9	10	16		8369
ENV	IGPGQTFYA	358	9	10	16		8370
ENV	FDITNWLWY	768	9	10	16		8371
ENV	RDFILIAAR	869	9	10	16		8372
ENV	NSAVSLLNA	916	9	10	16		8373
ENV	ILGLVIICSA	26	10	10	16		8374
ENV	LLGMLMICSA	26	10	10	16		8375
ENV	PIIYCTPAGF	260	10	10	16		8376
ENV	FAILKCNDKK	269	10	10	16		8377
ENV	RIGPGQTFYA	357	10	10	16		8378
ENV	MLQLTVWGIK	651	10	10	16		8379
ENV	RVLAVERYLR	665	10	10	16		8380
ENV	WFDITNWLW	767	10	10	16		8381

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	EGIEEEGGER	828	10	10	16		8382
ENV	PIIYCTPAGFA	260	11	10	16		8383
ENV	GFAILKCNDKK	268	11	10	16		8384
ENV	FAILKCNDKKF	269	11	10	16		8385
ENV	GDIIGDIRQAH	371	11	10	16		8386
ENV	NVPWNSSWSN	693	11	10	16		8387
ENV	WMEWEREIDN	723	11	10	16		8388
ENV	NSAVSLLNAT	916	11	10	16		8389
ENV	IAIAVAEGTDR	925	11	10	16		8390
ENV	RGWEALKY	886	8	11	18		8391
ENV	GIGAVFLGF	598	9	11	18		8392
ENV	KLWVTVYY	44	8	11	17		8393
ENV	AVGIGAVF	595	8	11	17		8394
ENV	RAVGIGAVF	594	9	11	17		8395
ENV	AVGIGAVFLGF	595	11	11	17		8396
ENV	TITQACPK	244	8	11	17		8397
ENV	YCTPAGFA	263	8	11	17		8398
ENV	RIGPGQTF	357	8	11	17		8399
ENV	IGPGQTFY	358	8	11	17		8400
ENV	LFLGFLGA	603	8	11	17		8401
ENV	LAVERYLR	667	8	11	17		8402
ENV	NLCLFSYH	859	8	11	17		8403
ENV	SAVSLLNA	917	8	11	17		8404
ENV	VSLLNATA	919	8	11	17		8405
ENV	LGMLMICSA	27	9	11	17		8406
ENV	RIGPGQTFY	357	9	11	17		8407
ENV	ITTHSFNCR	431	9	11	17		8408
ENV	NITLPCRIK	482	9	11	17		8409
ENV	ALFLGFLGA	602	9	11	17		8410
ENV	LFLGFLGAA	603	9	11	17		8411
ENV	VLAVERYLR	666	9	11	17		8412
ENV	ISNWLWYIK	770	9	11	17		8413
ENV	NLCLFSYHR	859	9	11	17		8414
ENV	AVSLLNATA	918	9	11	17		8415
ENV	GDIIGDIRQA	371	10	11	17		8416
ENV	EITTHSFNCR	430	10	11	17		8417
ENV	VGIGAVFLGF	596	10	11	17		8418
ENV	GALFLGFLGA	601	10	11	17		8419
ENV	ALFLGFLGAA	602	10	11	17		8420
ENV	SAVSLLNATA	917	10	11	17		8421
ENV	VSLLNATAIA	919	10	11	17		8422
ENV	YATGDIIGDIR	368	11	11	17		8423
ENV	GALFLGFLGAA	601	11	11	17		8424
ENV	ISNWLWYIKIF	770	11	11	17		8425
ENV	DLRNLCLFSYH	856	11	11	17		8426
ENV	NLCLFSYHRLR	859	11	11	17		8427
ENV	AVSLLNATAIA	918	11	11	17		8428
ENV	PTRIRQGLERA	951	11	11	17		8429
ENV	TGDIIGDIR	370	9	12	19		8430
ENV	DIIGDIRQA	372	9	12	19		8431

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	EAQQHLLK	646	8	12	19		8432
ENV	GMLMICSA	28	8	12	19		8433
ENV	ILKCNDKK	271	8	12	19		8434
ENV	TTHSFNCR	432	8	12	19		8435
ENV	IGAVFLGF	600	8	12	19		8436
ENV	MTWMEWER	721	8	12	19		8437
ENV	GGERDRDR	834	8	12	19		8438
ENV	AILKCNDKK	270	9	12	19		8439
ENV	ILKCNDKKF	271	9	12	19		8440
ENV	LAEEEVVIR	312	9	12	19	0.0002	8441
ENV	AMFLGFLGA	602	9	12	19		8442
ENV	NMTWMEWER	720	9	12	19		8443
ENV	GIEEEGGER	829	9	12	19		8444
ENV	EGGERDRDR	833	9	12	19		8445
ENV	RSIRLVNGF	841	9	12	19		8446
ENV	WGQELKNSA	910	9	12	19		8447
ENV	WSQELKNSA	910	9	12	19		8448
ENV	KTTLFCASDA	60	10	12	19		8449
ENV	AILKCNDKKF	270	10	12	19		8450
ENV	SLAEEEVVIR	311	10	12	19		8451
ENV	ATGDIIGDIR	369	10	12	19		8452
ENV	IINMWQEVGK	492	10	12	19		8453
ENV	GAMFLGFLGA	601	10	12	19		8454
ENV	AMFLGFLGAA	602	10	12	19		8455
ENV	AIEAQQHLLK	644	10	12	19		8456
ENV	QDLLALDKWA	753	10	12	19		8457
ENV	SIRLVSGFLA	842	10	12	19		8458
ENV	LLQYWSQELK	906	10	12	19		8459
ENV	AILIIPRRIR	946	10	12	19		8460
ENV	PTRIRQGLER	951	10	12	19		8461
ENV	KTTLFCASDA	60	11	12	19		8462
ENV	GSLAEEEVVIR	310	11	12	19		8463
ENV	TTHSFNCRGE	432	11	12	19		8464
ENV	QIINMWQEVG	491	11	12	19		8465
ENV	IINMWQEVGK	492	11	12	19		8466
ENV	GAMFLGFLGA	601	11	12	19		8467
ENV	ITKWLWYIKIF	770	11	12	19		8468
ENV	GIEEEGGERDR	829	11	12	19		8469
ENV	RSIRLVSGFLA	841	11	12	19		8470
ENV	NLLQYWSQEL	905	11	12	19		8471
ENV	RAILIIPRRIR	945	11	12	19		8472
ENV	NTSVITQA	241	8	13	20		8473
ENV	SVEINCTR	340	8	13	20		8474
ENV	GDIIGDIR	371	8	13	20		8475
ENV	MFLGFLGA	603	8	13	20		8476
ENV	KLTVWGIK	653	8	13	20		8477
ENV	SIRLVNGF	842	8	13	20		8478
ENV	SIRLVSGF	842	8	13	20		8479
ENV	RLVNGFLA	844	8	13	20		8480
ENV	RAILHIPR	945	8	13	20		8481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	AILIIPRR	946	8	13	20		8482
ENV	KAKRRVVQR	579	9	13	20	0.0002	8483
ENV	MFLGFLGAA	603	9	13	20		8484
ENV	RSIRLVSGF	841	9	13	20		8485
ENV	RAILHIPRR	945	9	13	20		8486
ENV	ILIIPRRIR	947	9	13	20		8487
ENV	SGGDPEIVMH	425	10	13	20		8488
ENV	LLKLTVWGIK	651	10	13	20		8489
ENV	NTSVITQACPK	241	11	13	20		8490
ENV	CTNVSTVQCT	285	11	13	20		8491
ENV	SSGGDLEITTH	424	11	13	20		8492
ENV	SSGGDPEIVMH	424	11	13	20		8493
ENV	VMHSFNCGGE	432	11	13	20		8494
ENV	PTKAKRRVVQ	576	11	13	20		8495
ENV	KAKRRVVQRE	579	11	13	20		8496
ENV	HLLKLTVWGI	650	11	13	20		8497
ENV	VGGLIGLRIIF	784	11	13	20		8498
ENV	SLLNATAIAVA	920	11	13	20		8499
ENV	TGEIIGDIR	370	9	14	23		8500
ENV	NTSAITQA	241	8	14	22		8501
ENV	AITQACPK	244	8	14	22		8502
ENV	GDPEIVMH	427	8	14	22		8503
ENV	QDLLALDK	753	8	14	22		8504
ENV	NATAIAVA	923	8	14	22		8505
ENV	SAITQACPK	243	9	14	22		8506
ENV	FAILKCNDK	269	9	14	22	0.0002	8507
ENV	GGDPEIVMH	426	9	14	22		8508
ENV	TITLPCRIK	482	9	14	22		8509
ENV	SLLNATAIA	920	9	14	22		8510
ENV	NCNTSAITQA	239	10	14	22		8511
ENV	TSAITQACPK	242	10	14	22		8512
ENV	TSVITQACPK	242	10	14	22		8513
ENV	GFAILKCNDK	268	10	14	22		8514
ENV	GDPEIVMHSF	427	10	14	22		8515
ENV	IFAVLSIVNR	793	10	14	22		8516
ENV	LLNATAIAVA	921	10	14	22		8517
ENV	NTSAITQACPK	241	11	14	22		8518
ENV	VITQACPKVSF	244	11	14	22		8519
ENV	AGFAILKCNDK	267	11	14	22		8520
ENV	GGDPEIVMHSF	426	11	14	22		8521
ENV	ITNWLWYIKIF	770	11	14	22		8522
ENV	IIFAVLSIVNR	792	11	14	22		8523
ENV	KIEPLGVAPTK	568	11	15	24		8524
ENV	FDPIPIHY	255	8	15	23		8525
ENV	PAGYAILK	266	8	15	23		8526
ENV	NMWQEVGK	494	8	15	23		8527
ENV	LLNATAIA	921	8	15	23		8528
ENV	NMWQEVGKA	494	9	15	23		8529
ENV	DLLALDKWA	754	9	15	23		8530
ENV	ITNWLWYIK	770	9	15	23		8531

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	GLIGLRIIF	786	9	15	23		8532
ENV	DDLRNLCLF	855	9	15	23		8533
ENV	SGGDLEITTH	425	10	15	23		8534
ENV	IFRPGGGDMR	545	10	15	23		8535
ENV	GGLIGLRIIF	785	10	15	23		8536
ENV	GLIGLRIIFA	786	10	15	23		8537
ENV	WDDLRNLCLF	854	10	15	23		8538
ENV	NMWQEVGKA	494	11	15	23		8539
ENV	EIFRPGGGDMR	544	11	15	23		8540
ENV	GGLIGLRIIFA	785	11	15	23		8541
ENV	DDLRNLCLFSY	855	11	15	23		8542
ENV	SFNCRGEF	437	8	16	25		8543
ENV	LIGLRIIF	787	8	16	25		8544
ENV	VSGFLALA	846	8	16	25		8545
ENV	HSFNCRGEF	434	9	16	25		8546
ENV	SFNCRGEFF	437	9	16	25		8547
ENV	ITKWLWYIK	770	9	16	25		8548
ENV	LIGLRIIFA	787	9	16	25		8549
ENV	LVSGFLALA	845	9	16	25		8550
ENV	HSFNCRGEFF	434	10	16	25		8551
ENV	SFNCRGEFFY	437	10	16	25		8552
ENV	RLVSGFLALA	844	10	16	25		8553
ENV	DLRNLCLFSY	856	10	16	25		8554
ENV	TTHSFNCGGE	432	11	16	25		8555
ENV	HSFNCRGEFFY	434	11	16	25		8556
ENV	RLINCNTSA	236	9	17	27		8557
ENV	KAYDTEVH	72	8	17	27		8558
ENV	LINCNTSA	237	8	17	27		8559
ENV	VITQACPK	244	8	17	27		8560
ENV	RVVQREKR	587	8	17	27	0.0003	8561
ENV	VVQREKRA	588	8	17	27		8562
ENV	IGLRIIFA	788	8	17	27		8563
ENV	DLRNLCLF	856	8	17	27		8564
ENV	SVITQACPK	243	9	17	27		8565
ENV	VAPTKAKRR	574	9	17	27	0.0002	8566
ENV	RVVQREKRA	587	9	17	27		8567
ENV	DAKAYDTEVH	70	10	17	27		8568
ENV	YDTEVHNVWA	74	10	17	27		8569
ENV	GVAPTKAKRR	573	10	17	27		8570
ENV	VFAVLSIVNR	793	10	17	27		8571
ENV	SDAKAYDTEV	69	11	17	27		8572
ENV	DTEVHNVWAT	75	11	17	27		8573
ENV	NCTRPNNNTR	344	11	17	27		8574
ENV	LGVAPTKAKR	572	11	17	27		8575
ENV	IVFAVLSIVNR	792	11	17	27		8576
ENV	PIHYCTPA	260	8	18	28		8577
ENV	EVGKAMYA	498	8	18	28		8578
ENV	DTEVHNVWA	75	9	18	28		8579
ENV	VLAVERYLK	666	9	18	28		8580
ENV	ELLELDKWA	754	9	18	28		8581

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	KIEPLGVA	568	8	23	37		8632
ENV	LGVAPTKA	572	8	23	36		8633
ENV	TVQCTHGIR	290	9	23	36	0.0008	8634
ENV	PLGVAPTKA	571	9	23	36		8635
ENV	STVQCTHGIR	289	10	23	36		8636
ENV	VVKIEPLGVA	566	10	23	36		8637
ENV	QSNLLRAIEA	638	10	23	36		8638
ENV	ATTTLFCASD	59	11	23	36		8639
ENV	VSTVQCTHGIR	288	11	23	36		8640
ENV	KVVKIEPLGVA	565	11	23	36		8641
ENV	ATTTLFCA	59	8	24	38		8642
ENV	EATTTLFCA	58	9	24	38		8643
ENV	TTTLFCASDA	60	10	24	38		8644
ENV	TFRPGGGDMR	545	10	24	38		8645
ENV	ALAWDDLR	851	8	25	39		8646
ENV	LALAWDDLR	850	9	25	39		8647
ENV	IVQQQNNLLR	634	10	25	39	0.0024	8648
ENV	FLALAWDDLR	849	10	25	39		8649
ENV	GIVQQQNNLLR	633	11	25	39		8650
ENV	IVQQQNNLLRA	634	11	25	39		8651
ENV	GFLALAWDDL	848	11	25	39		8652
ENV	ITLPCRIK	483	8	26	41		8653
ENV	PLGVAPTK	571	8	26	41		8654
ENV	LAVERYLK	667	8	26	41		8655
ENV	IVQQQSNLLR	634	10	26	41		8656
ENV	GIVQQQSNLLR	633	11	26	41		8657
ENV	IVQQQSNLLRA	634	11	26	41		8658
ENV	LDKWASLWN	758	11	26	41		8659
ENV	IIGDIRQAH	377	9	27	44		8660
ENV	ESQNQQEK	743	8	27	42		8661
ENV	PHYCAPAGF	260	10	27	42		8662
ENV	PHYCAPAGFA	260	11	27	42		8663
ENV	VGGLIGLRIVF	784	11	27	42		8664
ENV	IGDIRQAH	378	8	28	44		8665
ENV	YCAPAGFA	263	8	28	44		8666
ENV	TVQCTHGIK	290	9	28	44	0.0021	8667
ENV	CTRPNNNTR	345	9	28	44		8668
ENV	ASITLTVQA	619	9	28	44		8669
ENV	VSFEPIPIHY	253	10	28	44		8670
ENV	STVQCTHGIK	289	10	28	44		8671
ENV	AASITLTVQA	618	10	28	44		8672
ENV	ASITLTVQAR	619	10	28	44		8673
ENV	KVSFEPIPIHY	252	11	28	44		8674
ENV	YCAPAGFAILK	263	11	28	44		8675
ENV	VSTVQCTHGIK	288	11	28	44		8676
ENV	GAASITLTVQA	617	11	28	44		8677
ENV	AASITLTVQAR	618	11	28	44		8678
ENV	LIGLRIVF	787	8	29	45		8679
ENV	VSFEPIPIH	253	9	29	45		8680
ENV	GLIGLRIVF	786	9	29	45		8681

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	FSYHRLRDF	863	9	18	28		8582
ENV	PIPIIYCTPA	258	10	18	28		8583
ENV	RVLAVERYLK	665	10	18	28		8584
ENV	LFSYHRLRDF	862	10	18	28		8585
ENV	CLFSYHRLRDF	861	11	18	28		8586
ENV	NCRGEFFY	439	8	19	30		8587
ENV	GVAPTKAK	573	8	19	30		8588
ENV	VAPTKAKR	574	8	19	30		8589
ENV	VFLGFLGA	603	8	19	30		8590
ENV	LLALDKWA	755	8	19	30		8591
ENV	LGVAPTKAK	572	9	19	30		8592
ENV	GVAPTKAKR	573	9	19	30		8593
ENV	AVFLGFLGA	602	9	19	30		8594
ENV	VFLGFLGAA	603	9	19	30		8595
ENV	SGKLICTTA	685	9	19	30		8596
ENV	PLGVAPTKAK	571	10	19	30		8597
ENV	LGVAPTKAKR	572	10	19	30		8598
ENV	GAVFLGFLGA	601	10	19	30		8599
ENV	AVFLGFLGAA	602	10	19	30		8600
ENV	CSGKLICTTA	684	10	19	30		8601
ENV	SSNITGLLLTR	516	11	19	30		8602
ENV	PLGVAPTKAK	571	11	19	30		8603
ENV	GAVFLGFLGA	601	11	19	30		8604
ENV	GCSGKLICTTA	683	11	19	30		8605
ENV	AILKCNDK	270	8	20	31		8606
ENV	RLVSGFLA	844	8	20	31		8607
ENV	ETFRPGGGDM	544	11	20	31		8608
ENV	LIEESQNQQEK	740	11	20	31		8609
ENV	GDLEITTII	427	8	21	33		8610
ENV	YCNTSGLF	446	8	21	33		8611
ENV	LLELDKWA	755	8	21	33		8612
ENV	GGDLEITTH	426	9	21	33		8613
ENV	DLEITTHSF	428	9	21	33		8614
ENV	LIGLRIVFA	787	9	21	33		8615
ENV	GDLEITTHSF	427	10	21	33		8616
ENV	FFYCNTSGLF	444	10	21	33		8617
ENV	GLIGLRIVFA	786	10	21	33		8618
ENV	SFEPIPIIYCA	254	11	21	33		8619
ENV	GGDLEITTHSF	426	11	21	33		8620
ENV	EFFYCNTSGLF	443	11	21	33		8621
ENV	GGLIGLRIVFA	785	11	21	33		8622
ENV	TAIAVAEGTDR	925	11	21	33		8623
ENV	IGLRIVFA	788	8	22	34		8624
ENV	RIVELLGR	878	8	22	34		8625
ENV	IVELLGRR	879	8	22	34		8626
ENV	RIVELLGRR	878	9	22	34	0.0550	8627
ENV	NCTRPNNNTR	344	10	22	34		8628
ENV	CTRPNNNTRK	345	10	22	34		8629
ENV	PVWKEATTTL	54	11	22	34		8630
ENV	TTTLFCASDA	60	11	22	34		8631

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	ITQACPKVSF	245	10	29	45		8682
ENV	KVSFEPIPIH	252	10	29	45		8683
ENV	CAPAGFAILK	264	10	29	45		8684
ENV	GGLIGLRIVF	785	10	29	45		8685
ENV	RSELYKYKVV	558	11	29	45		8686
ENV	IIGDIRQA	377	8	30	49		8687
ENV	WASLWNWF	761	8	30	47		8688
ENV	AVLSIVNR	795	8	31	48		8689
ENV	AVAEGTDR	928	8	31	48		8690
ENV	VTENFNMWK	102	9	31	48		8691
ENV	SFEPIPIHY	254	9	31	48		8692
ENV	FAVLSIVNR	794	9	31	48		8693
ENV	SLCLFSYHR	859	9	31	48		8694
ENV	IAVAEGTDR	927	9	31	48	0.0004	8695
ENV	NVTENFNMW	101	10	31	48		8696
ENV	AVLSIVNRVR	795	10	31	48		8697
ENV	RSLCLFSYHR	858	10	31	48		8698
ENV	AIAVAEGTDR	926	10	31	48		8699
ENV	FAVLSIVNRVR	794	11	31	48		8700
ENV	DDLRSLCLFSY	855	11	31	48		8701
ENV	SLCLFSYHRLR	859	11	31	48		8702
ENV	ELYKYKVVK	560	9	32	51		8703
ENV	RVVEREKR	587	8	32	50		8704
ENV	VVEREKRA	588	8	32	50		8705
ENV	SITLTVQA	620	8	32	50		8706
ENV	ITLTVQAR	621	8	32	50		8707
ENV	SLCLFSYH	859	8	32	50		8708
ENV	RVVEREKRA	587	9	32	50		8709
ENV	SITLTVQAR	620	9	32	50		8710
ENV	RSLCLFSYH	858	9	32	50		8711
ENV	DLRSLCLFSYH	856	11	32	50		8712
ENV	SFEPIPIH	254	8	33	52		8713
ENV	RVLAVERY	665	8	33	52		8714
ENV	QARVLAVER	663	9	33	52	0.0009	8715
ENV	DDLRSLCLF	855	9	33	52		8716
ENV	QARVLAVERY	663	10	33	52		8717
ENV	WDDLRSLCLF	854	10	33	52		8718
ENV	QLQARVLAVE	661	11	33	52		8719
ENV	IMIVGGLIGLR	781	11	34	54		8720
ENV	GVPVWKEA	52	8	34	53		8721
ENV	YGVPVWKEA	51	9	34	53		8722
ENV	RIRQGLERA	953	9	34	53		8723
ENV	LLQLTVWGIK	651	10	34	53	0.0055	8724
ENV	HLLQLTVWGI	650	11	34	53		8725
ENV	LSIVNRVRQGY	797	11	34	53		8726
ENV	NLWVTVYY	44	8	35	56		8727
ENV	NCGGEFFY	439	8	35	55		8728
ENV	RSLCLFSY	858	8	35	55		8729
ENV	EVHNVWATH	77	9	35	55		8730
ENV	SFNCGGEFF	437	9	35	55		8731

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	NITGLLLTR	519	9	35	55	0.0004	8732
ENV	EVHNVWATHA	77	10	35	55		8733
ENV	HSFNCGGEFF	434	10	35	55		8734
ENV	SFNCGGEFFY	437	10	35	55		8735
ENV	DLRSLCLFSY	856	10	35	55		8736
ENV	HSFNCGGEFFY	434	11	35	55		8737
ENV	SFNCGGEF	437	8	36	56		8738
ENV	HSFNCGGEF	434	9	36	56		8739
ENV	PIPIHYCAPA	258	10	36	56		8740
ENV	GGGDMRDNW	549	10	36	56		8741
ENV	MIVGGLIGLR	782	10	36	56		8742
ENV	SIVNRVRQGY	798	10	36	56	0.0008	8743
ENV	PGGGDMRDN	548	11	36	56		8744
ENV	PIHYCAPA	260	8	37	58		8745
ENV	ITGLLLTR	520	8	37	58		8746
ENV	DMRDNWRSEL	552	11	37	58		8747
ENV	PAGFAILK	266	8	38	59		8748
ENV	LSIVNRVR	797	8	38	59		8749
ENV	DLRSLCLF	856	8	38	59		8750
ENV	VLSIVNRVR	796	9	38	59		8751
ENV	IVNRVRQGY	799	9	38	59		8752
ENV	HSLWDQSLK	121	10	38	59	0.0410	8753
ENV	DHSLWDQSLK	120	11	38	59		8754
ENV	GDMRDNWR	551	8	39	61		8755
ENV	GGDMRDNWR	550	9	39	61		8756
ENV	QACPKVSF	248	8	40	63		8757
ENV	PIPIHYCA	258	8	40	63		8758
ENV	RDNWRSELY	554	9	40	63	0.0003	8759
ENV	RDNWRSELYK	554	10	40	63	0.0008	8760
ENV	TLFCASDAKA	64	11	40	63		8761
ENV	RDNWRSELYK	554	11	40	63		8762
ENV	GIKQLQARVLA	658	11	40	63		8763
ENV	QLQARVLA	661	8	41	64		8764
ENV	TVYYGVPVWK	48	10	41	64	3.8000	8765
ENV	VTVYYGVPVW	47	11	41	64	0.8600	8766
ENV	CASDAKAY	67	8	42	66		8767
ENV	LCLFSYHR	860	8	42	66		8768
ENV	FCASDAKAY	66	9	42	66		8769
ENV	IVGGLIGLR	783	9	42	66		8770
ENV	CLFSYHRLR	861	9	42	66		8771
ENV	LFCASDAKAY	65	10	42	66	0.0004	8772
ENV	GAAGSTMGAA	610	10	42	66		8773
ENV	LCLFSYHRLR	860	10	42	66		8774
ENV	LGAAGSTMGA	609	11	42	66		8775
ENV	VGGLIGLR	784	8	43	67		8776
ENV	QLTVWGIK	653	8	44	69		8777
ENV	LFSYHRLR	862	8	44	69		8778
ENV	RIRQGLER	953	8	44	69		8779
ENV	TTLFCASDAK	61	11	44	69		8780
ENV	AAGSTMGAA	611	9	45	70		8781

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	TLFCASDAKA	64	10	46	72		8782
ENV	SLWDQSLK	123	8	47	75		8783
ENV	ISLWDQSLK	122	9	47	73	0.0048	8784
ENV	WDQSLKPCVK	125	10	47	73		8785
ENV	RVRQGYSPLSF	802	11	47	73		8786
ENV	QSLKPCVK	127	8	48	75		8787
ENV	FLGFLGAA	604	8	48	75		8788
ENV	QGYSPLSF	805	8	48	75		8789
ENV	TVWGIKQLQA	655	11	48	75		8790
ENV	GIKQLQAR	658	8	49	77		8791
ENV	WGIKQLQAR	657	9	49	77	0.0004	8792
ENV	TVWGIKQLQA	655	10	49	77		8793
ENV	LTVWGIKQLQ	654	11	49	77		8794
ENV	FCASDAKA	66	8	50	78		8795
ENV	AGSTMGAA	612	8	50	78		8796
ENV	WLWYIKIF	773	8	50	78		8797
ENV	LFCASDAKA	65	9	50	78		8798
ENV	LGIWGCSGK	679	9	50	78	0.0097	8799
ENV	TTLFCASDAK	61	10	50	78	0.0920	8800
ENV	LLGIWGCSGK	678	10	50	78	0.1200	8801
ENV	NLLRAIEAQQH	640	11	50	78		8802
ENV	QLLGIWGCSG	677	11	50	78		8803
ENV	VSTVQCTH	288	8	51	80		8804
ENV	NLLRAIEA	640	8	51	80		8805
ENV	RAIEAQQH	643	8	51	80		8806
ENV	WGIKQLQA	657	8	51	80		8807
ENV	NVSTVQCTH	287	9	51	80		8808
ENV	LLRAIEAQQH	641	10	51	80		8809
ENV	GIWGCSGK	680	8	52	81		8810
ENV	TTLFCASDA	61	9	52	81		8811
ENV	TLFCASDAK	64	9	52	81	0.0930	8812
ENV	TLFCASDA	64	8	54	84		8813
ENV	RSELYKYK	558	8	54	84		8814
ENV	LLLNGSLA	306	8	55	86		8815
ENV	QLLLNGSLA	305	9	55	86		8816
ENV	GAAGSTMGA	610	9	55	86		8817
ENV	LGAAGSTMGA	609	10	55	86		8818
ENV	STQLLLNGSLA	303	11	55	86		8819
ENV	FLGAAGSTMG	608	11	55	86		8820
ENV	LFCASDAK	65	8	57	89		8821
ENV	AAGSTMGA	611	8	58	91		8822
GAG	EDTSARQA	133	8	01	33		8823
GAG	AAAIMMQK	405	8	01	25		8824
GAG	SATIMMQR	405	8	01	25		8825
GAG	TAPPPESF	508	8	01	33		8826
GAG	KDKDKELY	535	8	01	25		8827
GAG	ETIDKDLY	537	8	01	25		8828
GAG	NSATIMMQR	404	9	01	33		8829
GAG	PTAPPPESF	507	9	01	33		8830
GAG	TAPPPESFR	508	9	01	33		8831

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NGKQANFLGK	461	10	01	25		8832
GAG	NGRQANFLGK	461	10	01	25		8833
GAG	PTAPPPESFR	507	10	01	33		8834
GAG	TAPPPESFRF	508	10	01	33		8835
GAG	TIDKDLYPLA	538	10	01	25		8836
GAG	AAAIMMQKSN	405	11	01	25		8837
GAG	SATIMMQRGN	405	11	01	25		8838
GAG	NGKQANFLGK	461	11	01	25		8839
GAG	NGRQANFLGK	461	11	01	25		8840
GAG	PTAPPPESFRF	507	11	01	33		8841
GAG	KDKDKELYPL	535	11	01	25		8842
GAG	ETIDKDLYPLA	537	11	01	25		8843
GAG	PAAADKEK	123	8	01	50		8844
GAG	ASAQQDLK	392	8	01	50		8845
GAG	ATAQQDLK	392	8	01	50		8846
GAG	PAEPTAPPA	492	9	01	50		8847
GAG	AADKGVSQNY	130	10	01	50		8848
GAG	SAQQDLKGGY	393	10	01	50		8849
GAG	TAQQDLKGGY	393	10	01	50		8850
GAG	GTRPGNYVQK	480	10	01	50		8851
GAG	GTRPGNYVQR	480	10	01	50		8852
GAG	ITSLPKQEQK	526	10	01	50		8853
GAG	PAAADKEKDS	123	11	01	50		8854
GAG	GANSIPVGDIY	276	11	01	50		8855
GAG	ASAQQDLKGG	392	11	01	50		8856
GAG	ATAQQDLKGG	392	11	01	50		8857
GAG	EITSLPKQEQK	525	11	01	50		8858
GAG	YTAVFMQR	405	8	02	50		8859
GAG	TAPPAESF	508	8	02	67		8860
GAG	PTAPPAESF	507	9	02	67		8861
GAG	TAPPAESFR	508	9	02	67		8862
GAG	PTAPPAESFR	507	10	02	67		8863
GAG	TAPPAESFRF	508	10	02	67		8864
GAG	PTAPPAESFRF	507	11	02	67		8865
GAG	EGRQANFLGK	462	10	02	100		8866
GAG	AADKGKVSQN	129	11	02	18		8867
GAG	EADGKVSQNY	129	10	04	36		8868
GAG	AAAIMMQK	400	8	04	19		8869
GAG	AAIMMQKSNF	406	10	06	15		8870
GAG	AAIMMQKSNF	406	11	06	15		8871
GAG	KTVKCFNCGK	421	10	08	16		8872
GAG	NIMMQRGNF	407	9	10	17		8873
GAG	GARASILR	2	8	10	16		8874
GAG	PGNFPQSR	483	8	10	16		8875
GAG	MGARASILR	1	9	10	16		8876
GAG	KIWPSSKGR	472	9	10	16		8877
GAG	TGNSSQVSQN	139	11	10	16		8878
GAG	NFLGKIWPSSK	468	11	10	16		8879
GAG	NFLQNRPEPTA	485	11	10	16		8880
GAG	PVAPGQMR	243	8	10	16		8881

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	MMQKSNFK	409	8	10	16		8882
GAG	MMQRGNFK	409	8	10	16		8883
GAG	KLDKWEKIR	12	9	10	16		8884
GAG	GGKKKYKLK	24	9	10	16	0.0001	8885
GAG	RDTKEALDK	97	9	10	16		8886
GAG	ALSPRTLNA	167	9	10	16		8887
GAG	IMMQKSNFK	408	9	10	16		8888
GAG	LGKIWPSSK	470	9	10	16		8889
GAG	PGGKKKYKLK	23	10	10	16		8890
GAG	GGKKKYKLKH	24	10	10	16		8891
GAG	QALSPRTLNA	166	10	10	16		8892
GAG	AGPVAPGQMR	241	10	10	16		8893
GAG	GASLEEMMTA	364	10	10	16		8894
GAG	FLGKIWPSSK	469	10	10	16		8895
GAG	FLQNRPEPTA	486	10	10	16		8896
GAG	TAPPAESFGF	496	10	10	16		8897
GAG	KLDKWEKIRL	12	11	10	16		8898
GAG	PGGKKKYKLK	23	11	10	16		8899
GAG	LGKIWPSSKGR	470	11	10	16		8900
GAG	PTAPPAESFGF	495	11	10	16		8901
GAG	ATIMMQRGNF	406	10	11	28		8902
GAG	ATIMMQRGNF	406	11	11	28		8903
GAG	PSQKQEPIDK	528	10	11	18		8904
GAG	SSKGRPGNF	476	9	11	18		8905
GAG	TTSTLQEQIA	260	10	11	17		8906
GAG	DVKDTKEA	95	8	11	17		8907
GAG	PIPVGDIY	279	8	11	17		8908
GAG	SLEEMMTA	366	8	11	17		8909
GAG	MSQVTNSA	391	8	11	17		8910
GAG	IMMQKSNF	408	8	11	17		8911
GAG	IDVKDTKEA	94	9	11	17		8912
GAG	ASLEEMMTA	365	9	11	17		8913
GAG	AMSQVTNSA	390	9	11	17		8914
GAG	TIKCFNCGK	422	9	11	17		8915
GAG	TVKCFNCGK	422	9	11	17		8916
GAG	EAMSQVTNSA	389	10	11	17		8917
GAG	PSSKGRPGNF	475	10	11	17		8918
GAG	GTTSTLQEQIA	259	11	11	17		8919
GAG	TIMMQRGNFR	407	10	12	21		8920
GAG	QTGSEELR	71	8	12	19		8921
GAG	KSKKKAQQAA	112	10	12	19		8922
GAG	KSKKKAQQAA	112	11	12	19		8923
GAG	PGGKKKYK	23	8	12	19		8924
GAG	TLYCVHQK	86	8	12	19		8925
GAG	DTKEALEK	98	8	12	19		8926
GAG	MLNIVGGH	208	8	12	19		8927
GAG	NIVGGHQA	210	8	12	19		8928
GAG	IVGGHQAA	211	8	12	19		8929
GAG	STLQEQIA	262	8	12	19		8930
GAG	PTSILDIR	303	8	12	19		8931

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LTSLRSLF	549	8	12	19		8932
GAG	GSEELRSLY	73	9	12	19		8933
GAG	ATLYCVHQK	85	9	12	19		8934
GAG	KDTKEALEK	97	9	12	19		8935
GAG	MMLNIVGGH	207	9	12	19		8936
GAG	NIVGGHQAA	210	9	12	19		8937
GAG	TSTLQEQIA	261	9	12	19		8938
GAG	PLTSLKSLF	548	9	12	19		8939
GAG	PLTSLRSLF	548	9	12	19		8940
GAG	TGSEELRSLY	72	10	12	19		8941
GAG	VATLYCVHQK	84	10	12	19		8942
GAG	NAQGQMVHQA	158	10	12	19		8943
GAG	NMMLNIVGGH	206	10	12	19		8944
GAG	MLNIVGGHQA	208	10	12	19		8945
GAG	YSPTSILDIR	301	10	12	19		8946
GAG	RAEQASQEVK	329	10	12	19		8947
GAG	RLRPGGKKKY	20	11	12	19		8948
GAG	TVATLYCVHQ	83	11	12	19		8949
GAG	MMLNIVGGHQ	207	11	12	19		8950
GAG	MLNIVGGHQA	208	11	12	19		8951
GAG	TSILDIRQGPK	304	11	12	19		8952
GAG	TIMMQRGNF	407	9	13	22		8953
GAG	PGNFLQNR	483	8	13	21		8954
GAG	IARNCRAPR	434	9	13	21		8955
GAG	KIWPSNKGR	472	9	13	21		8956
GAG	NCGKEGHAR	427	10	13	21		8957
GAG	IARNCRAPRK	434	10	13	21		8958
GAG	IARNCRAPRKK	434	11	13	21		8959
GAG	NFLGKIWPSNK	468	11	13	21		8960
GAG	KGRPGNFLQN	478	11	13	21		8961
GAG	KLKHIVWA	31	8	13	20		8962
GAG	RIEVKDTK	93	8	13	20		8963
GAG	HARNCRA	433	8	13	20		8964
GAG	LTSLKSLF	549	8	13	20		8965
GAG	IVKCFNCGK	422	9	13	20		8966
GAG	CGKEGHAR	428	9	13	20		8967
GAG	EGHARNCR	431	9	13	20		8968
GAG	LGKIWPSNK	470	9	13	20		8969
GAG	KLKHIVWASR	31	10	13	20		8970
GAG	RIEVKDTKEA	93	10	13	20		8971
GAG	TILRALGPGA	356	10	13	20		8972
GAG	EGHARNCRA	431	10	13	20		8973
GAG	HIARNCRAPR	433	10	13	20		8974
GAG	FLGKIWPSNK	469	10	13	20		8975
GAG	EVKDTKEALD	95	11	13	20		8976
GAG	FSPEVIPMFTA	185	11	13	20		8977
GAG	AAEWDRVHPV	230	11	13	20		8978
GAG	KTILRALGPGA	355	11	13	20		8979
GAG	HIARNCRAPRK	433	11	13	20		8980
GAG	LGKIWPSNKG	470	11	13	20		8981

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NSSQVSQNY	144	9	14	31		8982
GAG	KSKKKAQQA	112	9	14	22		8983
GAG	NCGKEGHAK	427	10	14	22		8984
GAG	IAKNCRAPRKK	434	11	14	22		8985
GAG	EVIPMFTA	188	8	14	22		8986
GAG	RGNFRNQRK	412	9	14	22		8987
GAG	CGKEGHAK	428	9	14	22		8988
GAG	EGHAKNCR	431	9	14	22		8989
GAG	EGHAKNCRA	431	10	14	22		8990
GAG	PSNKGRPGNF	475	10	14	22		8991
GAG	TAPPEESFRF	496	10	14	22		8992
GAG	TVATLYCVHQ	83	11	14	22		8993
GAG	IVQNAQGQMV	155	11	14	22		8994
GAG	PTAPPEESFRF	495	11	14	22		8995
GAG	SSQVSQNY	145	8	15	31		8996
GAG	VSQNYPIVQNA	149	11	15	26		8997
GAG	RSLYNTVATL	78	11	15	24		8998
GAG	TLYCVHQR	86	8	15	23		8999
GAG	FTALSEGA	193	8	15	23		9000
GAG	AAEWDRVH	230	8	15	23		9001
GAG	WDRVHPVH	233	8	15	23		9002
GAG	RGNFRNQR	412	8	15	23		9003
GAG	TAPPEESF	496	8	15	23		9004
GAG	LASLKSLF	549	8	15	23		9005
GAG	VLSGGKLDA	7	9	15	23		9006
GAG	LFNTVATLY	80	9	15	23		9007
GAG	ATLYCVHQR	85	9	15	23	0.0150	9008
GAG	MFTALSEGA	192	9	15	23		9009
GAG	EAAEWDRVH	229	9	15	23		9010
GAG	WDRVHPVHA	233	9	15	23		9011
GAG	PTAPPEESF	495	9	15	23		9012
GAG	TAPPEESFR	496	9	15	23		9013
GAG	PLASLKSLF	548	9	15	23		9014
GAG	SVLSGGKLDA	6	10	15	23		9015
GAG	SGGKLDAWEK	9	10	15	23		9016
GAG	ELRSLYNTVA	76	10	15	23		9017
GAG	SLFNTVATLY	79	10	15	23		9018
GAG	VATLYCVHQR	84	10	15	23		9019
GAG	KIEEEQNKSK	105	10	15	23		9020
GAG	PMFTALSEGA	191	10	15	23		9021
GAG	RAEQATQDVK	329	10	15	23		9022
GAG	PTAPPEESFR	495	10	15	23		9023
GAG	ASVLSGGKLD	5	11	15	23		9024
GAG	LSGGKLDAWE	8	11	15	23		9025
GAG	PGLLETSEGCR	50	11	15	23		9026
GAG	KIEEEQNKSKK	105	11	15	23		9027
GAG	RLHPVHAGPIA	235	11	15	23		9028
GAG	MMQRGNFRN	409	11	15	23		9029
GAG	IAKNCRAPRK	434	10	16	25		9030
GAG	LSGGKLDA	8	8	16	25		9031

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LDAWEKIR	13	8	16	25		9032
GAG	NAQGQMVH	158	8	16	25		9033
GAG	PVSILDIK	303	8	16	25		9034
GAG	ILKALGPA	357	8	16	25		9035
GAG	KLDAWEKIR	12	9	16	25		9036
GAG	GGKKKYRLK	24	9	16	25		9037
GAG	TILKALGPA	356	9	16	25		9038
GAG	ILKALGPAA	357	9	16	25	0.0003	9039
GAG	VLAEAMSQA	386	9	16	25		9040
GAG	LDAWEKIRLR	13	10	16	25		9041
GAG	PGGKKKYRLK	23	10	16	25		9042
GAG	GGKKKYRLKH	24	10	16	25		9043
GAG	GLLETSEGCR	51	10	16	25		9044
GAG	YSPVSILDIK	301	10	16	25		9045
GAG	KTILKALGPA	355	10	16	25	0.0045	9046
GAG	TILKALGPAA	356	10	16	25		9047
GAG	AATLEEMMTA	364	10	16	25		9048
GAG	RVLAEAMSQA	385	10	16	25		9049
GAG	GGKLDAWEKI	10	11	16	25		9050
GAG	KLDAWEKIRL	12	11	16	25		9051
GAG	PGGKKKYRLK	23	11	16	25		9052
GAG	VSILDIKQGPK	304	11	16	25		9053
GAG	KTILKALGPAA	355	11	16	25		9054
GAG	PAATLEEMMT	363	11	16	25		9055
GAG	HAKNCRAPRK	433	11	16	25		9056
GAG	LAEAMSQA	387	8	17	27		9057
GAG	RLKHLVWA	31	8	17	27		9058
GAG	LSPRTLNA	168	8	17	27		9059
GAG	PIPPGQMR	243	8	17	27		9060
GAG	GGKLDAWEK	10	9	17	27		9061
GAG	DAWEKIRLR	14	9	17	27		9062
GAG	LLETSEGCR	52	9	17	27		9063
GAG	RLKHLVWASR	31	10	17	27		9064
GAG	LDKIEEEQNK	103	10	17	27		9065
GAG	AGPIPPGQMR	241	10	17	27		9066
GAG	ALDKIEEEQNK	102	11	17	27		9067
GAG	LSPRTLNAWV	168	11	17	27		9068
GAG	HAGPIPPGQMR	240	11	17	27		9069
GAG	PIPPGQMREPR	243	11	17	27		9070
GAG	PGATLEEMMT	363	11	17	27		9071
GAG	RSLYNTVA	78	8	18	29		9072
GAG	IAKNCRAPR	434	9	18	29	0.0009	9073
GAG	LDKWEKIR	13	8	18	28		9074
GAG	PVGDIYKR	281	8	18	28		9075
GAG	PDCKTILR	352	8	18	28		9076
GAG	DCKTILRA	353	8	18	28		9077
GAG	HAKNCRA	433	8	18	28		9078
GAG	PDCKTILRA	352	9	18	28		9079
GAG	ILRALGPGA	357	9	18	28		9080
GAG	LDKWEKIRLR	13	10	18	28		9081

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	SILDIKQGPK	305	10	18	28		9082
GAG	HAKNCRAPR	433	10	18	28		9083
GAG	HAGPIAPGQM	240	11	18	28		9084
GAG	NANPDCKTILR	349	11	18	28		9085
GAG	LARNCRAPRK	434	11	19	30		9086
GAG	PVHAGPIA	238	8	19	30		9087
GAG	PIAPGQMR	243	8	19	30		9088
GAG	LDIKQGPK	307	8	19	30		9089
GAG	ILDIKQGPK	306	9	19	30		9090
GAG	PSHKARVLA	380	9	19	30		9091
GAG	AGPIAPGQMR	241	10	19	30		9092
GAG	IAPGQMREPR	244	10	19	30		9093
GAG	DIKQGPKEPF	308	10	19	30		9094
GAG	RLRPGGKKKY	20	11	19	30		9095
GAG	IVWASRELERF	35	11	19	30		9096
GAG	PIAPGQMREPR	243	11	19	30		9097
GAG	LDIKQGPKEPF	307	11	19	30		9098
GAG	DIKQGPKEPFR	308	11	19	30		9099
GAG	GGPSHKARVL	378	11	19	30		9100
GAG	PSHKARVLAE	380	11	19	30		9101
GAG	LARNCRAPR	434	9	20	32		9102
GAG	LARNCRAPRK	434	10	20	32		9103
GAG	PGGKKKYR	23	8	20	31		9104
GAG	TAPPAESF	496	8	20	31		9105
GAG	IMMQRGNFR	408	9	20	31		9106
GAG	PTAPPAESF	495	9	20	31		9107
GAG	IVWASRELER	35	10	20	31	0.0099	9108
GAG	HLARNCRAPR	433	10	20	31		9109
GAG	HIVWASRELER	34	11	20	31		9110
GAG	HLARNCRAPR	433	11	20	31		9111
GAG	HLARNCRA	433	8	21	33		9112
GAG	EGHLARNCR	431	9	21	33		9113
GAG	NLQGQMVHQA	158	10	21	33		9114
GAG	EGHLARNCRA	431	10	21	33		9115
GAG	QSRPEPTAPPA	488	11	21	33		9116
GAG	KIWPSHKGR	472	9	22	35	0.0770	9117
GAG	EVKDTKEA	95	8	22	34		9118
GAG	ETINEEAA	224	8	22	34		9119
GAG	DTLLVQNA	343	8	22	34		9120
GAG	GGPSHKAR	378	8	22	34		9121
GAG	TDTLLVQNA	342	9	22	34		9122
GAG	VGGPSHKAR	377	9	22	34		9123
GAG	SLYNTVATLY	79	10	22	34		9124
GAG	MLKETINEEA	221	10	22	34		9125
GAG	MTDTLLVQNA	341	10	22	34		9126
GAG	GVGGPSHKAR	376	10	22	34		9127
GAG	QMLKETINEEA	220	11	22	34		9128
GAG	MLKETINEEAA	221	11	22	34		9129
GAG	WMTDTLLVQ	340	11	22	34		9130
GAG	QGVGGPSHKA	375	11	22	34		9131

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LGKIWPSHKG	470	11	22	34		9132
GAG	NFLGKIWPSHK	468	11	23	37		9133
GAG	KIEEEQNK	105	8	23	36		9134
GAG	QGVGGPSH	375	8	23	36		9135
GAG	GVGGPSHK	376	8	23	36		9136
GAG	VGGPSHKA	377	8	23	36		9137
GAG	MMQRGNFR	409	8	23	36		9138
GAG	QGVGGPSHK	375	9	23	36		9139
GAG	GVGGPSHKA	376	9	23	36		9140
GAG	LGKIWPSHK	470	9	23	36		9141
GAG	ACQGVGGPSH	373	10	23	36		9142
GAG	QGVGGPSHKA	375	10	23	36		9143
GAG	FLGKIWPSHK	469	10	23	36	0.0200	9144
GAG	PSHKGRPGNF	475	10	23	36		9145
GAG	TACQGVGGPS	372	11	23	36		9146
GAG	ACQGVGGPSH	373	11	23	36		9147
GAG	NCGKEGHLAR	427	10	24	38		9148
GAG	KVIEEKAF	178	8	24	38		9149
GAG	CGKEGHLAR	428	9	24	38		9150
GAG	WVKVIEEKAF	176	10	24	38		9151
GAG	YSPVSILDIR	301	10	24	38		9152
GAG	NFLGKIWPSH	468	10	25	40		9153
GAG	PVSILDIR	303	8	25	39		9154
GAG	LGKIWPSH	470	8	25	39		9155
GAG	KDTKEALDK	97	9	25	39		9156
GAG	WVKVIEEKA	176	9	25	39		9157
GAG	FLGKIWPSH	469	9	25	39		9158
GAG	LVWASRELER	35	11	25	39		9159
GAG	NAWVKVIEEK	174	11	25	39		9160
GAG	VSILDIRQGPK	304	11	25	39		9161
GAG	LVWASRELER	35	10	26	41		9162
GAG	HLVWASRELE	34	11	26	41		9163
GAG	CFNCGKEGHIA	425	11	26	41		9164
GAG	NCGKEGHIA	427	9	27	43		9165
GAG	NCGKEGHLA	427	9	27	43		9166
GAG	RFFKTLRA	323	8	27	42		9167
GAG	IMMQRGNF	408	8	27	42		9168
GAG	CGKEGHIA	428	8	27	42		9169
GAG	CGKEGHLA	428	8	27	42		9170
GAG	MVHQAISPR	163	9	27	42	0.1800	9171
GAG	VDRFFKTLR	321	9	27	42		9172
GAG	QMVHQAISPR	162	10	27	42	0.0260	9173
GAG	YVDRFFKTLR	320	10	27	42		9174
GAG	VDRFFKTLRA	321	10	27	42		9175
GAG	FFKTLRAEQA	324	10	27	42		9176
GAG	RAEQATQEVK	329	10	27	42		9177
GAG	NAWVKVVEEK	174	11	27	42		9178
GAG	YVDRFFKTLR	320	11	27	42		9179
GAG	RFFKTLRAEQ	323	11	27	42		9180
GAG	RFYKTLRAEQ	323	11	27	42		9181

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NANPDCKTILK	349	11	27	42		9182
GAG	CFNCGKEGHL	425	11	27	42		9183
GAG	KGRPGNFLQS	478	11	28	44		9184
GAG	NFLQSRPEPTA	485	11	28	44		9185
GAG	KVVEEKAF	178	8	28	44		9186
GAG	RFYKTLRA	323	8	28	44		9187
GAG	PDCKTILK	352	8	28	44		9188
GAG	DCKTILKA	353	8	28	44		9189
GAG	WVKVVEEKA	176	9	28	44		9190
GAG	VDRFYKTLR	321	9	28	44		9191
GAG	PDCKTILKA	352	9	28	44		9192
GAG	WVKVVEEKAF	176	10	28	44		9193
GAG	PFRDYVDRFY	316	10	28	44		9194
GAG	YVDRFYKTLR	320	10	28	44	0.0003	9195
GAG	VDRFYKTLRA	321	10	28	44		9196
GAG	GATLEEMMTA	364	10	28	44		9197
GAG	FLQSRPEPTA	486	10	28	44	0.0005	9198
GAG	PFRDYVDRFY	316	11	28	44		9199
GAG	YVDRFYKTLR	320	11	28	44		9200
GAG	GARASVLSGG	2	11	29	46		9201
GAG	ASVLSGGK	5	8	29	45		9202
GAG	NLQGQMVH	158	8	29	45		9203
GAG	WVKVIEEK	176	8	29	45		9204
GAG	WDRLHPVH	233	8	29	45		9205
GAG	RDYVDRFY	318	8	29	45		9206
GAG	RASVLSGGK	4	9	29	45		9207
GAG	AISPRTLNA	167	9	29	45	0.0050	9208
GAG	WDRLHPVHA	233	9	29	45		9209
GAG	RDYVDRFYK	318	9	29	45	0.0007	9210
GAG	QAISPRTLNA	166	10	29	45		9211
GAG	NAWVKVIEEK	174	10	29	45		9212
GAG	IVQNLQGQMV	155	11	29	45		9213
GAG	AAEWDRLHPV	230	11	29	45		9214
GAG	PGNFLQSR	483	8	30	48		9215
GAG	NAWVKVVEEK	174	10	30	47	0.0004	9216
GAG	KIRLRPGGKKK	18	11	30	47		9217
GAG	WVKVVEEK	176	8	31	48	0.0003	9218
GAG	MLKDTINEEA	221	10	32	50		9219
GAG	QMLKDTINEEA	220	11	32	50		9220
GAG	MLKDTINEEAA	221	11	32	50		9221
GAG	KDTINEEA	223	8	33	52		9222
GAG	DTINEEAA	224	8	33	52		9223
GAG	KDTINEEAA	223	9	33	52		9224
GAG	RDYVDRFFK	318	9	33	52		9225
GAG	PFRDYVDRFF	316	11	33	52		9226
GAG	RLRPGGKKK	20	9	34	53		9227
GAG	RLRPGGKKKY	20	10	34	53		9228
GAG	PIPVGEIYKR	279	10	34	53	0.0003	9229
GAG	PIPVGEIY	279	8	35	55		9230
GAG	RDYVDRFF	318	8	35	55		9231

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	PIPVGEIYK	279	9	35	55	0.0002	9232
GAG	PGHKARVLA	380	9	35	55		9233
GAG	PFRDYVDRFF	316	10	35	55		9234
GAG	WMTETLLVQN	340	11	35	55		9235
GAG	GGPGHKARVL	378	11	35	55		9236
GAG	PGHKARVLAE	380	11	35	55		9237
GAG	DTKEALDK	98	8	36	56	0.0003	9238
GAG	ISPRTLNA	168	8	36	56		9239
GAG	QGVGGPGH	375	8	36	56		9240
GAG	QSRPEPTA	488	8	36	56		9241
GAG	QGVGGPGHK	375	9	36	56	0.0004	9242
GAG	MTETLLVQNA	341	10	36	56		9243
GAG	ACQGVGGPGH	373	10	36	56		9244
GAG	QGVGGPGHKA	375	10	36	56		9245
GAG	ISPRTLNAWV	168	11	36	56		9246
GAG	TACQGVGGPG	372	11	36	56	0.0001	9247
GAG	ACQGVGGPGH	373	11	36	56		9248
GAG	QGVGGPGHKA	375	11	36	56		9249
GAG	QGQMVHQA	160	8	37	58		9250
GAG	ETLLVQNA	343	8	37	58		9251
GAG	GVGGPGHK	376	8	37	58	0.0012	9252
GAG	VGGPGHKA	377	8	37	58		9253
GAG	GGPGHKAR	378	8	37	58		9254
GAG	GVGGPGHKA	376	9	37	58		9255
GAG	VGGPGHKAR	377	9	37	58		9256
GAG	GVGGPGHKAR	376	10	37	58	0.0003	9257
GAG	AAEWDRLH	230	8	39	61		9258
GAG	EAAEWDRLH	229	9	39	61		9259
GAG	PVGEIYKR	281	8	40	63	0.0003	9260
GAG	TVATLYCVH	83	9	40	63		9261
GAG	NTVATLYCVH	82	10	40	63		9262
GAG	SILDIRQGPK	305	10	40	63	0.3100	9263
GAG	FSPEVIPMFSA	185	11	40	63		9264
GAG	DIRQGPKEPF	308	10	41	64		9265
GAG	LDIRQGPKEPF	307	11	41	64		9266
GAG	DIRQGPKEPFR	308	11	41	64		9267
GAG	VATLYCVH	84	8	42	66		9268
GAG	LDIRQGPK	307	8	42	66		9269
GAG	ILDIRQGPK	306	9	42	66	0.0420	9270
GAG	NTMLNTVGGH	206	10	42	66		9271
GAG	TMLNTVGGH	207	9	43	67		9272
GAG	TMLNTVGGHQ	207	11	43	67		9273
GAG	KGCWKCGK	444	8	44	69		9274
GAG	KIRLRPGGK	18	9	44	69		9275
GAG	ASRELERFA	38	9	44	69		9276
GAG	KIRLRPGGKK	18	10	44	69	1.9000	9277
GAG	WASRELERFA	37	10	44	69		9278
GAG	QMREPRGSDIA	248	11	44	69		9279
GAG	KGCWKCGKEG	444	11	44	69		9280
GAG	FSALSEGA	193	8	45	70		9281

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	PGQMREPR	246	8	45	70		9282
GAG	MFSALSEGA	192	9	45	70		9283
GAG	CGKEGHQMK	449	9	45	70		9284
GAG	PMFSALSEGA	191	10	45	70		9285
GAG	KCGKEGHQMK	448	10	45	70		9286
GAG	ASRELERF	38	8	46	72		9287
GAG	EVIPMFSA	188	8	46	72		9288
GAG	TLEEMMTA	366	8	46	72		9289
GAG	WASRELERF	37	9	46	72		9290
GAG	ATLEEMMTA	365	9	46	72	0.0003	9291
GAG	MLNTVGGH	208	8	47	73		9292
GAG	NTVGGHQA	210	8	47	73		9293
GAG	TVGGHQAA	211	8	47	73		9294
GAG	NTVGGHQAA	210	9	47	73		9295
GAG	MLNTVGGHQA	208	10	47	73	0.0005	9296
GAG	MLNTVGGHQA	208	11	47	73		9297
GAG	WASRELER	37	8	48	75		9298
GAG	GCWKCGKEGH	445	10	48	75		9299
GAG	RLRPGGKK	20	8	49	77		9300
GAG	QMKDCTER	455	8	49	77		9301
GAG	QMKDCTERQA	455	10	49	77		9302
GAG	EGHQMKDCTE	452	11	49	77		9303
GAG	AFSPEVIPMF	184	10	50	78	0.0007	9304
GAG	KAFSPEVIPMF	183	11	50	78		9305
GAG	RAPRKKGCWK	439	10	51	80		9306
GAG	KDCTERQA	457	8	52	83		9307
GAG	KDCTERQANF	457	10	52	83		9308
GAG	CTERQANFLG	459	11	52	83		9309
GAG	DCTERQANF	458	9	52	81		9310
GAG	NCRAPRKK	437	8	53	84		9311
GAG	TINEEAAEWD	225	11	53	83		9312
GAG	KTLRAEQA	326	8	54	84		9313
GAG	FSPEVIPMF	185	9	54	84		9314
GAG	CTERQANF	459	8	55	87		9315
GAG	WHLGLNK	289	8	57	89		9316
GAG	KARVLAEA	383	8	57	89		9317
GAG	CFNCGKEGH	425	9	57	89		9318
GAG	HLGLNKIVR	290	10	57	89	0.0003	9319
GAG	KCFNCGKEGH	424	10	57	89		9320
GAG	WHLGLNKIVR	289	11	57	89		9321
GAG	ILGLNKIVRMY	291	11	57	89		9322
GAG	ILGLNKIVR	291	9	58	91	0.0008	9323
GAG	LGLNKIVRMY	292	10	58	91	0.0004	9324
GAG	LLVQNANPDC	345	11	58	91		9325
GAG	LGLNKIVR	292	8	59	92		9326
GAG	LVQNANPDCK	346	10	59	92	0.0002	9327
GAG	GLNKIVRMY	293	9	60	94	0.0100	9328
GAG	QAAMQMLK	216	8	61	95		9329
GAG	GGHQAAMQM	213	11	61	95		9330
GAG	RTLNAWVK	171	8	63	98	0.0410	9331

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	QGPKEPFR	311	8	63	98		9332
GAG	PFRDYVDR	316	8	63	98		9333
GAG	PFRDYVDRF	316	9	63	98		9334
GAG	QGPKEPFRDY	311	10	63	98	0.0004	9335
NEF	QAEPAAAGVG	34	11	01	33		9336
NEF	RAQAEPAA	32	8	01	17		9337
NEF	RAQAEPAAA	32	9	01	17		9338
NEF	QTEPAAVGVG	32	11	01	17		9339
NEF	RAEPAADGVG	32	11	01	17		9340
NEF	RTEPAAVGVG	32	11	01	17		9341
NEF	QAEPAAEGVG	33	11	01	17		9342
NEF	QAPTAAKGVG	33	11	01	17		9343
NEF	AADGVGAVSR	42	10	09	15		9344
NEF	SSIVGWPA	8	8	09	15		9345
NEF	VGWPAIRER	11	9	10	17		9346
NEF	AAEGVGAA	42	8	10	16		9347
NEF	FDSRLAFH	310	8	10	16		9348
NEF	FDSRLAFHH	310	9	10	16		9349
NEF	DSRLAFHH	311	8	10	16		9350
NEF	AVSQDLDK	48	8	10	16		9351
NEF	PLRPMTFK	102	8	10	16		9352
NEF	KGAFDLSF	109	8	10	16		9353
NEF	GAFDLSFF	110	8	10	16		9354
NEF	GAVSQDLDK	47	9	10	16		9355
NEF	QVPLRPMTF	100	9	10	16		9356
NEF	KGAFDLSFF	109	9	10	16		9357
NEF	GLEGLIYSK	125	9	10	16		9358
NEF	MARELHPEY	321	9	10	16		9359
NEF	VGAVSQDLDK	46	10	10	16		9360
NEF	QVPLRPMTFK	100	10	10	16		9361
NEF	GAFDLSFFLK	110	10	10	16		9362
NEF	GGLEGLIYSK	124	10	10	16		9363
NEF	CFKLVPVDPR	226	10	10	16		9364
NEF	HMARELHPEY	320	10	10	16		9365
NEF	MARELHPEYY	321	10	10	16		9366
NEF	GVGAVSQDLD	45	11	10	16		9367
NEF	KGAFDLSFFLK	109	11	10	16		9368
NEF	KGGLEGLIYSK	122	11	10	16		9369
NEF	WCFKLVPVDP	225	11	10	16		9370
NEF	HMARELHPEY	320	11	10	16		9371
NEF	MARELHPEYY	321	11	10	16		9372
NEF	AVSRDLEK	48	8	11	17		9373
NEF	VSRDLEKH	49	8	11	17		9374
NEF	KLVPVDPR	228	8	11	17		9375
NEF	GAVSRDLEK	47	9	11	17	0.0002	9376
NEF	AVSRDLEKH	48	9	11	17		9377
NEF	VGAVSRDLEK	46	10	11	17		9378
NEF	GAVSRDLEKH	47	10	11	17		9379
NEF	VSRDLEKHGA	49	10	11	17		9380
NEF	NSLLHPICQH	255	10	11	17		9381

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
NEF	GVGAVSRDLE	45	11	11	17		9382
NEF	VGAVSRDLEK	46	11	11	17		9383
NEF	AVSRDLEKHG	48	11	11	17		9384
NEF	AATNADCA	70	8	12	22		9385
NEF	ATNADCAWLE	71	11	12	22		9386
NEF	EGENNCLLH	251	9	12	19		9387
NEF	PMTYKGAF	105	8	12	19		9388
NEF	YTPGPGVR	207	8	12	19		9389
NEF	TAATNADCA	69	9	12	19		9390
NEF	DILDLWVYH	185	9	12	19		9391
NEF	NTAATNADCA	68	10	12	19		9392
NEF	QDILDLWVYH	184	10	12	19		9393
NEF	ITSSNTAATNA	64	11	12	19		9394
NEF	PLRPMTYKGA	102	11	12	19		9395
NEF	PGIRYPLTF	211	9	13	21		9396
NEF	PGTRFPLTF	211	9	13	21		9397
NEF	EGENNSLLH	251	9	13	21		9398
NEF	WVYHTQGF	191	8	13	20		9399
NEF	GIRYPLTF	213	8	13	20		9400
NEF	GTRFPLTF	213	8	13	20		9401
NEF	SSNTAATNA	66	9	13	20		9402
NEF	WVYHTQGFF	191	9	13	20		9403
NEF	YTPGPGTRF	207	9	13	20		9404
NEF	TSSNTAATNA	65	10	13	20		9405
NEF	VDLSHFLKEK	112	10	13	20		9406
NEF	DLWVYHTQGF	188	10	13	20		9407
NEF	AVDLSHFLKEK	111	11	13	20		9408
NEF	LDLWVYHTQG	187	11	13	20		9409
NEF	DLWVYHTQGF	188	11	13	20		9410
NEF	PGPGIRYPLTF	209	11	13	20		9411
NEF	PGPGTRFPLTF	209	11	13	20		9412
NEF	VDLSHFLK	112	8	14	22		9413
NEF	DGLIYSKK	172	8	14	22		9414
NEF	ELHPEFYK	324	8	14	22		9415
NEF	AITSSNTAA	63	9	14	22	0.0003	9416
NEF	AVDLSHFLK	111	9	14	22	0.0740	9417
NEF	LDGLIYSKK	171	9	14	22		9418
NEF	DGLIYSKKR	172	9	14	22		9419
NEF	SLLHPICQH	256	9	14	22		9420
NEF	GAITSSNTAA	62	10	14	22		9421
NEF	GLDGLIYSKK	125	10	14	22		9422
NEF	LDGLIYSKKR	171	10	14	22		9423
NEF	HGAITSSNTAA	61	11	14	22		9424
NEF	GGLDGLIYSKK	124	11	14	22		9425
NEF	GLDGLIYSKKR	125	11	14	22		9426
NEF	PAADGVGA	41	8	15	23		9427
NEF	ITSSNTAA	64	8	15	23		9428
NEF	CLLHPMSQH	256	9	15	23		9429
NEF	NCLLHPMSQH	255	10	15	23		9430
NEF	EAQEEEEVGF	82	10	16	25		9431

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
NEF	RDLEKHGA	51	8	16	25		9432
NEF	LDGLIYSK	171	8	16	25		9433
NEF	GLDGLIYSK	125	9	16	25		9434
NEF	GGLDGLIYSK	124	10	16	25		9435
NEF	KGGLDGLIYSK	122	11	16	25		9436
NEF	RFPLTFGWCF	216	10	17	27		9437
NEF	RFPLTFGWCF	216	11	17	27		9438
NEF	ADCAWLEA	74	8	17	27		9439
NEF	FFPDWQNY	199	8	17	27		9440
NEF	LLHPMSQH	257	8	17	27		9441
NEF	NADCAWLEA	73	9	17	27		9442
NEF	GFFPDWQNY	198	9	17	27		9443
NEF	YTPGPGIRY	207	9	17	27		9444
NEF	FDLSFFLKEK	112	10	17	27		9445
NEF	QGFFPDWQNY	196	10	17	27		9446
NEF	AFDLSFFLKEK	111	11	17	27		9447
NEF	FDLSFFLK	112	8	18	28		9448
NEF	LLHPICQH	257	8	18	28		9449
NEF	AFDLSFFLK	111	9	18	28		9450
NEF	GGLEGLIY	124	8	19	30		9451
NEF	KGGLEGLIY	122	9	19	30		9452
NEF	DILDLWVY	185	8	20	31		9453
NEF	YTPGPGIR	207	8	20	31		9454
NEF	QDILDLWVY	184	9	20	31		9455
NEF	PLRPMTYKAA	102	10	20	31		9456
NEF	QVPLRPMTYK	100	11	20	31		9457
NEF	PAAEGVGA	41	8	21	33		9458
NEF	GGLDGLIY	124	8	21	33		9459
NEF	WVYHTQGY	191	8	21	33		9460
NEF	YTPGPGTR	207	8	21	33		9461
NEF	PLRPMTYKA	102	9	21	33		9462
NEF	KGGLDGLIY	122	9	21	33		9463
NEF	WVYHTQGYF	191	9	21	33		9464
NEF	DLWVYHTQGY	188	10	21	33		9465
NEF	LDLWVYHTQG	187	11	21	33		9466
NEF	DLWVYHTQGY	188	11	21	33		9467
NEF	LSFFLKEK	114	8	22	34		9468
NEF	ELHPEYYK	324	8	22	34		9469
NEF	DLSFFLKEK	113	9	22	34		9470
NEF	EILDLWVYH	185	9	22	34		9471
NEF	GLIYSKKR	173	8	23	36		9472
NEF	PLRPMTYKGA	102	10	25	39		9473
NEF	AITSSNTA	63	8	27	42		9474
NEF	LSHFLKEK	114	8	27	42		9475
NEF	GAITSSNTA	62	9	27	42		9476
NEF	DLSHFLKEK	113	9	27	42		9477
NEF	HGAITSSNTA	61	10	27	42		9478
NEF	EILDLWVY	185	8	33	52		9479
NEF	ILDLWVYH	186	8	34	53		9480
NEF	YFPDWQNY	199	8	36	56		9481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
NEF	QGYFPDWQNY	196	10	36	56	0.0004	9482
NEF	LTFGWCFK	221	8	39	61		9483
NEF	PLTFGWCFK	219	9	39	61		9484
NEF	PLTFGWCF	219	8	43	67		9485
NEF	QVPLRPMTY	100	9	46	72		9486
NEF	QVPLRPMTYK	100	10	46	72	0.6100	9487
NEF	PVRPQVPLR	95	9	48	75		9488
NEF	GFPVRPQVPLR	93	11	48	75		9489
NEF	PLRPMTYK	102	8	49	77	0.0010	9490
POL	STNSPTSR	32	8	01	33		9491
POL	RANSPSSR	35	8	01	33		9492
POL	NSTNSPTSR	31	9	01	33		9493
POL	PTSRELQVR	36	9	01	33		9494
POL	QTRANSPSSR	33	10	01	33		9495
POL	QTRANSPTTR	35	10	01	33		9496
POL	NSPTSRELQVR	34	11	01	33		9497
POL	RANSPTTR	37	8	01	50		9498
POL	PSSRELQVR	39	9	01	50		9499
POL	PSRANSPTSR	24	10	01	50		9500
POL	NSPSSRELQVR	37	11	01	50		9501
POL	NSPTTRELQV	39	11	01	50		9502
POL	ADRQGIVSF	71	9	01	20		9503
POL	DDRQGPVSF	71	9	01	20		9504
POL	GADRQGIVSF	70	10	01	20		9505
POL	GDDRQGPVSF	70	10	01	20		9506
POL	ADRQGIVSFNF	71	11	01	20		9507
POL	DDRQGPVSFSF	71	11	01	20		9508
POL	AGADRQGIVSF	69	11	01	17		9509
POL	AGDDRQGPVS	69	11	01	17		9510
POL	GTTLNFPQITF	79	11	01	17		9511
POL	NLAFPQGEA	5	9	10	16		9512
POL	NLAFPQGEAR	5	10	10	16		9513
POL	KTGKYAKMRT	542	11	10	16		9514
POL	ILIEICGH	149	8	10	16		9515
POL	LIEICGHK	150	8	10	16		9516
POL	YAKMRTAH	546	8	10	16		9517
POL	LIEICGHKA	150	9	10	16		9518
POL	RSAHTNDVK	550	9	10	16		9519
POL	AFPQGEAREF	7	10	10	16		9520
POL	LIEALLDTGA	106	10	10	16		9521
POL	TGKYAKMRTA	543	10	10	16		9522
POL	ETWETWWTD	588	10	10	16		9523
POL	ETWETWWTE	588	10	10	16		9524
POL	ETWWTDYWQ	591	10	10	16		9525
POL	VSLTDTTNQK	659	10	10	16		9526
POL	LAFPQGEAREF	6	11	10	16		9527
POL	QLIEALLDTGA	105	11	10	16		9528
POL	MLTQLGCTLN	176	11	10	16		9529
POL	TGKYAKMRTA	543	11	10	16		9530
POL	VVSLTDTTNQ	658	11	10	16		9531

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QTKELQKQIIK	961	11	10	16		9532
POL	QTRANSPTRR	21	10	11	18		9533
POL	LDGIDKAQEDII	754	11	11	17		9534
POL	IGGFIKVK	137	8	11	17		9535
POL	RIGPENPY	238	8	11	17		9536
POL	VIPLTEEA	481	8	11	17		9537
POL	TAIITNDVK	551	8	11	17		9538
POL	QLTEVVQK	559	8	11	17		9539
POL	IDKAQEDII	757	8	11	17		9540
POL	WAGIQQEF	884	8	11	17		9541
POL	VVPRRKVK	1012	8	11	17		9542
POL	KIIKDYGK	1019	8	11	17		9543
POL	GIGGFIKVK	136	9	11	17		9544
POL	EVIPLTEEA	480	9	11	17		9545
POL	SLTDTTNQK	660	9	11	17		9546
POL	GIDKAQEDII	756	9	11	17		9547
POL	KVVPRRKVK	1011	9	11	17		9548
POL	GGIGGFIKVK	135	10	11	17		9549
POL	ISRIGPENPY	236	10	11	17		9550
POL	STNNETPGIR	323	10	11	17		9551
POL	ESWTVNDIQK	439	10	11	17		9552
POL	ETTNQKTELII	663	10	11	17		9553
POL	DGIDKAQEDII	755	10	11	17		9554
POL	GSNFTSTTVK	870	10	11	17		9555
POL	GIQQEFGIPY	886	10	11	17		9556
POL	SDIQTKELQK	958	10	11	17		9557
POL	IIKDYGKQMA	1020	10	11	17		9558
POL	IGGIGGFIKVK	134	11	11	17		9559
POL	KISRIGPENPY	235	11	11	17		9560
POL	PSTNNETPGIR	322	11	11	17		9561
POL	STNNETPGIRY	323	11	11	17		9562
POL	LTEVIPLTEEA	478	11	11	17		9563
POL	VVSLTETTNQ	658	11	11	17		9564
POL	ETTNQKTELII	663	11	11	17		9565
POL	NGSNFTSTTV	869	11	11	17		9566
POL	GSNFTSTTVK	870	11	11	17		9567
POL	ACWWAGIQQE	881	11	11	17		9568
POL	AGIQQEFGIPY	885	11	11	17		9569
POL	IDIIASDIQTK	953	11	11	17		9570
POL	VDIIATDIQTK	953	11	11	17		9571
POL	ASDIQTKELQK	957	11	11	17		9572
POL	NSEIKVVPRRK	1007	11	11	17		9573
POL	KIIKDYGKQMA	1019	11	11	17		9574
POL	NSLSEAGA	60	8	12	20		9575
POL	QTRANSPTSR	21	10	12	19		9576
POL	IIKIQNFR	969	8	12	19		9577
POL	QIYPGIKVK	458	9	12	19		9578
POL	QDQWTYQIY	526	9	12	19		9579
POL	IIKIQNFRVY	969	10	12	19		9580
POL	ASQIYPGIKVK	456	11	12	19		9581

Table XVI
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	IIKIQNFRVYY	969	11	12	19		9582
POL	LAFPQGEA	6	8	12	19		9583
POL	LAFPQGKA	6	8	12	19		9584
POL	AFPQGEAR	7	8	12	19		9585
POL	KTELQAIY	668	8	12	19		9586
POL	ELQAIYLA	670	8	12	19		9587
POL	QIIKIQNF	968	8	12	19		9588
POL	KDYGKQMA	1022	8	12	19		9589
POL	LAFPQGEAR	6	9	12	19		9590
POL	EINLPGKWK	122	9	12	19		9591
POL	TTNQKTELII	664	9	12	19		9592
POL	QIIKIQNFR	968	9	12	19		9593
POL	VIQDNSEIK	1003	9	12	19		9594
POL	NSEIKVVPR	1007	9	12	19		9595
POL	VLEEINLPGK	119	10	12	19		9596
POL	TTNQKTELIIA	664	10	12	19		9597
POL	KTELQAIYLA	668	10	12	19		9598
POL	VVIQDNSEIK	1002	10	12	19		9599
POL	NSEIKVVPRR	1007	10	12	19		9600
POL	TVLEEINLPGK	118	11	12	19		9601
POL	EINLPGKWKPK	122	11	12	19		9602
POL	ELRQHLLRWG	393	11	12	19		9603
POL	QGQDQWTYQI	524	11	12	19		9604
POL	RMRGAHTNDV	548	11	12	19		9605
POL	QIIKIQNFRVY	968	11	12	19		9606
POL	AVVIQDNSEIK	1000	11	12	19		9607
POL	QDNSEIKVVPR	1005	11	12	19		9608
POL	ELQKQIIK	964	8	13	21		9609
POL	EFSSEQTRA	16	9	13	21		9610
POL	KTGKYARMR	542	9	13	21		9611
POL	NLKTGKYARM	540	11	13	21		9612
POL	KTGKYARMRG	542	11	13	21		9613
POL	EDINLPGK	121	8	13	20		9614
POL	IVPLTEEA	481	8	13	20		9615
POL	TGKYARMR	543	8	13	20		9616
POL	YARMRGAH	546	8	13	20		9617
POL	IGQVREQA	914	8	13	20		9618
POL	QVREQAEH	916	8	13	20		9619
POL	DINLPGKWK	122	9	13	20		9620
POL	LIEICGKKA	150	9	13	20		9621
POL	DIVPLTEEA	480	9	13	20		9622
POL	IIGQVREQA	913	9	13	20		9623
POL	VLEDINLPGK	119	10	13	20		9624
POL	EDINLPGKWK	121	10	13	20		9625
POL	ILIEICGKKA	149	10	13	20		9626
POL	RAKIEELREH	388	10	13	20		9627
POL	TVQPIVLPEK	429	10	13	20	0.1600	9628
POL	TDIVPLTEEA	479	10	13	20		9629
POL	TGKYARMRGA	543	10	13	20		9630
POL	AGRWPVKTIH	857	10	13	20		9631

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KHGQVREQA	912	10	13	20		9632
POL	IGQVREQAEH	914	10	13	20		9633
POL	QVREQAEHLK	916	10	13	20		9634
POL	EIKVVPRRKA	1009	10	13	20		9635
POL	TLWQRPLVTV	91	11	13	20		9636
POL	LVTIKIGGQLK	97	11	13	20		9637
POL	TVLEDINLPGK	118	11	13	20		9638
POL	DINLPGKWKP	122	11	13	20		9639
POL	QILIEICGKKA	148	11	13	20		9640
POL	KIEELREHLLK	390	11	13	20		9641
POL	WTVQPIVLPEK	428	11	13	20	0.0011	9642
POL	LTDIVPLTEEA	478	11	13	20		9643
POL	TGKYARMRGA	543	11	13	20		9644
POL	LAGRWPVKTI	856	11	13	20		9645
POL	HGQVREQAEH	913	11	13	20		9646
POL	DSRDPLWKGP	981	11	13	20		9647
POL	EIKVVPRRKAK	1009	11	13	20		9648
POL	EFSSEQTR	16	8	14	22		9649
POL	QIYPGIKVR	458	9	14	22		9650
POL	ASQIYPGIKVR	456	11	14	22		9651
POL	IATESIVIWGK	567	11	14	22		9652
POL	ILIEICGK	149	8	14	22		9653
POL	LIEICGKK	150	8	14	22		9654
POL	NFTSTTVK	872	8	14	22		9655
POL	FTSTTVKA	873	8	14	22		9656
POL	TSTTVKAA	874	8	14	22		9657
POL	IASDIQTK	956	8	14	22		9658
POL	DSRDPLWK	981	8	14	22		9659
POL	QILIEICGK	148	9	14	22		9660
POL	ILIEICGKK	149	9	14	22		9661
POL	NFTSTTVKA	872	9	14	22		9662
POL	FTSTTVKAA	873	9	14	22	0.0003	9663
POL	HASDIQTK	955	9	14	22		9664
POL	RDSRDPLWK	980	9	14	22		9665
POL	RDPLWKGPA	983	9	14	22		9666
POL	QILIEICGKK	148	10	14	22		9667
POL	RTKIEELRQH	388	10	14	22		9668
POL	PGIKVRQLCK	461	10	14	22		9669
POL	THTDNGSNF	864	10	14	22		9670
POL	NFTSTTVKAA	872	10	14	22		9671
POL	TTVKAACWW	876	10	14	22	0.0006	9672
POL	AGERIVDIIA	948	10	14	22		9673
POL	DIIASDIQTK	954	10	14	22		9674
POL	RDPLWKGPAK	983	10	14	22		9675
POL	FSFPQITLWQR	85	11	14	22		9676
POL	YDQILIEICGK	146	11	14	22		9677
POL	ELREHLLKWG	393	11	14	22		9678
POL	KTPKFKLPIQK	577	11	14	22		9679
POL	GIDKAQEEHER	756	11	14	22		9680
POL	STTVKAACW	875	11	14	22		9681

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	SAGERIVDIIA	947	11	14	22		9682
POL	QTRANSPTR	21	9	15	24		9683
POL	LVEICTEMEK	221	10	15	24	0.0002	9684
POL	FFREDLAF	1	8	15	23		9685
POL	FSSEQTRA	17	8	15	23		9686
POL	ELRQIILLR	393	8	15	23		9687
POL	QGQDQWTY	524	8	15	23		9688
POL	KTELQAIII	668	8	15	23		9689
POL	AGIRKVLF	746	8	15	23		9690
POL	PIQKETWEA	584	9	15	23		9691
POL	SAGIRKVLF	745	9	15	23		9692
POL	EIKVVPRRK	1009	9	15	23		9693
POL	LTQLGCTLNF	177	10	15	23		9694
POL	KTELQAIILA	668	10	15	23		9695
POL	LGIIQAQPDR	695	10	15	23		9696
POL	VDKLVSAGIR	740	10	15	23		9697
POL	VSAGIRKVLF	744	10	15	23		9698
POL	IDKAQEEIIER	757	10	15	23		9699
POL	ALVEICTEMEK	220	11	15	23		9700
POL	KIEELRQIILLR	390	11	15	23		9701
POL	ALGIIQAQPDR	694	11	15	23		9702
POL	LVNQIIEQLIK	709	11	15	23		9703
POL	QVDKLVSAGIR	739	11	15	23		9704
POL	VDKLVSAGIRK	740	11	15	23		9705
POL	LVSAGIRKVLF	743	11	15	23		9706
POL	IDKAQEEIIERY	757	11	15	23		9707
POL	KAQEEIIER	759	8	16	25		9708
POL	NLAFQQGEA	5	9	16	25		9709
POL	KAQEEIIERY	759	9	16	25		9710
POL	NLAFQQGEAR	5	10	16	25		9711
POL	KAQEEIIERYII	759	10	16	25		9712
POL	LAFQQGEA	6	8	16	25		9713
POL	AFQQGEAR	7	8	16	25		9714
POL	RANSPTRR	26	8	16	25		9715
POL	QLGCTLNF	179	8	16	25		9716
POL	SAIITNDVK	551	8	16	25		9717
POL	ELQAIILA	670	8	16	25		9718
POL	IIQAQPDR	697	8	16	25		9719
POL	QVDKLVSA	739	8	16	25		9720
POL	KLVSAGIR	742	8	16	25		9721
POL	LVSAGIRK	743	8	16	25	0.0091	9722
POL	EIKVVPRR	1009	8	16	25		9723
POL	LAFQQGEAR	6	9	16	25		9724
POL	GIIQAQPDR	696	9	16	25		9725
POL	KLVSAGIRK	742	9	16	25	0.1300	9726
POL	QLEKEPIVGA	620	10	16	25		9727
POL	RANSPTSR	26	8	17	27		9728
POL	KIEELRQII	390	8	17	27		9729
POL	ELREHLLK	393	8	17	27		9730
POL	WGKTPKFK	575	8	17	27		9731

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	TIKIGGQLK	99	9	17	27	0.2700	9732
POL	VTIKIGGQLK	98	10	17	27	0.0370	9733
POL	TVQPIQLPEK	429	10	17	27		9734
POL	VIWGKTPKFK	573	10	17	27		9735
POL	TLWQRPLVTI	91	11	17	27		9736
POL	TIKIGGQLKEA	99	11	17	27		9737
POL	MLTQIGCTLNF	176	11	17	27		9738
POL	WTVQPIQLPEK	428	11	17	27		9739
POL	IVIWGKTPKFK	572	11	17	27		9740
POL	ETTNQKTELQ	663	11	17	27		9741
POL	KDFRKYTAF	311	9	18	29		9742
POL	YFSVPLDKDF	304	10	18	29		9743
POL	YFSVPLDKDFR	304	11	18	29		9744
POL	NLKTGKYAKM	540	11	18	29		9745
POL	SVPLDKDF	306	8	18	28		9746
POL	PDIVIYQY	365	8	18	28		9747
POL	FSVPLDKDF	305	9	18	28		9748
POL	SVPLDKDFR	306	9	18	28		9749
POL	FSVPLDKDFR	305	10	18	28		9750
POL	SVPLDKDFRK	306	10	18	28		9751
POL	AGIKVKQLCK	461	10	18	28		9752
POL	FSVPLDKDFRK	305	11	18	28		9753
POL	SVPLDKDFRK	306	11	18	28		9754
POL	LDKDFRKYTA	309	11	18	28		9755
POL	YAGIKVKQLCK	460	11	18	28		9756
POL	LVSQHEQLIK	709	11	18	28		9757
POL	PLDKDFRK	308	8	19	30		9758
POL	KDFRKYTA	311	8	19	30		9759
POL	PLDKDFRKY	308	9	19	30		9760
POL	KTGKYAKMR	542	9	19	30		9761
POL	PLDKDFRKYT	308	11	19	30		9762
POL	LDKDFRKY	309	8	19	30		9763
POL	KIEELREH	390	8	19	30		9764
POL	TGKYAKMR	543	8	19	30		9765
POL	GAHTNDVK	551	8	19	30		9766
POL	LTDTTNQK	661	8	19	30		9767
POL	PLWKGPAK	985	8	19	30		9768
POL	GIKVRQLCK	462	9	19	30		9769
POL	RGAHTNDVK	550	9	19	30		9770
POL	LDKDFRKYTA	309	10	19	30		9771
POL	KVRQLCKLLR	464	10	19	30		9772
POL	ATESIVIWGK	568	10	19	30		9773
POL	VSQHEQLIK	710	10	19	30	0.0007	9774
POL	MAGDDCVASR	1028	10	19	30		9775
POL	VSQHEQLIKK	710	11	19	30		9776
POL	QLIKKEKVYLA	716	11	19	30		9777
POL	QMAGDDCVAS	1027	11	19	30		9778
POL	QIYAGIKVK	458	9	20	32		9779
POL	KVYLAWVPA	722	9	20	32	0.0750	9780
POL	KVYLAWVPAH	722	10	20	32	0.0280	9781

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KAACWWAGIK	879	10	20	32	0.0300	9782
POL	ASQIYAGIKVK	456	11	20	32		9783
POL	KVYLAWVPAII	722	11	20	32	8.6000	9784
POL	KFKLPIQK	580	8	20	31		9785
POL	GDDCVASR	1030	8	20	31		9786
POL	AGDDCVASR	1029	9	20	31		9787
POL	VSLTETTNQK	659	10	20	31		9788
POL	LIKKEKVYLA	717	10	20	31		9789
POL	LLKLAGRWPV	853	11	20	31		9790
POL	YFSVPLDK	304	8	21	33		9791
POL	KVIITDNGSNF	863	11	21	33		9792
POL	ACWWAGIK	881	8	21	33		9793
POL	WAGIKQEF	884	8	21	33		9794
POL	SLTETTNQK	660	9	21	33		9795
POL	AACWWAGIK	880	9	21	33	0.0130	9796
POL	DAYFSVPLDK	302	10	21	33		9797
POL	DLEIGQHRTK	381	10	21	33		9798
POL	QLCKLLRGTK	467	10	21	33		9799
POL	SDFNLPPIVA	776	10	21	33		9800
POL	LLTQIGCTLNF	176	11	21	33		9801
POL	IFAIKKKDSTK	249	11	21	33		9802
POL	GDAYFSVPLD	301	11	21	33		9803
POL	SDLEIGQHRTK	380	11	21	33		9804
POL	QLCKLLRGTK	467	11	21	33		9805
POL	ASDFNLPPIVA	775	11	21	33		9806
POL	SDFNLPPIVAK	776	11	21	33		9807
POL	ACWWAGIKQE	881	11	21	33		9808
POL	AGIKQEFGIPY	885	11	21	33		9809
POL	EDFRKYTA	311	8	22	35		9810
POL	EDFRKYTAF	311	9	22	35		9811
POL	EIGQHRTK	383	8	22	34		9812
POL	RTKIEELR	388	8	22	34		9813
POL	YLAWVPAII	724	8	22	34		9814
POL	LAWVPAIIK	725	8	22	34		9815
POL	YLAWVPAIIK	724	9	22	34	0.0770	9816
POL	NFPQITLWQR	86	10	22	34		9817
POL	MTKILEPFRK	353	10	22	34	0.0150	9818
POL	KVILVAVHVA	823	10	22	34		9819
POL	AGRWPVKVHI	857	10	22	34		9820
POL	GIKQEFGIPY	886	10	22	34	0.0002	9821
POL	SMTKILEPFRK	352	11	22	34		9822
POL	KTPKFRLPIQK	577	11	22	34		9823
POL	LAGRWPVKVI	856	11	22	34		9824
POL	KVYLSWVPA	722	9	23	37		9825
POL	KVYLSWVPAII	722	10	23	37		9826
POL	KVYLSWVPAII	722	11	23	37		9827
POL	KILEPFRK	355	8	23	36		9828
POL	EGKVILVA	821	8	23	36		9829
POL	KVILVAVH	823	8	23	36		9830
POL	KIGGQLKEA	101	9	23	36		9831

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	DFNLPPIVA	777	9	23	36		9832
POL	VILVAVHVA	824	9	23	36		9833
POL	TVKAACWWA	877	9	23	36		9834
POL	SFPQITLWQR	86	10	23	36		9835
POL	DFNLPPIVAK	777	10	23	36		9836
POL	HLEGKVILVA	819	10	23	36		9837
POL	EGKVILVAVH	821	10	23	36		9838
POL	LLKWGFTTPD	398	11	23	36		9839
POL	LLRWGFTTPD	398	11	23	36		9840
POL	IDHATDIQTK	953	11	23	36		9841
POL	KLLRGTKA	470	8	24	38		9842
POL	NTPIFAIK	246	8	24	38		9843
POL	GDDCVAGR	1030	8	24	38		9844
POL	NTPIFAIKK	246	9	24	38		9845
POL	LCKLLRGTK	468	9	24	38	0.0004	9846
POL	AGDDCVAGR	1029	9	24	38		9847
POL	NTPIFAIKKK	246	10	24	38		9848
POL	LCKLLRGTKA	468	10	24	38		9849
POL	VIHTDNGSNF	864	10	24	38		9850
POL	MAGDDCVAGR	1028	10	24	38		9851
POL	QLCKLLRGAK	467	11	24	38		9852
POL	QGQGQWTYQI	524	11	24	38		9853
POL	KLGKAGYVTD	643	11	24	38		9854
POL	TAYFLLKLAG	849	11	24	38		9855
POL	QMAGDDCVAG	1027	11	24	38		9856
POL	KLLRGAKA	470	8	25	40		9857
POL	QGQWTYQIY	526	9	25	40	0.0004	9858
POL	IGGQLKEA	102	8	25	39		9859
POL	PIFAIKKK	248	8	25	39		9860
POL	QGQGQWTY	524	8	25	39		9861
POL	FLLKLAGR	852	8	25	39		9862
POL	QLCKLLRGA	467	9	25	39		9863
POL	PIVAKEIVA	782	9	25	39		9864
POL	YFLLKLAGR	851	9	25	39		9865
POL	QLCKLLRGAK	467	10	25	39		9866
POL	LCKLLRGAKA	468	10	25	39		9867
POL	LGKAGYVTDR	644	10	25	39		9868
POL	IDKAQEEHEK	757	10	25	39		9869
POL	SDFNLPPVVA	776	10	25	39		9870
POL	PSKDLIAEIQK	513	11	25	39		9871
POL	DTTNQKTELQ	663	11	25	39		9872
POL	GIDKAQEEHEK	756	11	25	39		9873
POL	IDKAQEEHEKY	757	11	25	39		9874
POL	ASDFNLPPVVA	775	11	25	39		9875
POL	SDFNLPPVVAK	776	11	25	39		9876
POL	RAKIEELR	388	8	26	41		9877
POL	LCKLLRGA	468	8	26	41		9878
POL	KFRLPIQK	580	8	26	41		9879
POL	NLPPIVAK	779	8	26	41		9880
POL	IVAKEIVA	783	8	26	41		9881

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	LCKLLRGAK	468	9	26	41		9882
POL	LTEAVQKIA	560	9	26	41		9883
POL	SSGIRKVLF	745	9	26	41		9884
POL	DFNLPPVVA	777	9	26	41		9885
POL	QLTEAVQKIA	559	10	26	41		9886
POL	VSSGIRKVLF	744	10	26	41		9887
POL	DFNLPPVVAK	777	10	26	41		9888
POL	GSNFTSAAVK	870	10	26	41		9889
POL	LVSSGIRKVLF	743	11	26	41		9890
POL	TGQETAYFLL	845	11	26	41		9891
POL	NGSNFTSAAV	869	11	26	41		9892
POL	GSNFTSAAVK	870	11	26	41		9893
POL	KAQEEHEK	759	8	27	43		9894
POL	ASQIYAGIK	456	9	27	43	0.0013	9895
POL	KAQEEHEKY	759	9	27	43		9896
POL	KAQEEHEKYH	759	10	27	43		9897
POL	EICTEMEK	223	8	27	42		9898
POL	EIGQHRAK	383	8	27	42		9899
POL	LVSSGIRK	743	8	27	42		9900
POL	SGIRKVLF	746	8	27	42		9901
POL	NLPPVVAK	779	8	27	42		9902
POL	ETAYFLLK	848	8	27	42	0.0037	9903
POL	TSAAVKAA	874	8	27	42		9904
POL	KLVSSGIRK	742	9	27	42		9905
POL	TAYFLLKLA	849	9	27	42	0.0027	9906
POL	FTSAAVKAA	873	9	27	42		9907
POL	DLEIGQHRAK	381	10	27	42		9908
POL	KLNWASQIYA	452	10	27	42	0.0052	9909
POL	WASQIYAGIK	455	10	27	42		9910
POL	KVKQLCKLLR	464	10	27	42		9911
POL	ETAYFLLKLA	848	10	27	42		9912
POL	NFTSAAVKAA	872	10	27	42		9913
POL	EICTEMEKEGK	223	11	27	42		9914
POL	SDLEIGQHRAK	380	11	27	42		9915
POL	VDKLVSSGIRK	740	11	27	42		9916
POL	ASQIYPGIK	456	9	28	44		9917
POL	KDLIAEIQK	515	9	28	44		9918
POL	NLKTGKYAK	540	9	28	44		9919
POL	DLIAEIQK	516	8	28	44		9920
POL	PIVGAETF	625	8	28	44		9921
POL	IVGAETFY	626	8	28	44		9922
POL	GSNFTSAA	870	8	28	44		9923
POL	NFTSAAVK	872	8	28	44		9924
POL	FTSAAVKA	873	8	28	44		9925
POL	CTEMEKEGK	225	9	28	44	0.0002	9926
POL	DLEIGQHRA	381	9	28	44		9927
POL	GIKVKQLCK	462	9	28	44		9928
POL	PIVGAETFY	625	9	28	44		9929
POL	QLIKKEKVY	716	9	28	44		9930
POL	PVVAKEIVA	782	9	28	44		9931

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NGSNFTSAA	869	9	28	44		9932
POL	NFTSAAVKA	872	9	28	44		9933
POL	ICTEMEKEGK	224	10	28	44		9934
POL	SDLEIGQHRA	380	10	28	44		9935
POL	WASQIYPGIK	455	10	28	44		9936
POL	AAVKAACWW	876	10	28	44		9937
POL	GSDLEIGQHRA	379	11	28	44		9938
POL	VGAETFYVDG	627	11	28	44		9939
POL	TDNGSNFTSA	867	11	28	44		9940
POL	SAAVKAACW	875	11	28	44		9941
POL	NLKTGKYAR	540	9	29	46	0.0008	9942
POL	KLVSSGIR	742	8	29	45		9943
POL	VIWGKTPKFR	573	10	29	45		9944
POL	VDKLVSSGIR	740	10	29	45		9945
POL	PLTEEAELELA	483	11	29	45		9946
POL	IVIWGKTPKFR	572	11	29	45		9947
POL	QVDKLVSSGIR	739	11	29	45		9948
POL	WGKTPKFR	575	8	30	47		9949
POL	LTETTNQK	661	8	30	47		9950
POL	IILVAVHVA	824	9	30	47		9951
POL	AANRETKLGK	637	10	30	47	0.0007	9952
POL	IIEQLIKKEK	713	10	30	47	0.0004	9953
POL	KIILVAVHVA	823	10	30	47		9954
POL	GAANRETKLG	636	11	30	47		9955
POL	AANRETKLGK	637	11	30	47		9956
POL	QIIEQLIKKEK	712	11	30	47		9957
POL	ILKLAGRWPV	853	11	30	47		9958
POL	VVAKEIVA	783	8	31	48		9959
POL	EGKIILVA	821	8	31	48		9960
POL	KIILVAVH	823	8	31	48		9961
POL	ETAYFILK	848	8	31	48		9962
POL	YFILKLAGR	851	9	31	48		9963
POL	HLEGKIILVA	819	10	31	48		9964
POL	EGKIILVAVH	821	10	31	48		9965
POL	ETAYFILKLA	848	10	31	48		9966
POL	PSINNETPGIR	322	11	31	48		9967
POL	TGQETAYFILK	845	11	31	48		9968
POL	TAYFILKLAGR	849	11	31	48		9969
POL	FILKLAGR	852	8	32	50		9970
POL	NDVKQLTEA	555	9	32	50		9971
POL	TAYFILKLA	849	9	32	50		9972
POL	AVKAACWWA	877	9	32	50		9973
POL	SINNETPGIR	323	10	32	50		9974
POL	SINNETPGIRY	323	11	32	50		9975
POL	SSMTKILEPFR	351	11	32	50		9976
POL	IITNDVKQLTE	553	11	32	50		9977
POL	IISNWRAMAS	768	11	32	50		9978
POL	QTKELQKQITK	961	11	32	50	0.0050	9979
POL	DVKQLTEA	556	8	33	52		9980
POL	NGSNFTSA	869	8	33	52		9981

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	EMEKEGKISK	229	10	33	52	0.0004	9982
POL	SSMTKILEPF	351	10	33	52	0.0004	9983
POL	TDNGSNFTSA	867	10	33	52		9984
POL	QSSMTKILEPF	350	11	33	52		9985
POL	DVKQLTEAVQ	556	11	33	52	0.0048	9986
POL	HTDNGSNFTS	866	11	33	52		9987
POL	YDPSKDLIA	511	9	34	53		9988
POL	DIIATDIQTK	954	10	34	53	0.0056	9989
POL	QLKEALLDTG	105	11	34	53		9990
POL	ELQKQITK	964	8	35	56		9991
POL	LIKKEKVY	717	8	35	55		9992
POL	QITKIQNF	968	8	35	55		9993
POL	DSRDPIWK	981	8	35	55		9994
POL	ETKLGKAGY	641	9	35	55		9995
POL	IIATDIQTK	955	9	35	55	0.0250	9996
POL	QITKIQNFR	968	9	35	55	0.0021	9997
POL	RDSRDPIWK	980	9	35	55		9998
POL	TDIQTKELQK	958	10	35	55	0.0007	9999
POL	RDPIWKGPAK	983	10	35	55		10000
POL	ATDIQTKELQK	957	11	35	55	0.0051	10001
POL	QITKIQNFRVY	968	11	35	55		10002
POL	DSRDPIWKGP	981	11	35	55		10003
POL	SDIKVVPRRKA	1008	11	35	55		10004
POL	ITKIQNFR	969	8	36	57		10005
POL	ITKIQNFRVY	969	10	36	57	0.0016	10006
POL	ITKIQNFRVYY	969	11	36	57		10007
POL	IATDIQTK	956	8	36	56		10008
POL	PIWKGPAK	985	8	36	56		10009
POL	NLPGKWKPK	124	9	36	56		10010
POL	AIFQSSMTK	347	9	36	56	1.1000	10011
POL	PAIFQSSMTK	346	10	36	56	0.0760	10012
POL	LTEEAELELA	484	10	36	56		10013
POL	VFAIKKKDSTK	249	11	36	56		10014
POL	NTPVFAIK	246	8	37	58	0.0003	10015
POL	PVFAIKKK	248	8	37	58	0.0003	10016
POL	QLTEAVQK	559	8	37	58		10017
POL	QIHEQLIK	712	8	37	58		10018
POL	HEQLIKK	713	8	37	58		10019
POL	YLSWVPAH	724	8	37	58		10020
POL	LSWVPAHK	725	8	37	58		10021
POL	NTPVFAIKK	246	9	37	58	0.0330	10022
POL	QIHEQLIKK	712	9	37	58	0.0091	10023
POL	YLSWVPAHK	724	9	37	58		10024
POL	RDPIWKGPA	983	9	37	58		10025
POL	VIQDNSDIK	1003	9	37	58	0.0009	10026
POL	NTPVFAIKKK	246	10	37	58	0.0006	10027
POL	VVIQDNSDIK	1002	10	37	58	0.0005	10028
POL	AVVIQDNSDIK	1000	11	37	58	0.0004	10029
POL	IFQSSMTK	348	8	38	59	0.0055	10030
POL	ILKEPVHGVYY	498	11	38	59		10031

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	LDGIDKAQEEH	754	11	39	62		10032
POL	HSNWRAMA	768	8	39	61		10033
POL	AGYVTDRGR	647	9	39	61		10034
POL	YVTDRGRQK	649	9	39	61	0.0011	10035
POL	KAGYVTDRGR	646	10	39	61		10036
POL	LGHQAQPDK	695	10	39	61	0.0007	10037
POL	DGIDKAQEEH	755	10	39	61		10038
POL	DIKVVPRRKA	1009	10	39	61		10039
POL	PVHGVYYDPS	505	11	39	61		10040
POL	AGYVTDRGRQ	647	11	39	61		10041
POL	ALGHQAQPDK	694	11	39	61		10042
POL	DIKVVPRRKAK	1009	11	39	61		10043
POL	VTDRGRQK	650	8	40	63	0.0090	10044
POL	HQAQPDK	697	8	40	63		10045
POL	GHQAQPDK	696	9	40	63	0.0009	10046
POL	GIDKAQEEH	756	9	40	63		10047
POL	NSDIKVVPR	1007	9	40	63		10048
POL	ILKEPVHGVY	498	10	40	63		10049
POL	NSDIKVVPRR	1007	10	40	63	0.0007	10050
POL	EILKEPVHGVY	497	11	40	63		10051
POL	WTYQIYQEPF	529	11	40	63	0.9200	10052
POL	QIYQEPFKNLK	532	11	40	63	0.2800	10053
POL	SAGERHDHA	947	11	40	63		10054
POL	QDNSDIKVVPR	1005	11	40	63		10055
POL	NSDIKVVPRRK	1007	11	40	63		10056
POL	ESIVIWGKTPK	570	11	41	65		10057
POL	FFRENLAF	1	8	41	64		10058
POL	QIGCTLNF	179	8	41	64		10059
POL	QIYQEPFK	532	8	41	64	0.0010	10060
POL	IDKAQEEH	757	8	41	64		10061
POL	KAKHRDY	1017	8	41	64		10062
POL	LTQIGCTLNF	177	10	41	64	0.0081	10063
POL	AGERHDHA	948	10	41	64		10064
POL	KAKHRDYGK	1017	10	41	64	0.0048	10065
POL	KISKIGPENPY	235	11	41	64		10066
POL	SIVIWGKTPKF	571	11	41	64		10067
POL	DFRKYTAF	312	8	42	66		10068
POL	KAGYVTDR	646	8	42	66		10069
POL	ISKIGPENPY	236	10	42	66		10070
POL	SMTKILEPFR	352	10	42	66	0.0004	10071
POL	WTYQIYQEPF	529	10	42	66		10072
POL	SIVIWGKTPK	571	10	42	66		10073
POL	TTNQKTELQA	664	10	42	66	0.0004	10074
POL	IVIYQYMDDLY	367	11	42	66		10075
POL	VVPRRKAKIIR	1012	11	42	66		10076
POL	GVYYDPSK	508	8	43	67		10077
POL	SCDKCQLK	791	8	43	67		10078
POL	SMTKILEPF	352	9	43	67	0.0004	10079
POL	MTKILEPFR	353	9	43	67	0.0008	10080
POL	HGVYYDPSK	507	9	43	67	0.0004	10081

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	ASCDKCQLK	790	9	43	67	0.0027	10082
POL	DSWTVNDIQK	439	10	43	67	0.0007	10083
POL	TFYVDGAANR	631	10	43	67	0.0003	10084
POL	VASCDKCQLK	789	10	43	67	0.0004	10085
POL	KIIGQVRDQA	912	10	43	67		10086
POL	KDSWTVNDIQ	438	11	43	67		10087
POL	ETFYVDGAAN	630	11	43	67		10088
POL	IVASCDKCQLK	788	11	43	67	0.0970	10089
POL	SCDKCQLKGE	791	11	43	67		10090
POL	MTKILEPF	353	8	44	69		10091
POL	IGQVRDQA	914	8	44	69		10092
POL	SDIKVVPR	1008	8	44	69		10093
POL	MAGDDCVA	1028	8	44	69		10094
POL	IIGQVRDQA	913	9	44	69		10095
POL	SDIKVVPRR	1008	9	44	69	0.0002	10096
POL	QMAGDDCVA	1027	9	44	69	0.0003	10097
POL	VDGAANRETK	634	10	44	69		10098
POL	IGQVRDQAEH	914	10	44	69		10099
POL	QVRDQAEHLK	916	10	44	69	0.0089	10100
POL	SDIKVVPRRK	1008	10	44	69	0.0004	10101
POL	PFKNLKTGKY	537	11	44	69		10102
POL	GAETFYVDGA	628	11	44	69		10103
POL	YVDGAANRET	633	11	44	69		10104
POL	IIGQVRDQAEH	913	11	44	69		10105
POL	VAKEIVASCDK	784	11	45	71		10106
POL	GAANRETK	636	8	45	70		10107
POL	EIVASCDK	787	8	45	70		10108
POL	DGAANRETK	635	9	45	70		10109
POL	PFKNLKTGKY	537	10	45	70	0.0004	10110
POL	RDQAEHLKTA	918	10	45	70		10111
POL	PLVKLWYQLE	613	11	45	70		10112
POL	EILKEPVH	497	8	46	72		10113
POL	KLWYQLEK	616	8	46	72		10114
POL	RDQAEHLK	918	8	46	72		10115
POL	PFKNLKTGK	537	9	46	72		10116
POL	DIQTKELQK	959	9	46	72	0.0009	10117
POL	LVKLWYQLEK	614	10	46	72	0.0560	10118
POL	KVKQWPLTEE	207	11	46	72	0.0750	10119
POL	VIWGKTPKF	573	9	47	73		10120
POL	IVIWGKTPKF	572	10	47	73		10121
POL	VIWGKTPK	573	8	48	75		10122
POL	QVRDQAEH	916	8	48	75		10123
POL	DIKVVPRR	1009	8	48	75		10124
POL	IVIWGKTPK	572	9	48	75	0.0850	10125
POL	DIKVVPRRK	1009	9	48	75	0.0002	10126
POL	GAETFYVDGA	628	10	48	75		10127
POL	KVLFLDGIDK	750	10	48	75	0.3600	10128
POL	CDKCQLKGEA	792	10	48	75		10129
POL	KCQLKGEAMH	794	10	48	75		10130
POL	VVESMNKELK	902	10	48	75		10131

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KVLFLDGIDKA	750	11	48	75		10132
POL	GVVESMNKEL	901	11	48	75		10133
POL	VVESMNKELK	902	11	48	75		10134
POL	GVVESMNK	901	8	49	77		10135
POL	RDYGKQMA	1022	8	49	77		10136
POL	QGVVESMNK	900	9	49	77		10137
POL	KLKPGMDGPK	197	10	49	77	0.3900	10138
POL	HRDYGKQMA	1020	10	49	77		10139
POL	QSQGVVESMN	898	11	49	77		10140
POL	KHRDYGKQMA	1019	11	49	77		10141
POL	ESIVIWGK	570	8	50	79		10142
POL	YVDGAANR	633	8	50	78	0.0003	10143
POL	LAGRWPVK	856	8	50	78		10144
POL	KHRDYGK	1019	8	50	78		10145
POL	KLAGRWPVK	855	9	50	78	2.7000	10146
POL	GMDGPKVK	201	8	51	80	0.0007	10147
POL	KIGPENPY	238	8	51	80		10148
POL	FTTPDKKH	403	8	51	80		10149
POL	TFYVDGAA	631	8	51	80		10150
POL	HTDNGSNF	866	8	51	80		10151
POL	PGMDGPKVK	200	9	51	80	0.0004	10152
POL	GFTTPDKKH	402	9	51	80		10153
POL	ETFYVDGAA	630	9	51	80		10154
POL	VLFLDGIDK	751	9	51	80	0.0380	10155
POL	VIYQYMDDLY	368	10	51	80	0.0007	10156
POL	WGFTTPDKKH	401	10	51	80		10157
POL	FTTPDKKHQK	403	10	51	80	0.0002	10158
POL	VLFLDGIDKA	751	10	51	80	0.0004	10159
POL	KSVTVLDVGD	293	11	51	80		10160
POL	GFTTPDKKHQ	402	11	51	80		10161
POL	QATWIPEWEF	599	10	52	83	0.0004	10162
POL	PAGLKKKK	286	8	52	81		10163
POL	SDLEIGQH	380	8	52	81		10164
POL	DLEIGQHR	381	8	52	81		10165
POL	WGFTTPDK	401	8	52	81		10166
POL	GFTTPDKK	402	8	52	81		10167
POL	KCQLKGEA	794	8	52	81		10168
POL	VASGYIEA	831	8	52	81		10169
POL	KIQNFRVY	971	8	52	81		10170
POL	KVVPRRKA	1011	8	52	81		10171
POL	VVPRRKAK	1012	8	52	81	0.0027	10172
POL	ETPGIRYQY	327	9	52	81		10173
POL	GSDLEIGQH	379	9	52	81		10174
POL	SDLEIGQHR	380	9	52	81	0.0003	10175
POL	WGFTTPDKK	401	9	52	81	0.0004	10176
POL	ATWIPEWEF	600	9	52	81		10177
POL	HVASGYIEA	830	9	52	81	0.0003	10178
POL	KIQNFRVYY	971	9	52	81	0.1200	10179
POL	KVVPRRKAK	1011	9	52	81	0.0290	10180
POL	VGSDLEIGQH	378	10	52	81		10181

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	GSDLEIGQHR	379	10	52	81		10182
POL	KIQNFRVYYR	971	10	52	81	0.0320	10183
POL	NFRVYYRDSR	974	10	52	81		10184
POL	IGGIGGFIKVR	134	11	52	81		10185
POL	VGPTPVNIIGR	164	11	52	81		10186
POL	YVGSDLEIGQH	377	11	52	81		10187
POL	VGSDLEIGQHR	378	11	52	81		10188
POL	AVHVASGYIEA	828	11	52	81		10189
POL	SGYIEAEVIPA	833	11	52	81		10190
POL	GIPHPAGLKKK	282	11	53	84		10191
POL	IGGFIKVR	137	8	53	83		10192
POL	GFIKVRQY	139	8	53	83		10193
POL	PIETVPVK	190	8	53	83		10194
POL	ETVPVKLK	192	8	53	83	0.0049	10195
POL	ELELAENR	489	8	53	83		10196
POL	QLKGEAMH	796	8	53	83		10197
POL	ESMNKELK	904	8	53	83		10198
POL	SMNKELKK	905	8	53	83		10199
POL	GIGGFIKVR	136	9	53	83	0.0008	10200
POL	GGFIKVRQY	138	9	53	83	0.0004	10201
POL	YIEAEVIPA	835	9	53	83	0.0003	10202
POL	ESMNKELKK	904	9	53	83		10203
POL	GGIGGFIKVR	135	10	53	83	0.0004	10204
POL	IGGFIKVRQY	137	10	53	83	0.0004	10205
POL	ISPIETVPVK	188	10	53	83	0.0003	10206
POL	PIETVPVKLK	190	10	53	83	0.0002	10207
POL	EAELELAENR	487	10	53	83		10208
POL	LVAVHVASGY	826	10	53	83		10209
POL	GIGGFIKVRQY	136	11	53	83		10210
POL	PISPIETVPVK	187	11	53	83		10211
POL	ILVAVHVASGY	825	11	53	83		10212
POL	FVNTPPLVK	608	9	54	86	0.0120	10213
POL	GIPHPAGLKK	282	10	54	86	0.0110	10214
POL	LGIPHPAGLKK	281	11	54	86		10215
POL	ILVAVHVA	825	8	54	84		10216
POL	PTPVNIIGR	166	9	54	84	0.0008	10217
POL	PLTEEKIKA	212	9	54	84		10218
POL	LAENREILK	492	9	54	84	0.0002	10219
POL	EVQLGIPHPA	278	10	54	84		10220
POL	ELAENREILK	491	10	54	84	0.0002	10221
POL	EFVNTPPLVK	607	10	54	84		10222
POL	PLTEEKIK	212	8	55	86		10223
POL	ETFYVDGA	630	8	55	86		10224
POL	LFLDGIDK	752	8	55	86		10225
POL	FLDGIDKA	753	8	55	86		10226
POL	LFLDGIDKA	752	9	55	86		10227
POL	QLGIPHPA	280	8	56	89		10228
POL	GIPHPAGLK	282	9	56	89	0.2300	10229
POL	KGGIGGYSA	940	9	56	89		10230
POL	LGIPHPAGLK	281	10	56	89	0.0370	10231

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QLGIPHPAGLK	280	11	56	89		10232
POL	LTEEKIKA	213	8	56	88		10233
POL	VTVLDVGDAY	295	10	56	88	0.0001	10234
POL	ELKKIIGQVR	909	10	56	88		10235
POL	DFWEVQLGIPH	275	11	56	88		10236
POL	SVTVLDVGDA	294	11	56	88		10237
POL	VTVLDVGDAY	295	11	56	88		10238
POL	PAETGQETAY	842	11	56	88		10239
POL	KTAVQMAVFI	925	11	56	88		10240
POL	TGQETAYF	845	8	57	89		10241
POL	AIKKKDSTK	251	9	57	89	0.0017	10242
POL	ELNKRTQDF	268	9	57	89		10243
POL	VTVLDVGDA	295	9	57	89		10244
POL	TVLDVGDAY	296	9	57	89	0.0002	10245
POL	TTPDKKHQK	404	9	57	89	0.0002	10246
POL	ETGQETAYF	844	9	57	89		10247
POL	ILKTAVQMA	923	9	57	89	0.0003	10248
POL	KTAVQMAVF	925	9	57	89	0.0003	10249
POL	FAIKKKDSTK	250	10	57	89	0.0004	10250
POL	SVTVLDVGDA	294	10	57	89		10251
POL	TVLDVGDAYF	296	10	57	89	0.0004	10252
POL	NTPPLVKLWY	610	10	57	89	0.0002	10253
POL	AIKKKDSTKW	251	11	57	89		10254
POL	ILKTAVQMAV	923	11	57	89		10255
POL	MAVFIHNFKR	930	11	57	89		10256
POL	GGIGGYSAGER	941	11	57	89		10257
POL	NLKTGKYA	540	8	58	92		10258
POL	VLPQGWKGSP	337	11	58	92		10259
POL	KDSTKWRK	255	8	58	91		10260
POL	EVQLGIPH	278	8	58	91		10261
POL	TVLDVGDA	296	8	58	91		10262
POL	YALGIIQA	693	8	58	91		10263
POL	GGNEQVDK	735	8	58	91		10264
POL	FHNFKRK	933	8	58	91		10265
POL	GGYSAGER	944	8	58	91		10266
POL	RVYYRDSR	976	8	58	91		10267
POL	IGGNEQVDK	734	9	58	91	0.0004	10268
POL	PAETGQETA	842	9	58	91		10269
POL	VFIHNFKRK	932	9	58	91	0.0004	10270
POL	IGGYSAGER	943	9	58	91	0.0004	10271
POL	STKWRKLVDF	257	10	58	91	0.0003	10272
POL	GIGGNEQVDK	733	10	58	91	0.0005	10273
POL	PAETGQETAY	842	10	58	91		10274
POL	AVFIHNFKRK	931	10	58	91	0.6600	10275
POL	GIGGYSAGER	942	10	58	91	0.0003	10276
POL	DSTKWRKLVD	256	11	58	91		10277
POL	STKWRKLVDF	257	11	58	91		10278
POL	DSQYALGIIQA	690	11	58	91		10279
POL	KGIGGNEQVDK	732	11	58	91		10280
POL	VIPAETGQETA	840	11	58	91		10281

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QGWKGSPA	340	8	59	92		10282
POL	AVIIVASGY	828	8	59	92		10283
POL	ETGQETAY	844	8	59	92		10284
POL	QAEHLKTA	920	8	59	92		10285
POL	GGIGGYSA	941	8	59	92		10286
POL	GIWQLDCTH	811	9	59	92		10287
POL	VAVIIVASGY	827	9	59	92	0.0004	10288
POL	KGPAKLLWK	988	9	59	92	0.0021	10289
POL	QGWKGSPAIF	340	10	59	92	0.0004	10290
POL	EVNIVTDSQY	684	10	59	92		10291
POL	PGIWQLDCTH	810	10	59	92		10292
POL	TAVQMAVFHI	926	10	59	92	0.0004	10293
POL	VGKLNWASQI	450	11	59	92		10294
POL	EVNIVTDSQYA	684	11	59	92		10295
POL	NFKRKGGIGGY	936	11	59	92		10296
POL	PAKLLWKGEG	990	11	59	92		10297
POL	QLDCTHLEGK	814	10	60	95	0.0010	10298
POL	DFRELNKR	265	8	60	94		10299
POL	VLDVGDAY	297	8	60	94		10300
POL	MAVFHINF	930	8	60	94		10301
POL	VDFRELNKR	264	9	60	94		10302
POL	VLDVGDAYF	297	9	60	94		10303
POL	MGYELHPDK	419	9	60	94	0.0640	10304
POL	KLNWASQIY	452	9	60	94	0.1200	10305
POL	AVQMAVFHI	927	9	60	94		10306
POL	QMAVFHINF	929	9	60	94	0.0010	10307
POL	MAVFHINFK	930	9	60	94	0.0170	10308
POL	KLLWKGEGA	992	9	60	94	0.0003	10309
POL	LVDFRELNKR	263	10	60	94		10310
POL	WMGYELHPDK	418	10	60	94	0.0005	10311
POL	QMAVFHINFK	929	10	60	94	0.6100	10312
POL	MAVFHINFKR	930	10	60	94	0.0068	10313
POL	KLVDFRELNK	262	11	60	94		10314
POL	PDKKHQKEPPF	406	11	60	94		10315
POL	AVQMAVFHIN	927	11	60	94		10316
POL	QMAVFHINFK	929	11	60	94		10317
POL	EALLDTGA	108	8	61	95		10318
POL	LDVGDAYF	298	8	61	95		10319
POL	LVGKLNWA	449	8	61	95		10320
POL	IVTDSQYA	687	8	61	95		10321
POL	TAVQMAVF	926	8	61	95		10322
POL	NDIQKLVGK	444	9	61	95		10323
POL	KLVGKLNWA	448	9	61	95	0.0003	10324
POL	NIVTDSQYA	686	9	61	95		10325
POL	LDCTHLEGK	815	9	61	95		10326
POL	TVNDIQKLVGK	442	11	61	95	0.0400	10327
POL	MIGGIGGF	133	8	62	97		10328
POL	VDFRELNK	264	8	62	97		10329
POL	WTVNDIQK	441	8	62	97	0.0003	10330
POL	DIQKLVGK	445	8	62	97		10331

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NIVTDSQY	686	8	62	97		10332
POL	DCTHLEGK	816	8	62	97		10333
POL	AVFIHNFK	931	8	62	97	0.0280	10334
POL	VFIHNFKR	932	8	62	97		10335
POL	LLWKGEGA	993	8	62	97		10336
POL	KMIGGIGGF	132	9	62	97	0.0004	10337
POL	LVDFRELNK	263	9	62	97	0.0110	10338
POL	AVFIHNFKR	931	9	62	97	0.1700	10339
POL	MIGGIGGFIK	133	10	62	97	0.0099	10340
POL	KLVDFRELNK	262	10	62	97	0.5100	10341
POL	KMIGGIGGFIK	132	11	62	97	2.3000	10342
POL	NVLPQGWK	336	8	63	100	0.0003	10343
POL	IGGIGGFIK	134	9	63	98	0.0004	10344
POL	GGIGGFIK	135	8	64	100		10345
POL	FLWMGYELH	416	9	64	100		10346
POL	PFLWMGYELH	415	10	64	100		10347
REV	GTRQTRKNR	37	9	01	50		10348
REV	TTRQARRNR	37	9	01	50		10349
REV	GTRQTRKNRR	37	10	01	50		10350
REV	TTRQARRNRR	37	10	01	50		10351
REV	GTRQTRKNRR	37	11	01	50		10352
REV	TTRQARRNRR	37	11	01	50		10353
REV	GTETGVGR	103	8	06	19		10354
REV	QGTETGVGR	102	9	06	19		10355
REV	LLKTVRLIK	12	9	10	16		10356
REV	GDSDEELLK	6	9	11	17		10357
REV	PLQLPPIER	76	9	11	17		10358
REV	SGDSDEELLK	5	10	11	17		10359
REV	RSGDSDEELLK	4	11	11	17		10360
REV	PVPLQLPPIER	74	11	11	17		10361
REV	RARQRQIR	50	8	12	19		10362
REV	DSDEELLK	7	8	12	19		10363
REV	ILSTCLGR	63	8	12	19		10364
REV	RILSTCLGR	62	9	12	19		10365
REV	AVRHKILY	17	9	13	20		10366
REV	PSPEGTRQA	31	9	13	20		10367
REV	QLPPLERLH	78	9	13	20		10368
REV	PSPEGTRQAR	31	10	13	20		10369
REV	PSPEGTRQAR	31	11	13	20		10370
REV	PLQLPPLERLH	76	11	13	20		10371
REV	GTRQARKNRR	36	11	14	22		10372
REV	RARQRQHI	50	8	15	24		10373
REV	GTRQARKNR	36	9	15	23		10374
REV	GTRQARKNRR	36	10	15	23		10375
REV	QARKNRRRR	40	9	16	25		10376
REV	QARKNRRRR	40	11	16	25		10377
REV	QARKNRRR	40	8	17	27		10378
REV	HKILYQSNPY	20	11	18	28		10379
REV	KILYQSNPY	22	9	26	41		10380
REV	ILYQSNPY	23	8	27	42		10381

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
REV	EGTRQARR	35	8	27	42		10382
REV	EGTRQARRNR	35	10	27	42		10383
REV	EGTRQARRNR	35	11	27	42		10384
REV	GTRQARRNR	36	9	34	53		10385
REV	GTRQARRNRR	36	10	34	53		10386
REV	GTRQARRNRR	36	11	34	53		10387
REV	PVPLQLPPLER	74	11	34	53		10388
REV	PLQLPPLER	76	9	35	55		10389
REV	QARRNRRRR	40	11	37	58		10390
REV	QARRNRRR	40	8	38	59		10391
REV	QARRNRRRR	40	9	38	59		10392
TAT	PGGYPRRK	104	8	01	50		10393
TAT	AGPGGYPRR	102	9	01	50		10394
TAT	TGPSGQPCH	102	9	01	50		10395
TAT	ETGPSGQPCH	101	10	01	50		10396
TAT	KAGPGGYPRR	101	10	01	50		10397
TAT	AGPGGYPRRK	102	10	01	50		10398
TAT	KAGPGGYPRR	101	11	01	50		10399
TAT	GGYPRRKGSC	105	11	01	50		10400
TAT	PGSQPRTA	17	8	10	16		10401
TAT	ACTNCYCK	24	8	10	16		10402
TAT	TACTNCYCK	23	9	10	16		10403
TAT	YCKKCCFH	29	8	11	17		10404
TAT	YCKKCCYH	29	8	11	17		10405
TAT	CFHCQVCF	34	8	11	17		10406
TAT	VDPRLEPWK	4	9	11	17		10407
TAT	ACNNCYCKK	24	9	11	17		10408
TAT	CCFHCQVCF	33	9	11	17		10409
TAT	PVDPRLEPWK	3	10	11	17	0.0005	10410
TAT	VDPRLEPWKH	4	10	11	17		10411
TAT	TACNNCYCKK	23	10	11	17		10412
TAT	PVDPRLEPWK	3	11	11	17		10413
TAT	RGDPTGPKES	84	11	11	17		10414
TAT	GDPTGPKESK	85	11	11	17		10415
TAT	ESKKKVESK	93	9	12	19		10416
TAT	GDPTGPKESK	85	10	12	19		10417
TAT	PTGPKESKKK	88	10	12	19		10418
TAT	TGPKESKKK	89	9	13	20		10419
TAT	FLNKGLGISY	41	10	14	22		10420
TAT	PVDPNLEPWN	3	11	14	22		10421
TAT	CFLNKGLGISY	40	11	14	22		10422
TAT	RGDPTGPK	84	8	16	25		10423
TAT	VDPNLEPWNH	4	10	16	25		10424
TAT	ACNNCYCK	24	8	17	27		10425
TAT	TACNNCYCK	23	9	17	27		10426
TAT	PTGPKESKK	88	9	18	28		10427
TAT	TGPKESKK	89	8	19	30		10428
TAT	PTGPKESK	88	8	20	31		10429
TAT	YGRKKRRQRR	50	11	22	34		10430
TAT	PGSQPKTA	17	8	26	41		10431

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
TAT	YGRKKRRQRR	50	10	38	59		10432
TAT	ISYGRKKRRQR	48	11	39	61		10433
TAT	YGRKKRRQR	50	9	41	64		10434
TAT	GISYGRKKRR	47	10	45	70	0.0003	10435
TAT	LGISYGRKKRR	46	11	45	70		10436
TAT	ISYGRKKRR	48	9	46	72	0.0008	10437
TAT	GLGISYGRKKR	45	11	54	86		10438
TAT	GLGISYGR	45	8	55	87		10439
TAT	GLGISYGRK	45	9	55	87	0.0340	10440
TAT	GLGISYGRKK	45	10	55	87		10441
TAT	KGLGISYGR	44	9	55	86	0.0006	10442
TAT	KGLGISYGRK	44	10	55	86	0.0100	10443
TAT	KGLGISYGRKK	44	11	55	86		10444
TAT	GISYGRKKR	47	9	57	89	0.0008	10445
TAT	LGISYGRKKR	46	10	57	89		10446
TAT	LGISYGRK	46	8	58	91		10447
TAT	GISYGRKK	47	8	58	91		10448
TAT	ISYGRKKR	48	8	58	91		10449
TAT	LGISYGRKK	46	9	58	91	0.0004	10450
VIF	LIVWQVDR	8	8	10	16		10451
VIF	RMRINTWK	15	8	10	16		10452
VIF	LIKPKKIK	158	8	10	16		10453
VIF	KGWFYRHHY	36	9	10	16		10454
VIF	ALIKPKKIK	157	9	10	16		10455
VIF	VDRMRINTWK	13	10	10	16		10456
VIF	GVSIEWRLRR	87	10	10	16		10457
VIF	QVDRMRINTW	12	11	10	16		10458
VIF	RLVITTYWGL	65	11	10	16		10459
VIF	QTGERDWHLG	75	11	10	16		10460
VIF	GVSIEWRLRR	87	11	10	16		10461
VIF	IDPDLADQLHP	103	11	10	16		10462
VIF	LVEDRWNKPQ	178	11	10	16		10463
VIF	YSTQIDPDLA	99	10	11	17		10464
VIF	YSTQVDPGLA	99	10	11	17		10465
VIF	SIEWRLRR	89	8	11	17		10466
VIF	TALIKPKK	156	8	11	17		10467
VIF	LVEDRWNK	178	8	11	17		10468
VIF	VSIEWRLRR	88	9	11	17		10469
VIF	SIEWRLRRY	89	9	11	17		10470
VIF	STQVDPGLA	100	9	11	17		10471
VIF	SLQYLALKA	149	9	11	17		10472
VIF	LTALIKPKK	155	9	11	17		10473
VIF	KLVEDRWNK	177	9	11	17		10474
VIF	VSIEWRLRRY	88	10	11	17		10475
VIF	GLADQLIHMH	106	10	11	17		10476
VIF	IVSPRCEYQA	133	10	11	17		10477
VIF	GSLQYLALKA	148	10	11	17		10478
VIF	ALTALIKPKK	154	10	11	17		10479
VIF	PGLADQLIHMH	105	11	11	17		10480
VIF	GLADQLIHMH	106	11	11	17		10481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	VGSLQYLALK	147	11	11	17		10482
VIF	LALTALIKPKK	153	11	11	17		10483
VIF	WFYRHHYESR	38	11	12	19		10484
VIF	KGWFYRHH	36	8	12	19		10485
VIF	WGLQTGER	72	8	12	19		10486
VIF	QTGERDWH	75	8	12	19		10487
VIF	SDSAIRKA	121	8	12	19		10488
VIF	SLQYLALA	149	8	12	19		10489
VIF	IVWQVDRMK	9	9	12	19		10490
VIF	STQIDPDLA	100	9	12	19		10491
VIF	FSDSAIRKA	120	9	12	19		10492
VIF	FSESAIRNA	120	9	12	19		10493
VIF	GSLQYLALA	148	9	12	19		10494
VIF	SLQYLALAA	149	9	12	19		10495
VIF	KIRTWNSLVK	17	10	12	19		10496
VIF	LVKHHMYVSK	24	10	12	19		10497
VIF	GLQTGERDWH	73	10	12	19		10498
VIF	TGERDWHLGH	77	10	12	19		10499
VIF	HGVSIEWRLR	86	10	12	19		10500
VIF	CFSDSAIRKA	119	10	12	19		10501
VIF	CFSESAIRNA	119	10	12	19		10502
VIF	VGSLQYLALA	147	10	12	19		10503
VIF	GSLQYLALAA	148	10	12	19		10504
VIF	IVWQVDRMKI	9	11	12	19		10505
VIF	KIRTWNSLVK	17	11	12	19		10506
VIF	SLVKHHMYVS	23	11	12	19		10507
VIF	LVKHHMYVSK	24	11	12	19		10508
VIF	WGLQTGERD	72	11	12	19		10509
VIF	DCFSESAIRKA	118	11	12	19		10510
VIF	DCFSESAIRNA	118	11	12	19		10511
VIF	KVGSLQYLAL	146	11	12	19		10512
VIF	VGSLQYLALA	147	11	12	19		10513
VIF	WFYRHHYESR	38	10	13	21		10514
VIF	QVDRMKIR	12	8	13	20		10515
VIF	HMYVSKKA	28	8	13	20		10516
VIF	HIPLGDAR	56	8	13	20		10517
VIF	ADQLHHMH	108	8	13	20		10518
VIF	CFSDSAIR	119	8	13	20		10519
VIF	FSDSAIRK	120	8	13	20		10520
VIF	SLQYLALK	149	8	13	20		10521
VIF	LTALIKPK	155	8	13	20		10522
VIF	LADQLHHMH	107	9	13	20		10523
VIF	ADQLHHMHY	108	9	13	20		10524
VIF	CFSDSAIRK	119	9	13	20		10525
VIF	FSESAIRKA	120	9	13	20		10526
VIF	GSLQYLALK	148	9	13	20		10527
VIF	ALTALIKPK	154	9	13	20		10528
VIF	SVKKLTEDR	174	9	13	20		10529
VIF	EVHIPLGDAR	54	10	13	20		10530
VIF	LADQLHHMHY	107	10	13	20		10531

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	ADQLIHMHYF	108	10	13	20		10532
VIF	DCFSESAIRK	118	10	13	20		10533
VIF	CFSESAIRKA	119	10	13	20		10534
VIF	VGSLQYLALK	147	10	13	20		10535
VIF	LALTALIKPK	153	10	13	20		10536
VIF	PSVKKLTEDR	173	10	13	20		10537
VIF	LADQLIHMHYF	107	11	13	20		10538
VIF	QLIHLYYFDCF	110	11	13	20		10539
VIF	FDCFSESAIRK	117	11	13	20		10540
VIF	YLALTALIKPK	152	11	13	20		10541
VIF	QLIHLYYF	110	8	14	22		10542
VIF	QLIHMHYF	110	8	14	22		10543
VIF	FSESAIRK	120	8	14	22		10544
VIF	IVSPRCEY	133	8	14	22		10545
VIF	GVSIEWRLR	87	9	14	22		10546
VIF	ADQLIHLYY	108	9	14	22		10547
VIF	CFSESAIRK	119	9	14	22		10548
VIF	VDRMRIRTWK	13	10	14	22		10549
VIF	LADQLIHLYY	107	10	14	22		10550
VIF	ADQLIHLYYF	108	10	14	22		10551
VIF	RCDYQAGHNK	137	10	14	22		10552
VIF	QVDRMRIRTW	12	11	14	22		10553
VIF	RIRTWNSLVK	17	11	14	22		10554
VIF	LADQLIHLYYF	107	11	14	22		10555
VIF	QLIHMHYFDCF	110	11	14	22		10556
VIF	RMRIRTWK	15	8	15	23		10557
VIF	RTWKSLVK	19	8	15	23		10558
VIF	VSIEWRLR	88	8	15	23		10559
VIF	ADQLIHLY	108	8	15	23		10560
VIF	HMHYFDCF	113	8	15	23		10561
VIF	RTWKSLVKH	19	9	15	23		10562
VIF	QGVSIEWRK	86	9	15	23		10563
VIF	LADQLIHLY	107	9	15	23		10564
VIF	AIRKAILGH	124	9	15	23		10565
VIF	CDYQAGHNK	138	9	15	23		10566
VIF	RIRTWKSLVK	17	10	15	23		10567
VIF	RIRTWNSLVK	17	10	15	23		10568
VIF	RTWKSLVKHH	19	10	15	23		10569
VIF	LIHMHYFDCF	111	10	15	23		10570
VIF	SAIRKAILGH	123	10	15	23		10571
VIF	RIRTWKSLVK	17	11	15	23		10572
VIF	LGQGVSIEWR	84	11	15	23		10573
VIF	VDPGLADQLIH	103	11	15	23		10574
VIF	ITTYWGLH	68	8	16	25		10575
VIF	GVSIEWRK	87	8	16	25		10576
VIF	HLYYFDCF	113	8	16	25		10577
VIF	RCDYQAGH	137	8	16	25		10578
VIF	LALTALIK	153	8	16	25		10579
VIF	VITTYWGLH	67	9	16	25		10580
VIF	YLALTALIK	152	9	16	25		10581

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	KTKGHRGSH	188	9	16	25	0.0004	10582
VIF	LVITTYWGLH	66	10	16	25		10583
VIF	LHLYYFDCF	111	10	16	25		10584
VIF	EDRWNKPQKT	180	11	17	27		10585
VIF	KSLVKHHMY	22	9	18	28		10586
VIF	EDRWNKPQKT	180	11	18	28		10587
VIF	RCEYQAGHNK	137	10	19	30		10588
VIF	HIPLGEAR	56	8	20	31		10589
VIF	EVHIPLGEAR	54	10	20	31		10590
VIF	HTGERDWH	75	8	21	33		10591
VIF	DLADQLIH	106	8	21	33		10592
VIF	PDLADQLIH	105	9	21	33		10593
VIF	VSPRCEYQA	134	9	21	33		10594
VIF	GLHTGERDWH	73	10	21	33		10595
VIF	WGLHTGERD	72	11	21	33		10596
VIF	VSPRCEYQAG	134	11	21	33		10597
VIF	LTEDRWNKPQ	178	11	21	33	0.0390	10598
VIF	GSHTMNGH	194	8	22	34		10599
VIF	RGSHTMNGH	193	9	22	34		10600
VIF	TTYWGLHTGE	69	11	22	34		10601
VIF	HLGHGVSIEW	83	11	22	34		10602
VIF	SSEVHIPLGDA	52	11	23	36		10603
VIF	NSLVKHHMY	22	9	24	38		10604
VIF	EVHIPLGDA	54	9	24	38		10605
VIF	QGVSIEWR	86	8	25	39		10606
VIF	EVHIPLGEA	54	9	25	39		10607
VIF	LGQGVSIEWR	84	10	25	39		10608
VIF	SSEVHIPLGEA	52	11	25	39		10609
VIF	HLGQGVSIEW	83	11	25	39		10610
VIF	RCEYQAGH	137	8	26	41		10611
VIF	RTWNSLVKH	19	9	26	41		10612
VIF	RTWNSLVKHH	19	10	26	41		10613
VIF	RTWNSLVK	19	8	27	42		10614
VIF	HGVSIEWR	86	8	27	42		10615
VIF	GLADQLIH	106	8	27	42		10616
VIF	PGLADQLIH	105	9	27	42		10617
VIF	LGHGVSIEWR	84	10	27	42		10618
VIF	YFDCFSESAIR	116	11	27	42		10619
VIF	WGLHTGER	72	8	28	44		10620
VIF	YFDCFSESA	116	9	28	44		10621
VIF	DCFSESAIR	118	9	28	44		10622
VIF	FDCFSESAIR	117	10	28	44		10623
VIF	FDCFSESA	117	8	29	45		10624
VIF	CFSESAIR	119	8	29	45		10625
VIF	KLTEDRWNK	177	9	29	45	0.0130	10626
VIF	VGSLQYLALT	147	11	30	47		10627
VIF	LTEDRWNK	178	8	31	48	0.0003	10628
VIF	SLQYLALTA	149	9	31	48		10629
VIF	GSLQYLALTA	148	10	31	48		10630
VIF	IVWQVDRMRI	9	11	33	52		10631

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	QVDRMRIR	12	8	34	53		10632
VIF	EDRWNKPQK	180	9	39	61		10633
VIF	VMIVWQVDR	7	11	41	64		10634
VIF	QVMIVWQVDR	6	10	43	67		10635
VIF	MIVWQVDRM	8	10	43	67	0.0062	10636
VIF	AGHNKVGSLQ	142	11	43	67		10637
VIF	SLVKHHMY	23	8	44	69		10638
VIF	VMIVWQVDR	7	9	44	69	0.0034	10639
VIF	MIVWQVDR	8	8	46	72		10640
VIF	IVWQVDRMR	9	9	47	73	0.0008	10641
VIF	KVGSLQYLA	146	9	52	81	0.0036	10642
VIF	VGSLQYLA	147	8	58	91		10643
VPR	#LPGRRGR	85	8	01	50		10644
VPR	NIRGRRVR	85	8	01	50		10645
VPR	#LPGRRGRNG	85	11	01	50		10646
VPR	WALELLEELK	18	10	09	15		10647
VPR	QLLFVHFR	66	8	10	16		10648
VPR	HSRIGHR	79	8	10	16		10649
VPR	RIGITRQR	81	8	10	16		10650
VPR	IGITRQRR	82	8	10	16		10651
VPR	ALELLEELK	19	9	10	16		10652
VPR	RIGITRQRR	81	9	10	16		10653
VPR	HSRIGITRQR	79	10	10	16		10654
VPR	HSRIGITRQRR	79	11	10	16		10655
VPR	WLHGLGQY	38	8	11	17		10656
VPR	HFRIGCRH	71	8	11	17		10657
VPR	HSRIGITR	79	8	11	17		10658
VPR	FHHFRIGCR	69	9	11	17		10659
VPR	LFHHFRIGCR	68	10	11	17		10660
VPR	FHHFRIGCRH	69	10	11	17		10661
VPR	FVHFRIGCQH	69	10	11	17		10662
VPR	HFRIGCRHSR	71	10	11	17		10663
VPR	LLFHHFRIGCR	67	11	11	17		10664
VPR	LFHHFRIGCRH	68	11	11	17		10665
VPR	LFVHFRIGCQH	68	11	11	17		10666
VPR	RIGCRHSR	74	8	12	19		10667
VPR	LGQHHYNTY	42	9	13	20		10668
VPR	LGQYIYETY	42	9	13	20		10669
VPR	HFPRIWLH	33	8	14	22		10670
VPR	KSEAVRHFPR	27	10	14	22		10671
VPR	AVRHFPRIWL	30	11	14	22		10672
VPR	KSEAVRHF	27	8	15	23		10673
VPR	ELKSEAVRHF	25	10	15	23		10674
VPR	ELKSEAVR	25	8	16	25		10675
VPR	ETYGDTWA	48	8	16	25		10676
VPR	DTWAGVEA	52	8	16	25		10677
VPR	AGVEAHR	55	8	16	25		10678
VPR	LLEELKSEA	22	9	16	25		10679
VPR	ELKSEAVRH	25	9	16	25		10680
VPR	GDTWAGVEA	51	9	16	25		10681

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPR	WAGVEAIIR	54	9	16	25		10682
VPR	ELLEELKNEA	21	10	16	25		10683
VPR	ELLEELKSEA	21	10	16	25		10684
VPR	YGDTWAGVEA	50	10	16	25		10685
VPR	LLEELKSEAVR	22	11	16	25		10686
VPR	DTWAGVEAIIR	52	11	16	25		10687
VPR	ELKNEAVR	25	8	17	27		10688
VPR	LLEELKNEA	22	9	17	27		10689
VPR	ELKNEAVRH	25	9	17	27		10690
VPR	LGQHIYETY	42	9	17	27		10691
VPR	ELKNEAVRHF	25	10	17	27		10692
VPR	LLEELKNEAVR	22	11	17	27		10693
VPR	EGVEAIIR	55	8	18	28		10694
VPR	DTWEGVEAIIR	52	11	18	28		10695
VPR	RARNGASR	93	8	19	30		10696
VPR	WLHGLGQH	38	8	20	31		10697
VPR	HGLGQHIY	40	8	20	31		10698
VPR	WLHGLGQHIY	38	10	20	31		10699
VPR	DTWEGVEA	52	8	23	36		10700
VPR	GDTWEGVEA	51	9	23	36		10701
VPR	YGDTWEGVEA	50	10	23	36		10702
VPR	LFIHFRIGCQH	68	11	29	45		10703
VPR	FIHFRIGCQH	69	10	30	47		10704
VPR	HFPRPWLH	33	8	31	49		10705
VPR	AVRHFPRPWL	30	11	31	48		10706
VPR	RILQQLLFIHF	62	11	34	53		10707
VPR	ILQQLLFIHF	63	10	35	55	0.0130	10708
VPR	ILQQLLFIHFR	63	11	35	55		10709
VPR	RILQQLLFIH	62	10	36	56		10710
VPR	ILQQLLFIH	63	9	37	58		10711
VPR	EDQGPQREPY	6	10	37	58		10712
VPR	AIIRILQQLLF	59	11	38	59		10713
VPR	QAPEDQGPQR	3	10	39	62		10714
VPR	IIRILQQLLF	60	10	41	64		10715
VPR	WTLELLEELK	18	10	42	69		10716
VPR	QGPQREPY	8	8	43	68		10717
VPR	QLLFIHFR	66	8	44	69		10718
VPR	HFRIGCQH	71	8	44	69		10719
VPR	TLELLEELK	19	9	44	69		10720
VPR	HFRIGCQHSR	71	10	44	69		10721
VPR	RILQQLLF	62	8	45	70		10722
VPR	RIGCQHSR	74	8	47	73		10723
VPR	EAVRHFPR	29	8	59	92		10724
VPU	IDYRLGVGA	9	9	01	33		10725
VPU	VDYRIVIVA	9	9	01	33		10726
VPU	VDYRLGVGA	9	9	01	33		10727
VPU	KVDYRIVIVA	7	10	01	33		10728
VPU	KVDYRLGVGA	7	10	01	33		10729
VPU	RIDYRLGVGA	7	10	01	33		10730
VPU	VDYRIVIVAF	9	10	01	33		10731

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPU	KVDYRIVIVAF	7	11	01	33		10732
VPU	LVQRKQDR	43	8	01	50		10733
VPU	GVEMGHHA	91	8	01	50		10734
VPU	VTLLSSSK	94	8	01	50		10735
VPU	LVQRKQDRR	43	9	01	50		10736
VPU	LVTLLSSSK	91	9	01	50		10737
VPU	RIKEIRDDSDY	64	11	01	50		10738
VPU	RIREIRDDSDY	64	11	01	50		10739
VPU	LAIVALVVA	13	9	09	15		10740
VPU	WTIVFIEYR	34	9	10	16		10741
VPU	TIVFIEYR	35	8	10	16		10742
VPU	IDRLIDRIR	54	9	10	16		10743
VPU	RLIDRIRER	56	9	10	16		10744
VPU	KIDRLIDRIR	52	10	10	16		10745
VPU	VVWTIVFIEYR	31	11	10	16		10746
VPU	ESEGDQEELSA	75	11	10	16		10747
VPU	EGDQEELSA	77	9	11	17		10748
VPU	WTIVFIEY	34	8	12	19		10749
VPU	AIVALVVA	14	8	12	19		10750
VPU	IVFIEYRK	36	8	12	19		10751
VPU	IDRIRERA	59	8	12	19		10752
VPU	LIDRIRERA	58	9	12	19		10753
VPU	VVWTIVFIEY	31	10	12	19		10754
VPU	IVVWTIVFIEY	30	11	12	19		10755
VPU	GDQEELSA	78	8	14	22		10756
VPU	LIDRIRER	58	8	14	22		10757
VPU	AIVVWTIVF	29	9	14	22		10758
VPU	IVVWTIVF	30	8	15	23		10759
VPU	KIDRLIDR	52	8	15	23		10760
VPU	ILRQRKIDR	46	9	15	23		10761
VPU	KILRQRKIDR	45	10	15	23	0.0039	10762

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	IGPGQTFY	361	8	01	25		10763
ENV	IGSGQAFY	361	8	01	25		10764
ENV	GTAGNSSR	375	8	01	33		10765
ENV	NNTSPRSR	375	8	01	33		10766
ENV	ADNLWVTVY	42	9	01	33		10767
ENV	GIGPGQTFY	360	9	01	33		10768
ENV	SIGSGQAFY	360	9	01	33		10769
ENV	ADNLWVTVYY	42	10	01	33		10770
ENV	EGKNEINDTY	217	10	01	33		10771
ENV	NTSPRSRVAY	376	10	01	33		10772
ENV	TAGNSSRAAY	376	10	01	33		10773
ENV	GTAGNSSRAA	375	11	01	33		10774
ENV	NNTSPRSRVA	375	11	01	33		10775
ENV	KLREIRQFENK	405	11	01	25		10776
ENV	KNNTETNK	535	8	01	50		10777
ENV	HINHITPH	584	8	01	50		10778
ENV	VISTRTHR	584	8	01	50		10779
ENV	INHITPHR	585	8	01	50		10780
ENV	STRTHREK	586	8	01	50		10781
ENV	SNNTSPRSR	374	9	01	50		10782
ENV	NANITIPCR	478	9	01	50		10783
ENV	HINHITPHR	584	9	01	50		10784
ENV	ISTRTHREK	585	9	01	50		10785
ENV	NHITPHREK	586	9	01	50		10786
ENV	STRTHREKR	586	9	01	50		10787
ENV	VISTRTHREK	584	10	01	50		10788
ENV	INHITPHREK	585	10	01	50		10789
ENV	ISTRTHREKR	585	10	01	50		10790
ENV	NHITPHREKR	586	10	01	50		10791
ENV	HTEGNITLQCR	478	11	01	50		10792
ENV	NANITIPCRIK	478	11	01	50		10793
ENV	GNSTNGTETF	535	11	01	50		10794
ENV	HINHITPHREK	584	11	01	50		10795
ENV	VISTRTHREKR	584	11	01	50		10796
ENV	INHITPHREKR	585	11	01	50		10797
ENV	DSSNSTGNY	218	9	01	20		10798
ENV	STNGTETFR	537	9	01	17		10799
ENV	TNSSYTNDTY	458	10	01	17		10800
ENV	NDTENNTEIFR	537	11	01	17		10801
ENV	NTETNKTETF	537	11	01	17		10802
ENV	NTTGNTTETF	537	11	01	17		10803
ENV	NGSENGTETF	537	11	02	33		10804
ENV	GSENGTETFR	538	10	02	18		10805
ENV	NDTITLPCR	477	9	03	20		10806
ENV	NDTITLPCRIK	477	11	03	20		10807
ENV	RGWEALKY	895	8	06	19		10808
ENV	KGLRLGWEGL	891	11	08	27		10809
ENV	LGWEGLKY	895	8	09	29		10810
ENV	RLGWEGLKY	894	9	09	29		10811
ENV	GLRLGWEGLK	892	11	09	29		10812

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	LGRRGWEALK	883	10	09	15		10813
ENV	LLGRRGWEAL	882	11	09	15		10814
ENV	RLGWEGLK	894	8	10	32		10815
ENV	GLRLGWEGLK	892	10	10	32		10816
ENV	ENLWVTVY	43	8	10	17		10817
ENV	ENLWVTVYY	43	9	10	17		10818
ENV	DIIGDIRQAH	372	10	10	16		10819
ENV	NNTRKSIR	350	8	10	16		10820
ENV	PLGVAPTR	571	8	10	16		10821
ENV	DITNWLWY	769	8	10	16		10822
ENV	DFILIAAR	870	8	10	16		10823
ENV	STITQACPK	243	9	10	16		10824
ENV	FDITNWLWY	768	9	10	16		10825
ENV	RDFILIAAR	869	9	10	16		10826
ENV	FAILKCNDKK	269	10	10	16		10827
ENV	MLQLTVWGIK	651	10	10	16		10828
ENV	RVLAVERYLR	665	10	10	16		10829
ENV	WFDITNWLW	767	10	10	16		10830
ENV	EGIEEEGGER	828	10	10	16		10831
ENV	GFAILKCNDKK	268	11	10	16		10832
ENV	GDIIGDIRQAH	371	11	10	16		10833
ENV	NVPWNSSWSN	693	11	10	16		10834
ENV	WMEWEREIDN	723	11	10	16		10835
ENV	IAIAVAEGTDR	925	11	10	16		10836
ENV	RGWEALKY	886	8	11	18		10837
ENV	KLWVTVYY	44	8	11	17		10838
ENV	WNSSWSNR	696	8	11	17		10839
ENV	TITQACPK	244	8	11	17		10840
ENV	IGPGQTFY	358	8	11	17		10841
ENV	LAVERYLR	667	8	11	17		10842
ENV	SNWLWYIK	771	8	11	17		10843
ENV	NLCLFSYH	859	8	11	17		10844
ENV	RIGPGQTFY	357	9	11	17		10845
ENV	ITTHSFNCR	431	9	11	17		10846
ENV	NITLPCRIK	482	9	11	17		10847
ENV	VLAVERYLR	666	9	11	17		10848
ENV	ISNWLWYIK	770	9	11	17		10849
ENV	RNLCLFSYH	858	9	11	17		10850
ENV	NLCLFSYHR	859	9	11	17		10851
ENV	EITTHSFNCR	430	10	11	17		10852
ENV	RNLCLFSYHR	858	10	11	17		10853
ENV	YATGDIIGDIR	368	11	11	17		10854
ENV	DLRNLCLFSYH	856	11	11	17		10855
ENV	NLCLFSYHRLR	859	11	11	17		10856
ENV	GNLWVTVY	43	8	12	20		10857
ENV	GNLWVTVYY	43	9	12	20		10858
ENV	TGDIIGDIR	370	9	12	19		10859
ENV	EAQQHLLK	646	8	12	19		10860
ENV	ILKCNDKK	271	8	12	19		10861
ENV	TTHSFNCR	432	8	12	19		10862

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	MTWMEWER	721	8	12	19		10863
ENV	GGERDRDR	834	8	12	19		10864
ENV	AILKCNDKK	270	9	12	19		10865
ENV	LAEEEVVIR	312	9	12	19	0.0002	10866
ENV	INMWQEVGK	493	9	12	19		10867
ENV	NMTWMEWER	720	9	12	19		10868
ENV	GIEEEGGER	829	9	12	19		10869
ENV	EGGERDRDR	833	9	12	19		10870
ENV	SLAEEEVVIR	311	10	12	19		10871
ENV	ATGDIIGDIR	369	10	12	19		10872
ENV	IINMWQEVGK	492	10	12	19		10873
ENV	AIEAQQHLLK	644	10	12	19		10874
ENV	LLQYWSQELK	906	10	12	19		10875
ENV	AILHIPRRIR	946	10	12	19		10876
ENV	PTRIRQGLER	951	10	12	19		10877
ENV	KTTLFCASDA	60	11	12	19		10878
ENV	GSLAEEEVVIR	310	11	12	19		10879
ENV	QIINMWQEVG	491	11	12	19		10880
ENV	KNEQELLELDK	750	11	12	19		10881
ENV	GIEEEGGERDR	829	11	12	19		10882
ENV	NLLQYWSQEL	905	11	12	19		10883
ENV	RAILHIPRRIR	945	11	12	19		10884
ENV	SVEINCTR	340	8	13	20		10885
ENV	GDIIGDIR	371	8	13	20		10886
ENV	KLTVWGIK	653	8	13	20		10887
ENV	RAILHIPR	945	8	13	20		10888
ENV	AILHIPRR	946	8	13	20		10889
ENV	KAKRRVVQR	579	9	13	20	0.0002	10890
ENV	RAILHIPRR	945	9	13	20		10891
ENV	ILHIPRRIR	947	9	13	20		10892
ENV	TNVSTVQCTH	286	10	13	20		10893
ENV	SGGDPEIVMH	425	10	13	20		10894
ENV	LLKLTVWGIK	651	10	13	20		10895
ENV	NTSVITQACPK	241	11	13	20		10896
ENV	CTNVSTVQCT	285	11	13	20		10897
ENV	SSGGDLEITTH	424	11	13	20		10898
ENV	SSGGDPEIVMH	424	11	13	20		10899
ENV	PTKAKRRVVQ	576	11	13	20		10900
ENV	KAKRRVVQRE	579	11	13	20		10901
ENV	HLLKLTVWGI	650	11	13	20		10902
ENV	KNEQDLLALD	750	11	13	20		10903
ENV	TGEIIGDIR	370	9	14	23		10904
ENV	AITQACPK	244	8	14	22		10905
ENV	GDPEIVMH	427	8	14	22		10906
ENV	QDLLALDK	753	8	14	22		10907
ENV	SAITQACPK	243	9	14	22		10908
ENV	FAILKCNDK	269	9	14	22	0.0002	10909
ENV	GGDPEIVMH	426	9	14	22		10910
ENV	TITLPCRIK	482	9	14	22		10911
ENV	TSAITQACPK	242	10	14	22		10912

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	TSVITQACPK	242	10	14	22		10913
ENV	GFAILKCNDK	268	10	14	22		10914
ENV	IFAVLSIVNR	793	10	14	22		10915
ENV	NTSAITQACPK	241	11	14	22		10916
ENV	AGFAILKCNDK	267	11	14	22		10917
ENV	HFAVLSIVNR	792	11	14	22		10918
ENV	KIEPLGVAPTK	568	11	15	24		10919
ENV	FDPIPIHY	255	8	15	23		10920
ENV	PAGYAILK	266	8	15	23		10921
ENV	NMWQEVGK	494	8	15	23		10922
ENV	TNWLWYIK	771	8	15	23		10923
ENV	ITNWLWYIK	770	9	15	23		10924
ENV	SGGDLEITTH	425	10	15	23		10925
ENV	IFRPGGGDMR	545	10	15	23		10926
ENV	NMWQEVGKA	494	11	15	23		10927
ENV	EIFRPGGGDMR	544	11	15	23		10928
ENV	DDLRNLCLFSY	855	11	15	23		10929
ENV	FNGTGPCK	279	8	16	25		10930
ENV	RNLCLFSY	858	8	16	25		10931
ENV	ITKWLWYIK	770	9	16	25		10932
ENV	SFNCRGEFFY	437	10	16	25		10933
ENV	DLRNLCLFSY	856	10	16	25		10934
ENV	HSFNCRGEFFY	434	11	16	25		10935
ENV	WNASWSNK	696	8	17	27		10936
ENV	KAYDTEVH	72	8	17	27		10937
ENV	VITQACPK	244	8	17	27		10938
ENV	RVVQREKR	587	8	17	27	0.0001	10939
ENV	SVITQACPK	243	9	17	27		10940
ENV	VAPTKAKRR	574	9	17	27	0.0002	10941
ENV	DAKAYDTEVH	70	10	17	27		10942
ENV	GVAPTKAKRR	573	10	17	27		10943
ENV	VFAVLSIVNR	793	10	17	27		10944
ENV	SDAKAYDTEV	69	11	17	27		10945
ENV	DTEVHNVWAT	75	11	17	27		10946
ENV	NCTRPNNNTR	344	11	17	27		10947
ENV	LGVAPTKAKR	572	11	17	27		10948
ENV	IVFAVLSIVNR	792	11	17	27		10949
ENV	WNSSWSNK	696	8	18	29		10950
ENV	ENVTENFNMW	100	11	18	29		10951
ENV	VLAVERYLK	666	9	18	28		10952
ENV	RVLAVERYLK	665	10	18	28		10953
ENV	NCRGEFFY	439	8	19	30		10954
ENV	GVAPTKAK	573	8	19	30		10955
ENV	VAPTKAKR	574	8	19	30		10956
ENV	FNCRGEFFY	438	9	19	30		10957
ENV	LGVAPTKAK	572	9	19	30		10958
ENV	GVAPTKAKR	573	9	19	30		10959
ENV	PLGVAPTKAK	571	10	19	30		10960
ENV	LGVAPTKAKR	572	10	19	30		10961
ENV	SSNITGLLLTR	516	11	19	30		10962

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	PLGVAPTKAK	571	11	19	30		10963
ENV	AILKCNDK	270	8	20	31		10964
ENV	ETFRPGGGDM	544	11	20	31		10965
ENV	LIEESQNQQEK	740	11	20	31		10966
ENV	GDLEITTH	427	8	21	33		10967
ENV	GGDLEITTH	426	9	21	33		10968
ENV	TAIAVAEGTDR	925	11	21	33		10969
ENV	RIVELLGR	878	8	22	34		10970
ENV	IVELLGRR	879	8	22	34		10971
ENV	RIVELLGRR	878	9	22	34	0.0100	10972
ENV	NCTRPNNNTR	344	10	22	34		10973
ENV	CTRPNNNTRK	345	10	22	34		10974
ENV	TTTLFCASDA	60	11	22	34		10975
ENV	INCTRPNNNTR	343	11	22	34		10976
ENV	TVQCTHGIR	290	9	23	36	0.0008	10977
ENV	STVQCTHGIR	289	10	23	36		10978
ENV	VSTVQCTHGIR	288	11	23	36		10979
ENV	TFRPGGGDMR	545	10	24	38		10980
ENV	ALAWDDLR	851	8	25	39		10981
ENV	LALAWDDLR	850	9	25	39		10982
ENV	KNVSTVQCTH	286	10	25	39		10983
ENV	IVQQQNNLLR	634	10	25	39	0.0190	10984
ENV	FLALAWDDLR	849	10	25	39		10985
ENV	GIVQQQNNLLR	633	11	25	39		10986
ENV	GFLALAWDDL	848	11	25	39		10987
ENV	ITLPCRIK	483	8	26	41		10988
ENV	PLGVAPTK	571	8	26	41		10989
ENV	LAVERYLK	667	8	26	41		10990
ENV	KNNMVEQMH	110	9	26	41		10991
ENV	IVQQQSNLLR	634	10	26	41		10992
ENV	GIVQQQSNLLR	633	11	26	41		10993
ENV	HGDIRQAH	377	9	27	44		10994
ENV	ESQNQQEK	743	8	27	42		10995
ENV	IGDIRQAH	378	8	28	44		10996
ENV	NNMVEQMH	111	8	28	44		10997
ENV	TVQCTHGIK	290	9	28	44	0.0460	10998
ENV	CTRPNNNTR	345	9	28	44		10999
ENV	VSFEPIPIHY	253	10	28	44		11000
ENV	STVQCTHGIK	289	10	28	44		11001
ENV	ASITLTVQAR	619	10	28	44		11002
ENV	KVSFEPIPIHY	252	11	28	44		11003
ENV	YCAPAGFAILK	263	11	28	44		11004
ENV	VSTVQCTHGIK	288	11	28	44		11005
ENV	AASITLTVQAR	618	11	28	44		11006
ENV	VSFEPIPIH	253	9	29	45		11007
ENV	KVSFEPIPIH	252	10	29	45		11008
ENV	CAPAGFAILK	264	10	29	45		11009
ENV	RSELYKYKVV	558	11	29	45		11010
ENV	AVLSIVNR	795	8	31	48		11011
ENV	AVAEGTDR	928	8	31	48		11012

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	VTENFNMWK	102	9	31	48		11013
ENV	SFEPIPHY	254	9	31	48		11014
ENV	FAVLSIVNR	794	9	31	48		11015
ENV	SLCLFSYHR	859	9	31	48		11016
ENV	IAVAEGTDR	927	9	31	48	0.0003	11017
ENV	NVTENFNMW	101	10	31	48		11018
ENV	AVLSIVNRVR	795	10	31	48		11019
ENV	RSLCLFSYHR	858	10	31	48		11020
ENV	AIAVAEGTDR	926	10	31	48		11021
ENV	FAVLSIVNRVR	794	11	31	48		11022
ENV	DDLRSLCLFSY	855	11	31	48		11023
ENV	SLCLFSYHRLR	859	11	31	48		11024
ENV	ELYKYKVVK	560	9	32	51		11025
ENV	RVVEREKR	587	8	32	50		11026
ENV	ITLTVQAR	621	8	32	50		11027
ENV	SLCLFSYH	859	8	32	50		11028
ENV	SITLTVQAR	620	9	32	50		11029
ENV	RSLCLFSYH	858	9	32	50		11030
ENV	DLRSLCLFSYH	856	11	32	50		11031
ENV	SFEPIPIH	254	8	33	52		11032
ENV	RVLAVERY	665	8	33	52		11033
ENV	QARVLAVER	663	9	33	52	0.0003	11034
ENV	QARVLAVERY	663	10	33	52		11035
ENV	QLQARVLAVE	661	11	33	52		11036
ENV	IMIVGGLIGLR	781	11	34	54		11037
ENV	LLQLTVWGIK	651	10	34	53	0.0110	11038
ENV	HLLQLTVWGI	650	11	34	53		11039
ENV	LSIVNRVRQGY	797	11	34	53		11040
ENV	NLWVTVYY	44	8	35	56		11041
ENV	NCGGEFFY	439	8	35	55		11042
ENV	RSLCLFSY	858	8	35	55		11043
ENV	EVHNVWATH	77	9	35	55		11044
ENV	FNCGGEFFY	438	9	35	55		11045
ENV	NITGLLLTR	519	9	35	55	0.0001	11046
ENV	SFNCGGEFFY	437	10	35	55		11047
ENV	SNITGLLLTR	517	10	35	55	0.0014	11048
ENV	DLRSLCLFSY	856	10	35	55		11049
ENV	HSFNCGGEFFY	434	11	35	55		11050
ENV	GGGDMRDNW	549	10	36	56		11051
ENV	MIVGGLIGLR	782	10	36	56		11052
ENV	SIVNRVRQGY	798	10	36	56	0.0008	11053
ENV	PGGGDMRDN	548	11	36	56		11054
ENV	ITGLLLTR	520	8	37	58		11055
ENV	DMRDNWRSEL	552	11	37	58		11056
ENV	PAGFAILK	266	8	38	59		11057
ENV	LSIVNRVR	797	8	38	59		11058
ENV	VLSIVNRVR	796	9	38	59		11059
ENV	IVNRVRQGY	799	9	38	59		11060
ENV	HSLWDQSLK	121	10	38	59	0.0540	11061
ENV	DHSLWDQSLK	120	11	38	59		11062

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	GDMRDNWR	551	8	39	61		11063
ENV	GGDMRDNWR	550	9	39	61		11064
ENV	RDNWRSELY	554	9	40	63	0.0001	11065
ENV	RDNWRSELYK	554	10	40	63	0.0028	11066
ENV	TLFCASDAKA	64	11	40	63		11067
ENV	RDNWRSELYK	554	11	40	63		11068
ENV	TVYYGVPVWK	48	10	41	64	7.8000	11069
ENV	VTVYYGVPVW	47	11	41	64	4.1000	11070
ENV	CASDAKAY	67	8	42	66		11071
ENV	LCLFSYHR	860	8	42	66		11072
ENV	FCASDAKAY	66	9	42	66		11073
ENV	IVGGLIGLR	783	9	42	66		11074
ENV	CLFSYHRLR	861	9	42	66		11075
ENV	LFCASDAKAY	65	10	42	66	0.0002	11076
ENV	LCLFSYHRLR	860	10	42	66		11077
ENV	VGGLIGLR	784	8	43	67		11078
ENV	QLTVWGIK	653	8	44	69		11079
ENV	LFSYHRLR	862	8	44	69		11080
ENV	RIRQGLER	959	8	44	69		11081
ENV	VNRVRQGY	800	8	45	71		11082
ENV	SLWDQSLK	123	8	47	75		11083
ENV	ISLWDQSLK	122	9	47	73	0.0890	11084
ENV	WDQSLKPCVK	125	10	47	73		11085
ENV	QSLKPCVK	127	8	48	75		11086
ENV	TVWGIKQLQA	655	11	48	75		11087
ENV	DNWRSELY	555	8	49	77		11088
ENV	GIKQLQAR	658	8	49	77		11089
ENV	DNWRSELYK	555	9	49	77	0.0014	11090
ENV	WGIKQLQAR	657	9	49	77	0.0001	11091
ENV	DNWRSELYKY	555	10	49	77	0.0001	11092
ENV	DNWRSELYKY	555	11	49	77		11093
ENV	LGIWGCSGK	679	9	50	78	0.0023	11094
ENV	TTLFCASDAK	61	10	50	78	0.2200	11095
ENV	LLGIWGCSGK	678	10	50	78	0.0120	11096
ENV	NLLRAIEAQQH	640	11	50	78		11097
ENV	QLLGIWGCSG	677	11	50	78		11098
ENV	VSTVQCTH	288	8	51	80		11099
ENV	RAIEAQQH	643	8	51	80		11100
ENV	NVSTVQCTH	287	9	51	80		11101
ENV	LLRAIEAQQH	641	10	51	80		11102
ENV	GIWGCSGK	680	8	52	81		11103
ENV	TLFCASDAK	64	9	52	81	0.5300	11104
ENV	RSELYKYK	558	8	54	84		11105
ENV	LFCASDAK	65	8	57	89		11106
GAG	AAAIMMQK	405	8	01	25		11107
GAG	SATIMMQR	405	8	01	25		11108
GAG	KDKDKELY	535	8	01	25		11109
GAG	ETIDKDLY	537	8	01	25		11110
GAG	NSATIMMQR	404	9	01	33		11111
GAG	TAPPPESFR	508	9	01	33		11112

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	NGKQANFLGK	461	10	01	25		11113
GAG	NGRQANFLGK	461	10	01	25		11114
GAG	PTAPPPESFR	507	10	01	33		11115
GAG	NGKQANFLGK	461	11	01	25		11116
GAG	NGRQANFLGK	461	11	01	25		11117
GAG	PAAADKEK	123	8	01	50		11118
GAG	ASAQQDLK	392	8	01	50		11119
GAG	ATAQQDLK	392	8	01	50		11120
GAG	AADKGVSQNY	130	10	01	50		11121
GAG	SAQQDLKGGY	393	10	01	50		11122
GAG	TAQQDLKGGY	393	10	01	50		11123
GAG	GTRPGNYVQK	480	10	01	50		11124
GAG	GTRPGNYVQR	480	10	01	50		11125
GAG	ITSLPKQEQK	526	10	01	50		11126
GAG	PAAADKEKDS	123	11	01	50		11127
GAG	GANSPVGDIY	276	11	01	50		11128
GAG	PNQPIPVGDIY	276	11	01	50		11129
GAG	ASAQQDLKGG	392	11	01	50		11130
GAG	ATAQQDLKGG	392	11	01	50		11131
GAG	EITSLPKQEQK	525	11	01	50		11132
GAG	YTAVFMQR	405	8	02	50		11133
GAG	TAPPAESFR	508	9	02	67		11134
GAG	PTAPPAESFR	507	10	02	67		11135
GAG	EGRQANFLGK	462	10	02	100		11136
GAG	AADKGKVSQN	129	11	02	18		11137
GAG	EADGKVSQNY	129	10	04	36		11138
GAG	AAAIMMQK	400	8	04	19		11139
GAG	AAIMMQKSNF	406	11	06	15		11140
GAG	KTVKCFNCGK	421	10	08	16		11141
GAG	GARASILR	2	8	10	16		11142
GAG	PGNFPQSR	483	8	10	16		11143
GAG	MGARASILR	1	9	10	16		11144
GAG	KIWPSSKGR	472	9	10	16		11145
GAG	TGNSSQVSQN	139	11	10	16		11146
GAG	NFLGKIWPSSK	468	11	10	16		11147
GAG	PVAPGQMR	243	8	10	16		11148
GAG	MMQKSNFK	409	8	10	16		11149
GAG	MMQRGNFK	409	8	10	16		11150
GAG	KLDKWEKIR	12	9	10	16		11151
GAG	GGKKKYKLK	24	9	10	16	0.0001	11152
GAG	RDTKEALDK	97	9	10	16		11153
GAG	IMMQKSNFK	408	9	10	16		11154
GAG	LGKIWPSSK	470	9	10	16		11155
GAG	PGGKKKYKLK	23	10	10	16		11156
GAG	GGKKKYKLKH	24	10	10	16		11157
GAG	AGPVAPGQMR	241	10	10	16		11158
GAG	FLGKIWPSSK	469	10	10	16		11159
GAG	KLDKWEKIRL	12	11	10	16		11160
GAG	PGGKKKYKLK	23	11	10	16		11161
GAG	LGKIWPSSKGR	470	11	10	16		11162

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	ATIMMQRGNF	406	11	11	28		11163
GAG	PSQKQEPIDK	528	10	11	18		11164
GAG	PIPVGDIY	279	8	11	17		11165
GAG	TIKCFNCGK	422	9	11	17		11166
GAG	TVKCFNCGK	422	9	11	17		11167
GAG	GNSSQVSQNY	140	10	12	23		11168
GAG	TIMMQRGNFR	407	10	12	21		11169
GAG	QTGSEELR	71	8	12	19		11170
GAG	FNCGKEGHIAR	426	11	12	19		11171
GAG	PGGKKKYK	23	8	12	19		11172
GAG	TLYCVHQK	86	8	12	19		11173
GAG	DTKEALEK	98	8	12	19		11174
GAG	MLNIVGGH	208	8	12	19		11175
GAG	PTSILDIR	303	8	12	19		11176
GAG	GSEELRSLY	73	9	12	19		11177
GAG	ATLYCVHQK	85	9	12	19		11178
GAG	KDTKEALEK	97	9	12	19		11179
GAG	MMLNIVGGH	207	9	12	19		11180
GAG	TGSEELRSLY	72	10	12	19		11181
GAG	VATLYCVHQK	84	10	12	19		11182
GAG	NMMLNIVGGH	206	10	12	19		11183
GAG	YSPTSILDIR	301	10	12	19		11184
GAG	RAEQASQEVK	329	10	12	19		11185
GAG	RLRPGGKKKY	20	11	12	19		11186
GAG	TVATLYCVHQ	83	11	12	19		11187
GAG	LNMMLNIVGG	205	11	12	19		11188
GAG	SNPPIPVGEIY	273	11	12	19		11189
GAG	TSILDIRQGPK	304	11	12	19		11190
GAG	PGNFLQNR	483	8	13	21		11191
GAG	IARNCRAPR	434	9	13	21		11192
GAG	KIWPSNKGR	472	9	13	21		11193
GAG	NCGKEGHIAR	427	10	13	21		11194
GAG	IARNCRAPRK	434	10	13	21		11195
GAG	IARNCRAPRKK	434	11	13	21		11196
GAG	NFLGKIWPSNK	468	11	13	21		11197
GAG	KGRPGNFLQN	478	11	13	21		11198
GAG	RIEVKDTK	93	8	13	20		11199
GAG	IVKCFNCGK	422	9	13	20		11200
GAG	CGKEGHIAR	428	9	13	20		11201
GAG	EGHIARNCR	431	9	13	20		11202
GAG	LGKIWPSNK	470	9	13	20		11203
GAG	KLKHIVWASR	31	10	13	20		11204
GAG	HIARNCRAPR	433	10	13	20		11205
GAG	FLGKIWPSNK	469	10	13	20		11206
GAG	EVKDTKEALD	95	11	13	20		11207
GAG	AAEWDRVHPV	230	11	13	20		11208
GAG	HIARNCRAPRK	433	11	13	20		11209
GAG	LGKIWPSNKG	470	11	13	20		11210
GAG	NSSQVSQNY	144	9	14	31		11211
GAG	NCGKEGHIAK	427	10	14	22		11212

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	FNCGKEGHIAK	426	11	14	22		11213
GAG	IAKNCRAPRKK	434	11	14	22		11214
GAG	QNAQGQMVH	157	9	14	22		11215
GAG	RGNFRNQRK	412	9	14	22		11216
GAG	CGKEGHIAK	428	9	14	22		11217
GAG	EGHIAKNCR	431	9	14	22		11218
GAG	FNTVATLYCV	81	11	14	22		11219
GAG	TVATLYCVHQ	83	11	14	22		11220
GAG	IVQNAQGQMV	155	11	14	22		11221
GAG	SSQVSQNY	145	8	15	31		11222
GAG	RSLYNTVATL	78	11	15	24		11223
GAG	FNTVATLY	81	8	15	23		11224
GAG	TLYCVHQR	86	8	15	23		11225
GAG	AAEWDRVH	230	8	15	23		11226
GAG	WDRVHPVH	233	8	15	23		11227
GAG	RGNFRNQR	412	8	15	23		11228
GAG	LFNTVATLY	80	9	15	23		11229
GAG	ATLYCVHQR	85	9	15	23	0.7100	11230
GAG	EAAEWDRVH	229	9	15	23		11231
GAG	TAPPEESFR	496	9	15	23		11232
GAG	SGGKLDAWEK	9	10	15	23		11233
GAG	SLFNTVATLY	79	10	15	23		11234
GAG	VATLYCVHQR	84	10	15	23		11235
GAG	KIEEEQNKSK	105	10	15	23		11236
GAG	RAEQATQDVK	329	10	15	23		11237
GAG	PTAPPEESFR	495	10	15	23		11238
GAG	LSGGKLDAWE	8	11	15	23		11239
GAG	PGLLETSEGCR	50	11	15	23		11240
GAG	KIEEEQNKSKK	105	11	15	23		11241
GAG	MMQRGNFRN	409	11	15	23		11242
GAG	IAKNCRAPRK	434	10	16	25		11243
GAG	LDAWEKIR	13	8	16	25		11244
GAG	NAQGQMVH	158	8	16	25		11245
GAG	PVSILDIK	303	8	16	25		11246
GAG	GNFRNQRK	413	8	16	25		11247
GAG	KLDAWEKIR	12	9	16	25		11248
GAG	GGKKKYRLK	24	9	16	25		11249
GAG	LDAWEKIRLR	13	10	16	25		11250
GAG	PGGKKKYRLK	23	10	16	25		11251
GAG	GGKKKYRLKH	24	10	16	25		11252
GAG	GLLETSEGCR	51	10	16	25		11253
GAG	YSPVSILDIK	301	10	16	25		11254
GAG	GGKLDAWEKI	10	11	16	25		11255
GAG	KLDAWEKIRL	12	11	16	25		11256
GAG	PGGKKKYRLK	23	11	16	25		11257
GAG	VSILDIKQGPK	304	11	16	25		11258
GAG	HIAKNCRAPRK	433	11	16	25		11259
GAG	PIPPGQMR	243	8	17	27		11260
GAG	GGKLDAWEK	10	9	17	27		11261
GAG	DAWEKIRLR	14	9	17	27		11262

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	LLETSEGCR	52	9	17	27		11263
GAG	RLKHLVWASR	31	10	17	27		11264
GAG	LDKIEEEQNK	103	10	17	27		11265
GAG	AGPIPPGQMR	241	10	17	27		11266
GAG	ALDKIEEEQNK	102	11	17	27		11267
GAG	LSPRTLNAWV	168	11	17	27		11268
GAG	HAGPIPPGQMR	240	11	17	27		11269
GAG	PIPPGQMREPR	243	11	17	27		11270
GAG	IAKNCRAPR	434	9	18	29	0.0003	11271
GAG	LDKWEKIR	13	8	18	28		11272
GAG	PVGDIYKR	281	8	18	28		11273
GAG	PDCKTILR	352	8	18	28		11274
GAG	LDKWEKIRLR	13	10	18	28		11275
GAG	SILDIKQGPK	305	10	18	28		11276
GAG	ANPDCKTILR	350	10	18	28		11277
GAG	HAKNCRAPR	433	10	18	28		11278
GAG	HAGPIAPGQM	240	11	18	28		11279
GAG	NNPPIPVGEIY	273	11	18	28		11280
GAG	NANPDCKTILR	349	11	18	28		11281
GAG	LARNCRAPRK	434	11	19	30		11282
GAG	PIAPGQMR	243	8	19	30		11283
GAG	LDIKQGPK	307	8	19	30		11284
GAG	ILDIKQGPK	306	9	19	30		11285
GAG	AGPIAPGQMR	241	10	19	30		11286
GAG	IAPGQMREPR	244	10	19	30		11287
GAG	RLRPGGKKKY	20	11	19	30		11288
GAG	PIAPGQMREPR	243	11	19	30		11289
GAG	DIKQGPKEPFR	308	11	19	30		11290
GAG	LARNCRAPR	434	9	20	32		11291
GAG	LARNCRAPRK	434	10	20	32		11292
GAG	PGGKKKYR	23	8	20	31		11293
GAG	IMMQRGNFR	408	9	20	31		11294
GAG	KNCRAPRKK	436	9	20	31		11295
GAG	IVWASRELER	35	10	20	31	0.0066	11296
GAG	HLARNCRAPR	433	10	20	31		11297
GAG	HVWASRELER	34	11	20	31		11298
GAG	HLARNCRAPR	433	11	20	31		11299
GAG	EGHLARNCR	431	9	21	33		11300
GAG	KIWPSHKGR	472	9	22	35	0.0005	11301
GAG	GGPSHKAR	378	8	22	34		11302
GAG	KNCRAPRK	436	8	22	34		11303
GAG	VGGPSHKAR	377	9	22	34		11304
GAG	SLYNTVATLY	79	10	22	34		11305
GAG	GVGGPSHKAR	376	10	22	34		11306
GAG	QGVGGPSHKA	375	11	22	34		11307
GAG	LGKIWPSHKG	470	11	22	34		11308
GAG	NFLGKIWPSHK	468	11	23	37		11309
GAG	YNTVATLY	81	8	23	36		11310
GAG	KIEEEQNK	105	8	23	36		11311
GAG	QGVGGPSH	375	8	23	36		11312

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	GVGGPSHK	376	8	23	36		11313
GAG	MMQRGNFR	409	8	23	36		11314
GAG	QGVGGPSHK	375	9	23	36		11315
GAG	LGKIWPSHK	470	9	23	36		11316
GAG	ACQGVGGPSH	373	10	23	36		11317
GAG	FLGKIWPSHK	469	10	23	36	0.0013	11318
GAG	YNTVATLYCV	81	11	23	36		11319
GAG	TACQGVGGPS	372	11	23	36		11320
GAG	ACQGVGGPSH	373	11	23	36		11321
GAG	NCGKEGHLAR	427	10	24	38		11322
GAG	FNCGKEGHLA	426	11	24	38		11323
GAG	CGKEGHLAR	428	9	24	38		11324
GAG	YSPVSILDIR	301	10	24	38		11325
GAG	NFLGKIWPSH	468	10	25	40		11326
GAG	PVSILDIR	303	8	25	39		11327
GAG	LGKIWPSH	470	8	25	39		11328
GAG	KDTKEALDK	97	9	25	39		11329
GAG	FLGKIWPSH	469	9	25	39		11330
GAG	VSILDIRQGPK	304	11	25	39		11331
GAG	ANFLGKIWPSH	467	11	25	39		11332
GAG	LVWASRELER	35	10	26	41		11333
GAG	HLVWASRELE	34	11	26	41		11334
GAG	MVHQAISPR	163	9	27	42	0.0670	11335
GAG	VDRFFKTLR	321	9	27	42		11336
GAG	QMVHQAISPR	162	10	27	42	0.0010	11337
GAG	YVDRFFKTLR	320	10	27	42		11338
GAG	RAEQATQEVK	329	10	27	42		11339
GAG	ANPDCKTILK	350	10	27	42	0.0002	11340
GAG	NANPDCKTILK	349	11	27	42		11341
GAG	KGRPGNFLQS	478	11	28	44		11342
GAG	PDCKTILK	352	8	28	44		11343
GAG	VDRFYKTLR	321	9	28	44		11344
GAG	PFRDYVDRFY	316	10	28	44		11345
GAG	YVDRFYKTLR	320	10	28	44	0.0006	11346
GAG	PFRDYVDRFY	316	11	28	44		11347
GAG	GARASVLSGG	2	11	29	46		11348
GAG	ASVLSGGK	5	8	29	45		11349
GAG	NLQGQMVH	158	8	29	45		11350
GAG	WVKVIEEK	176	8	29	45		11351
GAG	WDRLHPVH	233	8	29	45		11352
GAG	RDYVDRFY	318	8	29	45		11353
GAG	RASVLSGGK	4	9	29	45		11354
GAG	QNLQGQMVH	157	9	29	45		11355
GAG	RDYVDRFYK	318	9	29	45	0.0400	11356
GAG	NAWVKVIEEK	174	10	29	45		11357
GAG	IVQNLQGQMV	155	11	29	45		11358
GAG	LNAWVKVIEE	173	11	29	45		11359
GAG	AAEWDRLHPV	230	11	29	45		11360
GAG	PGNFLQSR	483	8	30	48		11361
GAG	NAWVKVVEEK	174	10	30	47	0.0002	11362

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	KIRLRPGGKKK	18	11	30	47		11363
GAG	LNAWVKVVEE	173	11	30	47		11364
GAG	WVKVVEEK	176	8	31	48	0.0001	11365
GAG	RDYVDRFFK	318	9	33	52		11366
GAG	RNCRAPRKK	436	9	33	52		11367
GAG	PFRDYVDRFF	316	11	33	52		11368
GAG	RNCRAPRK	436	8	34	53		11369
GAG	RLRPGGKKK	20	9	34	53		11370
GAG	RLRPGGKKKY	20	10	34	53		11371
GAG	PIPVGEIYKR	279	10	34	53	0.0001	11372
GAG	PIPVGEIY	279	8	35	55		11373
GAG	PIPVGEIYK	279	9	35	55	0.0012	11374
GAG	DTKEALDK	98	8	36	56	0.0001	11375
GAG	QGVGGPGH	375	8	36	56		11376
GAG	QGVGGPGHK	375	9	36	56	0.0001	11377
GAG	ACQGVGGPGH	373	10	36	56		11378
GAG	ISPRTLNAWV	168	11	36	56		11379
GAG	TACQGVGGPG	372	11	36	56	0.0001	11380
GAG	ACQGVGGPGH	373	11	36	56		11381
GAG	QGVGGPGHKA	375	11	36	56		11382
GAG	GVGGPGHK	376	8	37	58	0.0018	11383
GAG	GGPGHKAR	378	8	37	58		11384
GAG	VGGPGHKAR	377	9	37	58		11385
GAG	GVGGPGHKAR	376	10	37	58	0.0001	11386
GAG	AAEWDRLH	230	8	39	61		11387
GAG	EAAEWDRLH	229	9	39	61		11388
GAG	PVGEIYKR	281	8	40	63	0.0001	11389
GAG	TVATLYCVH	83	9	40	63		11390
GAG	NTVATLYCVH	82	10	40	63		11391
GAG	SILDIRQGPK	305	10	40	63	0.7100	11392
GAG	DIRQGPKEPFR	308	11	41	64		11393
GAG	VATLYCVH	84	8	42	66		11394
GAG	LDIRQGPK	307	8	42	66		11395
GAG	ILDIRQGPK	306	9	42	66	0.0048	11396
GAG	NTMLNTVGGH	206	10	42	66		11397
GAG	LNTMLNTVGG	205	11	42	66		11398
GAG	TMLNTVGGH	207	9	43	67		11399
GAG	KGCWKCGK	444	8	44	69		11400
GAG	KIRLRPGGK	18	9	44	69		11401
GAG	KIRLRPGGKK	18	10	44	69	0.0010	11402
GAG	KGCWKCGKEG	444	11	44	69		11403
GAG	PGQMREPR	246	8	45	70		11404
GAG	CGKEGHQMK	449	9	45	70		11405
GAG	KCGKEGHQMK	448	10	45	70		11406
GAG	MLNTVGGH	208	8	47	73		11407
GAG	WASRELER	37	8	48	75		11408
GAG	GCWKCGKEGH	445	10	48	75		11409
GAG	RLRPGGKK	20	8	49	77		11410
GAG	QMKDCTER	455	8	49	77		11411
GAG	EGHQMKDCTE	452	11	49	77		11412

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	RAPRKKGCWK	439	10	51	80		11413
GAG	CTERQANFLG	459	11	52	83		11414
GAG	NCRAPRKK	437	8	53	84		11415
GAG	TINEEAAEWD	225	11	53	83		11416
GAG	INEEAAEWDR	226	10	55	86		11417
GAG	FNCGKEGH	426	8	57	90		11418
GAG	WHLGLNK	289	8	57	89		11419
GAG	CFNCGKEGH	425	9	57	89		11420
GAG	HLGLNKIVR	290	10	57	89	0.0006	11421
GAG	KCFNCGKEGH	424	10	57	89		11422
GAG	WHLGLNKIVR	289	11	57	89		11423
GAG	ILGLNKIVRMY	291	11	57	89		11424
GAG	ILGLNKIVR	291	9	58	91	0.0001	11425
GAG	LGLNKIVRMY	292	10	58	91	0.0002	11426
GAG	LLVQNANPDC	345	11	58	91		11427
GAG	LGLNKIVR	292	8	59	92		11428
GAG	LVQNANPDCK	346	10	59	92	0.0110	11429
GAG	LNKIVRMY	294	8	60	94		11430
GAG	GLNKIVRMY	293	9	60	94	0.0002	11431
GAG	QAAMQMLK	216	8	61	95		11432
GAG	QNANPDCK	348	8	61	95		11433
GAG	GGHQAAMQM	213	11	61	95		11434
GAG	RTLNAWVK	171	8	63	98	0.0560	11435
GAG	QGPKEPFR	311	8	63	98		11436
GAG	PFRDYVDR	316	8	63	98		11437
GAG	QGPKEPFRDY	311	10	63	98	0.0002	11438
NEF	AADGVGAVSR	42	10	09	15		11439
NEF	ANEGENNSLLH	249	11	09	15		11440
NEF	VGWPAIRER	11	9	10	17		11441
NEF	FDSRLAFH	310	8	10	16		11442
NEF	FDSRLAFHH	310	9	10	16		11443
NEF	DSRLAFHH	311	8	10	16		11444
NEF	AVSQDLDK	48	8	10	16		11445
NEF	PLRPMTFK	102	8	10	16		11446
NEF	GAVSQDLDK	47	9	10	16		11447
NEF	GLEGLIYSK	125	9	10	16		11448
NEF	MARELHPEY	321	9	10	16		11449
NEF	VGAVSQDLDK	46	10	10	16		11450
NEF	QVPLRPMTFK	100	10	10	16		11451
NEF	GAFDLSFFLK	110	10	10	16		11452
NEF	GGLEGLIYSK	124	10	10	16		11453
NEF	CFKLVPVDPR	226	10	10	16		11454
NEF	HMARELHPEY	320	10	10	16		11455
NEF	MARELHPEYY	321	10	10	16		11456
NEF	GVGAVSQDLD	45	11	10	16		11457
NEF	KGAFDLSFFLK	109	11	10	16		11458
NEF	KGGLEGLIYSK	122	11	10	16		11459
NEF	WCFKLVPVDP	225	11	10	16		11460
NEF	NNSLLHPICQH	254	11	10	16		11461
NEF	HMARELHPEY	320	11	10	16		11462

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
NEF	MARELHPEYY	321	11	10	16		11463
NEF	ANEGENNCLL	249	11	11	18		11464
NEF	AVSRDLEK	48	8	11	17		11465
NEF	VSRDLEKH	49	8	11	17		11466
NEF	KLVPVDPR	228	8	11	17		11467
NEF	GAVSRDLEK	47	9	11	17	0.0009	11468
NEF	AVSRDLEKH	48	9	11	17		11469
NEF	VGAVSRDLEK	46	10	11	17		11470
NEF	GAVSRDLEKH	47	10	11	17		11471
NEF	QNYTPGPGVR	205	10	11	17		11472
NEF	NSLLHPICQH	255	10	11	17		11473
NEF	GVGAVSRDLE	45	11	11	17		11474
NEF	VGAVSRDLEK	46	11	11	17		11475
NEF	EGENNCLLH	251	9	12	19		11476
NEF	YTPGPGVR	207	8	12	19		11477
NEF	DILDLWVYH	185	9	12	19		11478
NEF	QDILDLWVYH	184	10	12	19		11479
NEF	EGENNSLLH	251	9	13	21		11480
NEF	VDLSHFLKEK	112	10	13	20		11481
NEF	AVDLSHFLKEK	111	11	13	20		11482
NEF	VDLSHFLK	112	8	14	22		11483
NEF	DGLIYSKK	172	8	14	22		11484
NEF	ELHPEFYK	324	8	14	22		11485
NEF	AVDLSHFLK	111	9	14	22	1.1000	11486
NEF	LDGLIYSKK	171	9	14	22		11487
NEF	DGLIYSKKR	172	9	14	22		11488
NEF	SLLHPICQH	256	9	14	22		11489
NEF	GLDGLIYSKK	125	10	14	22		11490
NEF	LDGLIYSKKR	171	10	14	22		11491
NEF	GGLDGLIYSKK	124	11	14	22		11492
NEF	GLDGLIYSKKR	125	11	14	22		11493
NEF	NNCLLHPMSQ	254	11	14	22		11494
NEF	CLLHPMSQH	256	9	15	23		11495
NEF	NCLLHPMSQH	255	10	15	23		11496
NEF	QNYTPGPGIRY	205	11	15	23		11497
NEF	LDGLIYSK	171	8	16	25		11498
NEF	GLDGLIYSK	125	9	16	25		11499
NEF	GGLDGLIYSK	124	10	16	25		11500
NEF	KGGLDGLIYSK	122	11	16	25		11501
NEF	RFPLTFGWCF	216	11	17	27		11502
NEF	FFPDWQNY	199	8	17	27		11503
NEF	LLHPMSQH	257	8	17	27		11504
NEF	GFFPDWQNY	198	9	17	27		11505
NEF	YTPGPGIRY	207	9	17	27		11506
NEF	FDLSFFLKEK	112	10	17	27		11507
NEF	QGFFPDWQNY	196	10	17	27		11508
NEF	AFDLSFFLKEK	111	11	17	27		11509
NEF	FDLSFFLK	112	8	18	28		11510
NEF	LLHPICQH	257	8	18	28		11511
NEF	AFDLSFFLK	111	9	18	28		11512

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
NEF	QNYTPGPGIR	205	10	18	28		11513
NEF	GGLEGLIY	124	8	19	30		11514
NEF	KGGLEGLIY	122	9	19	30		11515
NEF	DILDLWVY	185	8	20	31		11516
NEF	YTPGPGIR	207	8	20	31		11517
NEF	QDILDLWVY	184	9	20	31		11518
NEF	QNYTPGPGTR	205	10	20	31		11519
NEF	GGLDGLIY	124	8	21	33		11520
NEF	WVYHTQGY	191	8	21	33		11521
NEF	YTPGPGTR	207	8	21	33		11522
NEF	KGGLDGLIY	122	9	21	33		11523
NEF	DLWVYHTQGY	188	10	21	33		11524
NEF	LDLWVYHTQG	187	11	21	33		11525
NEF	LSFFLKEK	114	8	22	34		11526
NEF	ELHPEYYK	324	8	22	34		11527
NEF	DLSFFLKEK	113	9	22	34		11528
NEF	EILDLWVYH	185	9	22	34		11529
NEF	GLIYSKKR	173	8	23	36		11530
NEF	LSHFLKEK	114	8	27	42		11531
NEF	DLSHFLKEK	113	9	27	42		11532
NEF	EILDLWVY	185	8	33	52		11533
NEF	ILDLWVYH	186	8	34	53		11534
NEF	YFPDWQNY	199	8	36	56		11535
NEF	QGYFPDWQNY	196	10	36	56	0.0017	11536
NEF	LTFGWCFK	221	8	39	61		11537
NEF	PLTFGWCFK	219	9	39	61		11538
NEF	QVPLRPMTY	100	9	46	72		11539
NEF	QVPLRPMTYK	100	10	46	72	0.6300	11540
NEF	PVRPQVPLR	95	9	48	75		11541
NEF	GFPVRPQVPLR	93	11	48	75		11542
NEF	PLRPMTYK	102	8	49	77	0.0003	11543
POL	STNSPTSR	32	8	01	33		11544
POL	RANSPSSR	35	8	01	33		11545
POL	NSTNSPTSR	31	9	01	33		11546
POL	PTSRELQVR	36	9	01	33		11547
POL	QTRANSPSSR	33	10	01	33		11548
POL	QTRANSPTTR	35	10	01	33		11549
POL	NSPTSRELQVR	34	11	01	33		11550
POL	RANSPTTR	37	8	01	50		11551
POL	PSSRELQVR	39	9	01	50		11552
POL	PSRANSPTSR	24	10	01	50		11553
POL	NSPSSRELQVR	37	11	01	50		11554
POL	NSPTTRELQV	39	11	01	50		11555
POL	NNSLSEAGAD	55	11	05	25		11556
POL	NLAFPQGEAR	5	10	10	16		11557
POL	ILIEICGH	149	8	10	16		11558
POL	LIEICGHK	150	8	10	16		11559
POL	YAKMRTAH	546	8	10	16		11560
POL	RSAHTNDVK	550	9	10	16		11561
POL	ETWETWWTD	588	10	10	16		11562

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%).	A*1101	SEQ ID NO.
POL	ETWETWWTE	588	10	10	16		11563
POL	VSLTDTTNQK	659	10	10	16		11564
POL	ENLAFPQGEAR	4	11	10	16		11565
POL	TGKYAKMRTA	543	11	10	16		11566
POL	VVSLTDTTNQ	658	11	10	16		11567
POL	QTKELQKQIIK	961	11	10	16		11568
POL	QTRANSPTRR	21	10	11	18		11569
POL	TNNETPGIR	324	9	11	17		11570
POL	TNNETPGIRY	324	10	11	17		11571
POL	LDGIDKAQEDII	754	11	11	17		11572
POL	IGGFIKVK	137	8	11	17		11573
POL	RIGPENPY	238	8	11	17		11574
POL	TAIITNDVK	551	8	11	17		11575
POL	QLTEVVQK	559	8	11	17		11576
POL	IDKAQEDII	757	8	11	17		11577
POL	VVPRRKVK	1012	8	11	17		11578
POL	KIIKDYGK	1019	8	11	17		11579
POL	GIGGFIKVK	136	9	11	17		11580
POL	SLTDTTNQK	660	9	11	17		11581
POL	GIDKAQEDII	756	9	11	17		11582
POL	SNFTSTTVK	871	9	11	17		11583
POL	KVVPRRKVK	1011	9	11	17		11584
POL	GGIGGFIKVK	135	10	11	17		11585
POL	ISRIGPENPY	236	10	11	17		11586
POL	STNNETPGIR	323	10	11	17		11587
POL	ESWTVNDIQK	439	10	11	17		11588
POL	ETTNQKTELH	663	10	11	17		11589
POL	DGIDKAQEDII	755	10	11	17		11590
POL	GSNFTSTTVK	870	10	11	17		11591
POL	GIQQEFGIPY	886	10	11	17		11592
POL	SDIQTKELQK	958	10	11	17		11593
POL	FNFPQITLWQR	85	11	11	17		11594
POL	IGGIGGFIKVK	134	11	11	17		11595
POL	KISRIGPENPY	235	11	11	17		11596
POL	PSTNNETPGIR	322	11	11	17		11597
POL	STNNETPGIRY	323	11	11	17		11598
POL	VVSLTETTNQ	658	11	11	17		11599
POL	NGSNFTSTTV	869	11	11	17		11600
POL	AGIQQEFGIPY	885	11	11	17		11601
POL	IDIIASDIQTK	953	11	11	17		11602
POL	VDIIATDIQTK	953	11	11	17		11603
POL	ASDIQTKELQK	957	11	11	17		11604
POL	NSEIKVVPRRK	1007	11	11	17		11605
POL	QTRANSPTSR	21	10	12	19		11606
POL	IIKIQNFR	969	8	12	19		11607
POL	QIYPGIKVK	458	9	12	19		11608
POL	QDQWTYQIY	526	9	12	19		11609
POL	IIKIQNFRVY	969	10	12	19		11610
POL	ASQIYPGIKVK	456	11	12	19		11611
POL	IIKIQNFRVYY	969	11	12	19		11612

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HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	AFPQGEAR	7	8	12	19		11613
POL	TNQKTELH	665	8	12	19		11614
POL	KTELQAIY	668	8	12	19		11615
POL	LAFPQGEAR	6	9	12	19		11616
POL	EINLPGKWK	122	9	12	19		11617
POL	TTNQKTELH	664	9	12	19		11618
POL	QHKIQNFR	968	9	12	19		11619
POL	VIQDNSEIK	1003	9	12	19		11620
POL	NSEIKVVPR	1007	9	12	19		11621
POL	VLEEINLPGK	119	10	12	19		11622
POL	VVIQDNSEIK	1002	10	12	19		11623
POL	DNSEIKVVPR	1006	10	12	19		11624
POL	NSEIKVVPRR	1007	10	12	19		11625
POL	TVLEEINLPGK	118	11	12	19		11626
POL	EINLPGKWKPK	122	11	12	19		11627
POL	QGQDQWTYQI	524	11	12	19		11628
POL	RMRGAHTNDV	548	11	12	19		11629
POL	TNQKTELQAIY	665	11	12	19		11630
POL	QHKIQNFRVY	968	11	12	19		11631
POL	AVVIQDNSEIK	1000	11	12	19		11632
POL	QDNSEIKVVPR	1005	11	12	19		11633
POL	DNSEIKVVPRR	1006	11	12	19		11634
POL	ELQKQHK	964	8	13	21		11635
POL	KTGKYARMR	542	9	13	21		11636
POL	NLKTGKYARM	540	11	13	21		11637
POL	EDINLPGK	121	8	13	20		11638
POL	TGKYARMR	543	8	13	20		11639
POL	YARMRGAH	546	8	13	20		11640
POL	QVREQAEH	916	8	13	20		11641
POL	DINLPGKWK	122	9	13	20		11642
POL	VLEDINLPGK	119	10	13	20		11643
POL	EDINLPGKWK	121	10	13	20		11644
POL	RAKIEELREH	388	10	13	20		11645
POL	TVQPIVLPEK	429	10	13	20	5.6000	11646
POL	AGRWPVKTHI	857	10	13	20		11647
POL	IGQVREQAEH	914	10	13	20		11648
POL	QVREQAEHLK	916	10	13	20		11649
POL	TLWQRPLVTV	91	11	13	20		11650
POL	LVTIKIGGQLK	97	11	13	20		11651
POL	TVLEDINLPGK	118	11	13	20		11652
POL	DINLPGKWKP	122	11	13	20		11653
POL	KIEELREHLLK	390	11	13	20		11654
POL	WTVQPIVLPEK	428	11	13	20	0.0510	11655
POL	TGKYARMRGA	543	11	13	20		11656
POL	LAGRWPVKTI	856	11	13	20		11657
POL	HGQVREQAEH	913	11	13	20		11658
POL	EIKVVPRRKAK	1009	11	13	20		11659
POL	EFSSEQTR	16	8	14	22		11660
POL	QIYPGIKVR	458	9	14	22		11661
POL	ASQIYPGIKVR	456	11	14	22		11662

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HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	IATESIVIWGK	567	11	14	22		11663
POL	ILIEICGK	149	8	14	22		11664
POL	LIEICGKK	150	8	14	22		11665
POL	QNPDIVIY	363	8	14	22		11666
POL	NFTSTTVK	872	8	14	22		11667
POL	IASDIQTK	956	8	14	22		11668
POL	DSRDPLWK	981	8	14	22		11669
POL	QILIEICGK	148	9	14	22		11670
POL	ILIEICGKK	149	9	14	22		11671
POL	HASDIQTK	955	9	14	22		11672
POL	RDSRDPLWK	980	9	14	22		11673
POL	QILIEICGKK	148	10	14	22		11674
POL	QNPDIVIYQY	363	10	14	22		11675
POL	RTKIEELRQH	388	10	14	22		11676
POL	PGIKVRQLCK	461	10	14	22		11677
POL	DHASDIQTK	954	10	14	22		11678
POL	RDPLWKGPAK	983	10	14	22		11679
POL	FSFPQITLWQR	85	11	14	22		11680
POL	YDQILIEICGK	146	11	14	22		11681
POL	KTPKFKLPIQK	577	11	14	22		11682
POL	GIDKAQEEHER	756	11	14	22		11683
POL	QTRANSPTR	21	9	15	24		11684
POL	LVEICTEMEK	221	10	15	24	0.0120	11685
POL	ELRQHLLR	393	8	15	23		11686
POL	QGQDQWTY	524	8	15	23		11687
POL	KTELQAIH	668	8	15	23		11688
POL	EIKVVPRRK	1009	9	15	23		11689
POL	LGHQAQPDR	695	10	15	23		11690
POL	VDKLVSAGIR	740	10	15	23		11691
POL	IDKAQEEHER	757	10	15	23		11692
POL	ALVEICTEMEK	220	11	15	23		11693
POL	KIEELRQHLLR	390	11	15	23		11694
POL	TNQKTELQAIH	665	11	15	23		11695
POL	ALGHQAQPDR	694	11	15	23		11696
POL	LVNQIIEQLIK	709	11	15	23		11697
POL	QVDKLVSAGIR	739	11	15	23		11698
POL	VDKLVSAGIRK	740	11	15	23		11699
POL	IDKAQEEHERY	757	11	15	23		11700
POL	KAQEEHER	759	8	16	25		11701
POL	KAQEEHERY	759	9	16	25		11702
POL	NLAFQQGEAR	5	10	16	25		11703
POL	KAQEEHERYH	759	10	16	25		11704
POL	AFQQGEAR	7	8	16	25		11705
POL	RANSPTRR	26	8	16	25		11706
POL	SAHTNDVK	551	8	16	25		11707
POL	HQAQPDR	697	8	16	25		11708
POL	KLVSAGIR	742	8	16	25		11709
POL	LVSAGIRK	743	8	16	25	0.0054	11710
POL	EIKVVPRR	1009	8	16	25		11711
POL	LAFQQGEAR	6	9	16	25		11712

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GIIQAQPDR	696	9	16	25		11713
POL	KLVSAGIRK	742	9	16	25	0.0770	11714
POL	ENLAFQQGEA	4	11	16	25		11715
POL	RANSPTSR	26	8	17	27		11716
POL	KIEELRQH	390	8	17	27		11717
POL	ELREHLLK	393	8	17	27		11718
POL	WGKTPKFK	575	8	17	27		11719
POL	TIKIGGQLK	99	9	17	27	0.0330	11720
POL	VTIKIGGQLK	98	10	17	27	0.2100	11721
POL	TVQPIQLPEK	429	10	17	27		11722
POL	VIWGKTPKFK	573	10	17	27		11723
POL	TLWQRPLVTI	91	11	17	27		11724
POL	WTVQPIQLPEK	428	11	17	27		11725
POL	IVIWGKTPKFK	572	11	17	27		11726
POL	YFSVPLDKDFR	304	11	18	29		11727
POL	NLKTGKYAKM	540	11	18	29		11728
POL	PDIVIYQY	365	8	18	28		11729
POL	SVPLDKDFR	306	9	18	28		11730
POL	FSVPLDKDFR	305	10	18	28		11731
POL	SVPLDKDFRK	306	10	18	28		11732
POL	AGIKVKQLCK	461	10	18	28		11733
POL	VNQIIEQLIK	710	10	18	28		11734
POL	FSVPLDKDFRK	305	11	18	28		11735
POL	SVPLDKDFRK	306	11	18	28		11736
POL	YAGIKVKQLCK	460	11	18	28		11737
POL	LVSQIIEQLIK	709	11	18	28		11738
POL	VNQIIEQLIKK	710	11	18	28		11739
POL	PLDKDFRK	308	8	19	30		11740
POL	PLDKDFRKY	308	9	19	30		11741
POL	KTGKYAKMR	542	9	19	30		11742
POL	LDKDFRKY	309	8	19	30		11743
POL	KIEELREH	390	8	19	30		11744
POL	TGKYAKMR	543	8	19	30		11745
POL	GAHTNDVK	551	8	19	30		11746
POL	LTDTTNQK	661	8	19	30		11747
POL	PLWKGPAK	985	8	19	30		11748
POL	GIKVRQLCK	462	9	19	30		11749
POL	RGAHTNDVK	550	9	19	30		11750
POL	KVRQLCKLLR	464	10	19	30		11751
POL	ATESIVIWGK	568	10	19	30		11752
POL	VSQIIEQLIK	710	10	19	30	0.0370	11753
POL	MAGDDCVASR	1028	10	19	30		11754
POL	VSQIIEQLIKK	710	11	19	30		11755
POL	QMAGDDCVAS	1027	11	19	30		11756
POL	QIYAGIKVK	458	9	20	32		11757
POL	KVYLAWVPAH	722	10	20	32	0.0036	11758
POL	KAACWWAGIK	879	10	20	32	0.0740	11759
POL	ASQIYAGIKVK	456	11	20	32		11760
POL	KVYLAWVPAH	722	11	20	32	2.3000	11761
POL	KFKLPIQK	580	8	20	31		11762

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GDDCVASR	1030	8	20	31		11763
POL	AGDDCVASR	1029	9	20	31		11764
POL	VSLTETTNQK	659	10	20	31		11765
POL	LLKLAGRWPV	853	11	20	31		11766
POL	YFSVPLDK	304	8	21	33		11767
POL	ACWWAGIK	881	8	21	33		11768
POL	SLTETTNQK	660	9	21	33		11769
POL	AACWWAGIK	880	9	21	33	0.0470	11770
POL	DAYFSVPLDK	302	10	21	33		11771
POL	DLEIGQHRTK	381	10	21	33		11772
POL	QLCKLLRGTK	467	10	21	33		11773
POL	IFAIKKKDSTK	249	11	21	33		11774
POL	GDAYFSVPLD	301	11	21	33		11775
POL	SDLEIGQHRTK	380	11	21	33		11776
POL	SDFNLPPIVAK	776	11	21	33		11777
POL	AGIKQEFGIPY	885	11	21	33		11778
POL	EIGQHRTK	383	8	22	34		11779
POL	RTKIEELR	388	8	22	34		11780
POL	YLAWVPAH	724	8	22	34		11781
POL	LAWVPAHK	725	8	22	34		11782
POL	YLAWVPAHK	724	9	22	34	0.0570	11783
POL	NFPQITLWQR	86	10	22	34		11784
POL	MTKILEPFRK	353	10	22	34	0.0380	11785
POL	AGRWPVKVHI	857	10	22	34		11786
POL	GIKQEFGIPY	886	10	22	34	0.0002	11787
POL	SMTKILEPFRK	352	11	22	34		11788
POL	KTPKFRLPIQK	577	11	22	34		11789
POL	LAGRWPVKVI	856	11	22	34		11790
POL	KVYLSWVPAH	722	10	23	37		11791
POL	KVYLSWVPAH	722	11	23	37		11792
POL	KILEPFRK	355	8	23	36		11793
POL	KVILVAVH	823	8	23	36		11794
POL	SFPQITLWQR	86	10	23	36		11795
POL	DFNLPPIVAK	777	10	23	36		11796
POL	EGKVILVAVH	821	10	23	36		11797
POL	LLKWGFTTPD	398	11	23	36		11798
POL	LLRWGFTTPD	398	11	23	36		11799
POL	IDHATDIQTK	953	11	23	36		11800
POL	NTPIFAIK	246	8	24	38		11801
POL	GDDCVAGR	1030	8	24	38		11802
POL	YNTPIFAIK	245	9	24	38		11803
POL	NTPIFAIKK	246	9	24	38		11804
POL	LCKLLRGTK	468	9	24	38	0.0001	11805
POL	AGDDCVAGR	1029	9	24	38		11806
POL	YNTPIFAIKK	245	10	24	38		11807
POL	NTPIFAIKKK	246	10	24	38		11808
POL	MAGDDCVAGR	1028	10	24	38		11809
POL	YNTPIFAIKKK	245	11	24	38		11810
POL	QGQGQWTYQI	524	11	24	38		11811
POL	KLGKAGYVTD	643	11	24	38		11812

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HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	TAYFLLKLAG	849	11	24	38		11813
POL	QMAGDDCVAG	1027	11	24	38		11814
POL	QGQWTYQIY	526	9	25	40	0.0001	11815
POL	PIFAIKKK	248	8	25	39		11816
POL	QGQGQWTY	524	8	25	39		11817
POL	FLLKLAGR	852	8	25	39		11818
POL	YFLLKLAGR	851	9	25	39		11819
POL	QLCKLLRGAK	467	10	25	39		11820
POL	LGKAGYVTDR	644	10	25	39		11821
POL	IDKAQEEHEK	757	10	25	39		11822
POL	PSKDLIAEIQK	513	11	25	39		11823
POL	GIDKAQEEHEK	756	11	25	39		11824
POL	IDKAQEEHEKY	757	11	25	39		11825
POL	SDFNLPPVVAK	776	11	25	39		11826
POL	RAKIEELR	388	8	26	41		11827
POL	KFRLPIQK	580	8	26	41		11828
POL	NLPPIVAK	779	8	26	41		11829
POL	LCKLLRGAK	468	9	26	41		11830
POL	FNLPPIVAK	778	9	26	41		11831
POL	SNFTSAAVK	871	9	26	41		11832
POL	DFNLPPVVAK	777	10	26	41		11833
POL	GSNFTSAAVK	870	10	26	41		11834
POL	TGQETAYFLL	845	11	26	41		11835
POL	NGSNFTSAAV	869	11	26	41		11836
POL	KAQEEHEK	759	8	27	43		11837
POL	ASQIYAGIK	456	9	27	43	0.3400	11838
POL	KAQEEHEKY	759	9	27	43		11839
POL	KAQEEHEKYH	759	10	27	43		11840
POL	INLPGKWK	123	8	27	42		11841
POL	EICTEMEK	223	8	27	42		11842
POL	EIGQHRAK	383	8	27	42		11843
POL	LVSSGIRK	743	8	27	42		11844
POL	NLPPVVAK	779	8	27	42		11845
POL	ETAYFLLK	848	8	27	42	0.0430	11846
POL	KLVSSGIRK	742	9	27	42		11847
POL	FNLPPVVAK	778	9	27	42		11848
POL	INLPGKWKPK	123	10	27	42		11849
POL	DLEIGQHRAK	381	10	27	42		11850
POL	WASQIYAGIK	455	10	27	42		11851
POL	KVKQLCKLLR	464	10	27	42		11852
POL	EICTEMEKEGK	223	11	27	42		11853
POL	SDLEIGQHRAK	380	11	27	42		11854
POL	VDKLVSSGIRK	740	11	27	42		11855
POL	ASQIYPGIK	456	9	28	44		11856
POL	KDLIAEIQK	515	9	28	44		11857
POL	NLKTGKYAK	540	9	28	44		11858
POL	DLIAEIQK	516	8	28	44		11859
POL	IVGAETFY	626	8	28	44		11860
POL	NFTSAAVK	872	8	28	44		11861
POL	CTEMEKEGK	225	9	28	44	0.0001	11862

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GIKVKQLCK	462	9	28	44		11863
POL	PIVGAETFY	625	9	28	44		11864
POL	QLIKKEKVY	716	9	28	44		11865
POL	ICTEMEKEGK	224	10	28	44		11866
POL	WASQIYPGIK	455	10	28	44		11867
POL	KNLKTGKYAK	539	10	28	44		11868
POL	NLKTGKYAR	540	9	29	46	0.0001	11869
POL	KLVSSGIR	742	8	29	45		11870
POL	KNLKTGKYAR	539	10	29	45		11871
POL	VIWGKTPKFR	573	10	29	45		11872
POL	VDKLVSSGIR	740	10	29	45		11873
POL	IVIWGKTPKFR	572	11	29	45		11874
POL	QVDKLVSSGIR	739	11	29	45		11875
POL	WGKTPKFR	575	8	30	47		11876
POL	LTEITNQK	661	8	30	47		11877
POL	ANRETKLGK	638	9	30	47	0.0001	11878
POL	AANRETKLGK	637	10	30	47	0.0016	11879
POL	IIEQLIKKEK	713	10	30	47	0.0003	11880
POL	GAANRETKLG	636	11	30	47		11881
POL	QIIEQLIKKEK	712	11	30	47		11882
POL	ILKLAGRWPV	853	11	30	47		11883
POL	KIILVAVII	823	8	31	48		11884
POL	ETAYFILK	848	8	31	48		11885
POL	YFILKLAGR	851	9	31	48		11886
POL	EGKIILVAVII	821	10	31	48		11887
POL	PSINNETPGIR	322	11	31	48		11888
POL	TGQETAYFILK	845	11	31	48		11889
POL	TAYFILKLAGR	849	11	31	48		11890
POL	INNETPGIR	324	9	32	51		11891
POL	INNETPGIRY	324	10	32	51		11892
POL	FILKLAGR	852	8	32	50		11893
POL	SINNETPGIR	323	10	32	50		11894
POL	SINNETPGIRY	323	11	32	50		11895
POL	SSMTKILEPFR	351	11	32	50		11896
POL	QTKELQKQITK	961	11	32	50	0.0100	11897
POL	EMEKEGKISK	229	10	33	52	0.0001	11898
POL	DVKQLTEAVQ	556	11	33	52	0.0240	11899
POL	DIIATDIQTK	954	10	34	53	0.0130	11900
POL	ELQKQITK	964	8	35	56		11901
POL	LIKKEKVY	717	8	35	55		11902
POL	DSRDPIWK	981	8	35	55		11903
POL	ETKLGKAGY	641	9	35	55		11904
POL	IIATDIQTK	955	9	35	55	0.0980	11905
POL	QITKIQNFR	968	9	35	55	0.0045	11906
POL	RDSRDPIWK	980	9	35	55		11907
POL	TDIQTKELQK	958	10	35	55	0.0001	11908
POL	RDPIWKGPAK	983	10	35	55		11909
POL	ATDIQTKELQK	957	11	35	55	0.1800	11910
POL	QITKIQNFRVY	968	11	35	55		11911
POL	ITKIQNFR	969	8	36	57		11912

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HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ITKIQNFRVY	969	10	36	57	0.0012	11913
POL	ITKIQNFRVYY	969	11	36	57		11914
POL	IATDIQTK	956	8	36	56		11915
POL	PIWKGPAK	985	8	36	56		11916
POL	NLPGKWKPK	124	9	36	56		11917
POL	AIFQSSMTK	347	9	36	56	0.9600	11918
POL	PAIFQSSMTK	346	10	36	56	0.0830	11919
POL	VFAIKKKDSTK	249	11	36	56		11920
POL	NTPVFAIK	246	8	37	58	0.0003	11921
POL	PVFAIKKK	248	8	37	58	0.0001	11922
POL	QLTEAVQK	559	8	37	58		11923
POL	QIIEQLIK	712	8	37	58		11924
POL	IIEQLIKK	713	8	37	58		11925
POL	YLSWVPAH	724	8	37	58		11926
POL	LSWVPAHK	725	8	37	58		11927
POL	YNTPVFAIK	245	9	37	58	0.0002	11928
POL	NTPVFAIKK	246	9	37	58	0.0600	11929
POL	QIIEQLIKK	712	9	37	58	0.1600	11930
POL	YLSWVPAHK	724	9	37	58		11931
POL	VIQDNSDIK	1003	9	37	58	0.0068	11932
POL	YNTPVFAIKK	245	10	37	58		11933
POL	NTPVFAIKKK	246	10	37	58	0.0046	11934
POL	VVIQDNSDIK	1002	10	37	58	0.0210	11935
POL	YNTPVFAIKKK	245	11	37	58		11936
POL	AVVIQDNSDIK	1000	11	37	58	0.0150	11937
POL	IFQSSMTK	348	8	38	59	0.0073	11938
POL	ILKEPVHGVYY	498	11	38	59		11939
POL	LDGIDKAQEEH	754	11	39	62		11940
POL	AGYVTDRGR	647	9	39	61		11941
POL	YVTDRGRQK	649	9	39	61	0.0010	11942
POL	KAGYVTDRGR	646	10	39	61		11943
POL	LGIIQAQPDK	695	10	39	61	0.0001	11944
POL	DGIDKAQEEH	755	10	39	61		11945
POL	PVHGVYYDPS	505	11	39	61		11946
POL	AGYVTDRGRQ	647	11	39	61		11947
POL	ALGIIQAQPDK	694	11	39	61		11948
POL	DIKVVPRRKAK	1009	11	39	61		11949
POL	VTDRGRQK	650	8	40	63	0.0065	11950
POL	IIQAQPDK	697	8	40	63		11951
POL	GIIQAQPDK	696	9	40	63	0.0400	11952
POL	GIDKAQEEH	756	9	40	63		11953
POL	NSDIKVVPR	1007	9	40	63		11954
POL	ILKEPVHGVY	498	10	40	63		11955
POL	DNSDIKVVPR	1006	10	40	63		11956
POL	NSDIKVVPRR	1007	10	40	63	0.0001	11957
POL	EILKEPVHGVY	497	11	40	63		11958
POL	WTYQIYQEPF	529	11	40	63	0.0540	11959
POL	QIYQEPFKNLK	532	11	40	63	0.2900	11960
POL	QDNSDIKVVPR	1005	11	40	63		11961
POL	DNSDIKVVPRR	1006	11	40	63		11962

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	NSDIKVVPRRK	1007	11	40	63		11963
POL	ESIVIWGKTPK	570	11	41	65		11964
POL	QIYQEPFK	532	8	41	64	0.0013	11965
POL	IDKAQEEH	757	8	41	64		11966
POL	KAKIIRDY	1017	8	41	64		11967
POL	KAKIIRDYGK	1017	10	41	64	0.0018	11968
POL	KISKIGPENPY	235	11	41	64		11969
POL	KAGYVTDR	646	8	42	66		11970
POL	ISKIGPENPY	236	10	42	66		11971
POL	SMTKILEPFR	352	10	42	66	0.0004	11972
POL	SIVIWGKTPK	571	10	42	66		11973
POL	IVIYQYMDDLY	367	11	42	66		11974
POL	VVPRRKAKIIR	1012	11	42	66		11975
POL	GVYYDPSK	508	8	43	67		11976
POL	SCDKCQLK	791	8	43	67		11977
POL	MTKILEPFR	353	9	43	67	0.0160	11978
POL	HGVYYDPSK	507	9	43	67	0.0001	11979
POL	ASCDKCQLK	790	9	43	67	0.0140	11980
POL	DSWTVNDIQK	439	10	43	67	0.0002	11981
POL	TFYVDGAANR	631	10	43	67	0.0008	11982
POL	VASCDKCQLK	789	10	43	67	0.0004	11983
POL	KDSWTVNDIQ	438	11	43	67		11984
POL	ETFYVDGAAN	630	11	43	67		11985
POL	IVASCDKCQLK	788	11	43	67	0.1000	11986
POL	SDIKVVPR	1008	8	44	69		11987
POL	SDIKVVPRR	1008	9	44	69	0.0001	11988
POL	VDGAANRETK	634	10	44	69		11989
POL	IGQVRDQAEH	914	10	44	69		11990
POL	QVRDQAEHLK	916	10	44	69	0.0093	11991
POL	SDIKVVPRRK	1008	10	44	69	0.0001	11992
POL	ENREILKEPVH	494	11	44	69		11993
POL	YVDGAANRET	633	11	44	69		11994
POL	HGQVRDQAEH	913	11	44	69		11995
POL	VAKEIVASCDK	784	11	45	71		11996
POL	GAANRETK	636	8	45	70		11997
POL	EIVASCDK	787	8	45	70		11998
POL	DGAANRETK	635	9	45	70		11999
POL	PFKNLKTGKY	537	10	45	70	0.0002	12000
POL	PLVKLWYQLE	613	11	45	70		12001
POL	EILKEPVH	497	8	46	72		12002
POL	KLWYQLEK	616	8	46	72		12003
POL	RDQAEHLK	918	8	46	72		12004
POL	PFKNLKTGK	537	9	46	72		12005
POL	DIQTKELQK	959	9	46	72	0.0006	12006
POL	LVKLWYQLEK	614	10	46	72	0.0820	12007
POL	KVKQWPLTEE	207	11	46	72	0.0330	12008
POL	VIWGKTPK	573	8	48	75		12009
POL	QVRDQAEH	916	8	48	75		12010
POL	DIKVVPRR	1009	8	48	75		12011
POL	IVIWGKTPK	572	9	48	75	0.3700	12012

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	DIKVVPRRK	1009	9	48	75	0.0001	12013
POL	KVLFLDGIDK	750	10	48	75	0.7800	12014
POL	KCQLKGEAMH	794	10	48	75		12015
POL	VVESMNKELK	902	10	48	75		12016
POL	GVVESMNKEL	901	11	48	75		12017
POL	VVESMNKELK	902	11	48	75		12018
POL	GVVESMNK	901	8	49	77		12019
POL	QGVVESMNK	900	9	49	77		12020
POL	KLKPGMDGPK	197	10	49	77	0.0760	12021
POL	QSQGVVESMN	898	11	49	77		12022
POL	ESIVIWGK	570	8	50	79		12023
POL	YVDGAANR	633	8	50	78	0.0001	12024
POL	LAGRWPVK	856	8	50	78		12025
POL	KIIRDYGK	1019	8	50	78		12026
POL	KLAGRWPVK	855	9	50	78	0.0690	12027
POL	QNFRVYYRDS	973	11	50	78		12028
POL	GMDGPKVK	201	8	51	80	0.0004	12029
POL	KIGPENPY	238	8	51	80		12030
POL	NNETPGIR	325	8	51	80		12031
POL	FTTPDKKH	403	8	51	80		12032
POL	PGMDGPKVK	200	9	51	80	0.0001	12033
POL	NNETPGIRY	325	9	51	80		12034
POL	GFTTPDKKH	402	9	51	80		12035
POL	VLFLDGIDK	751	9	51	80	0.0320	12036
POL	VIYQYMDDLY	368	10	51	80	0.0090	12037
POL	WGFTTPDKKH	401	10	51	80		12038
POL	FTTPDKKHQK	403	10	51	80	0.0150	12039
POL	NNETPGIRYQY	325	11	51	80		12040
POL	GFTTPDKKHQ	402	11	51	80		12041
POL	PAGLKKKK	286	8	52	81		12042
POL	SDLEIGQH	380	8	52	81		12043
POL	DLEIGQHR	381	8	52	81		12044
POL	WGFTTPDK	401	8	52	81		12045
POL	GFTTPDKK	402	8	52	81		12046
POL	KIQNFRVY	971	8	52	81		12047
POL	VVPRRKAK	1012	8	52	81	0.0001	12048
POL	ETPGIRYQY	327	9	52	81		12049
POL	GSDLEIGQH	379	9	52	81		12050
POL	SDLEIGQHR	380	9	52	81	0.0001	12051
POL	WGFTTPDKK	401	9	52	81	0.0039	12052
POL	KIQNFRVYY	971	9	52	81	0.1400	12053
POL	KVVPRRKAK	1011	9	52	81	0.0039	12054
POL	VGSDLEIGQH	378	10	52	81		12055
POL	GSDLEIGQHR	379	10	52	81		12056
POL	KIQNFRVYYR	971	10	52	81	0.2100	12057
POL	NFRVYYRDSR	974	10	52	81		12058
POL	IGGIGGFIKVR	134	11	52	81		12059
POL	VGPTPVNIIGR	164	11	52	81		12060
POL	YVGSDLEIGQH	377	11	52	81		12061
POL	VGSDLEIGQHR	378	11	52	81		12062

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GIPHPAGLKKK	282	11	53	84		12063
POL	IGGFIKVR	137	8	53	83		12064
POL	GFIKVRQY	139	8	53	83		12065
POL	PIETVPVK	190	8	53	83		12066
POL	ETVPVKLK	192	8	53	83	0.0001	12067
POL	ELELAENR	489	8	53	83		12068
POL	QLKGEAMH	796	8	53	83		12069
POL	ESMNKELK	904	8	53	83		12070
POL	SMNKELKK	905	8	53	83		12071
POL	GIGGFIKVR	136	9	53	83	0.0005	12072
POL	GGFIKVRQY	138	9	53	83	0.0001	12073
POL	ESMNKELKK	904	9	53	83		12074
POL	GGIGGFIKVR	135	10	53	83	0.0002	12075
POL	IGGFIKVRQY	137	10	53	83	0.0002	12076
POL	ISPIETVPVK	188	10	53	83	0.0310	12077
POL	PIETVPVKLK	190	10	53	83	0.0001	12078
POL	EAELELAENR	487	10	53	83		12079
POL	LVAVHVASGY	826	10	53	83		12080
POL	GIGGFIKVRQY	136	11	53	83		12081
POL	PISPIETVPVK	187	11	53	83		12082
POL	ILVAVHVASGY	825	11	53	83		12083
POL	FVNTPPLVK	608	9	54	86	0.0660	12084
POL	GIPHPAGLKK	282	10	54	86	0.1700	12085
POL	LGIPHPAGLKK	281	11	54	86		12086
POL	QNFRVYYR	973	8	54	84		12087
POL	PTPVNHGR	166	9	54	84	0.0001	12088
POL	LAENREILK	492	9	54	84	0.0003	12089
POL	ELAENREILK	491	10	54	84	0.0003	12090
POL	EFVNTPPLVK	607	10	54	84		12091
POL	PLTEEKIK	212	8	55	86		12092
POL	LFLDGIDK	752	8	55	86		12093
POL	GIPHPAGLK	282	9	56	89	0.0650	12094
POL	LGIPHPAGLK	281	10	56	89	0.0150	12095
POL	QLGIPHPAGLK	280	11	56	89		12096
POL	VTVLDVGDAY	295	10	56	88	0.0004	12097
POL	ELKKIIGQVR	909	10	56	88		12098
POL	DFWEVQLGIPH	275	11	56	88		12099
POL	SVTVLDVGDA	294	11	56	88		12100
POL	KTAVQMAVFI	925	11	56	88		12101
POL	VNTPPLVK	609	8	57	89		12102
POL	AIKKKDSTK	251	9	57	89	0.0086	12103
POL	TVLDVGDAY	296	9	57	89	0.0056	12104
POL	TTPDKKHQK	404	9	57	89	0.0042	12105
POL	FAIKKKDSTK	250	10	57	89	0.0002	12106
POL	NTPPLVKLWY	610	10	57	89	0.0002	12107
POL	AIKKKDSTKW	251	11	57	89		12108
POL	VNTPPLVKLW	609	11	57	89		12109
POL	MAVFIHNFKR	930	11	57	89		12110
POL	GGIGGYSAGER	941	11	57	89		12111
POL	KDSTKWRK	255	8	58	91		12112

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	EVQLGIPH	278	8	58	91		12113
POL	GGNEQVDK	735	8	58	91		12114
POL	FIHNFKRK	933	8	58	91		12115
POL	GGYSAGER	944	8	58	91		12116
POL	RVYYRDSR	976	8	58	91		12117
POL	IGGNEQVDK	734	9	58	91	0.0001	12118
POL	VFIHNFKRK	932	9	58	91	0.0003	12119
POL	IGGYSAGER	943	9	58	91	0.0001	12120
POL	GIGGNEQVDK	733	10	58	91	0.0001	12121
POL	PAETGQETAY	842	10	58	91		12122
POL	AVFIHNFKRK	931	10	58	91	0.8500	12123
POL	GIGGYSAGER	942	10	58	91	0.0001	12124
POL	STKWRKLVDF	257	11	58	91		12125
POL	KGIGGNEQVDK	732	11	58	91		12126
POL	AVHVASGY	828	8	59	92		12127
POL	ETGQETAY	844	8	59	92		12128
POL	GIWQLDCTH	811	9	59	92		12129
POL	VAVHVASGY	827	9	59	92	0.0001	12130
POL	KGPAKLLWK	988	9	59	92	0.0007	12131
POL	EVNIVTDSQY	684	10	59	92		12132
POL	PGIWQLDCTH	810	10	59	92		12133
POL	TAVQMAVFIH	926	10	59	92	0.0110	12134
POL	VGKLNWASQI	450	11	59	92		12135
POL	NFKRKGGIGGY	936	11	59	92		12136
POL	QLDCTHLEGK	814	10	60	95	0.0003	12137
POL	DFRELNKR	265	8	60	94		12138
POL	VLDVGDAY	297	8	60	94		12139
POL	KNLKTGKY	539	8	60	94		12140
POL	VDFRELNKR	264	9	60	94		12141
POL	MGYELHPDK	419	9	60	94	0.0960	12142
POL	KLNWASQIY	452	9	60	94	0.0006	12143
POL	AVQMAVFIH	927	9	60	94		12144
POL	MAVFIHNFK	930	9	60	94	0.3000	12145
POL	LVDFRELNKR	263	10	60	94		12146
POL	WMGYELHPDK	418	10	60	94	0.0004	12147
POL	QMAVFIHNFK	929	10	60	94	0.6400	12148
POL	MAVFIHNFKR	930	10	60	94	0.0083	12149
POL	KLVDFRELNK	262	11	60	94		12150
POL	QMAVFIHNFK	929	11	60	94		12151
POL	LNWASQIY	453	8	61	95		12152
POL	NDIQKLVGK	444	9	61	95		12153
POL	LDCTHLEGK	815	9	61	95		12154
POL	VNDIQKLVGK	443	10	61	95		12155
POL	TVNDIQKLVGK	442	11	61	95	0.1700	12156
POL	VDFRELNK	264	8	62	97		12157
POL	WTVNDIQK	441	8	62	97	0.0001	12158
POL	DIQKLVGK	445	8	62	97		12159
POL	NIVTDSQY	686	8	62	97		12160
POL	DCTHLEGK	816	8	62	97		12161
POL	AVFIHNFK	931	8	62	97	0.0380	12162

Table XVII
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	VFIIINFKR	932	8	62	97		12163
POL	LVDFRELNK	263	9	62	97	0.0300	12164
POL	VNIVTDSQY	685	9	62	97		12165
POL	AVFIIINFKR	931	9	62	97	1.8000	12166
POL	MIGGIGGFIK	133	10	62	97	0.0550	12167
POL	KLVDFRELNK	262	10	62	97	0.0900	12168
POL	KMIGGIGGFIK	132	11	62	97	0.7000	12169
POL	NVLPQGWK	336	8	63	100	0.0012	12170
POL	IGGIGGFIK	134	9	63	98	0.0037	12171
POL	YNVLPQGWK	335	9	63	98	0.0001	12172
POL	GGIGGFIK	135	8	64	100		12173
POL	FLWMGYELII	416	9	64	100		12174
POL	PFLWMGYELII	415	10	64	100		12175
REV	GTRQTRKNR	37	9	01	50		12176
REV	TTRQARRNR	37	9	01	50		12177
REV	GTRQTRKNRR	37	10	01	50		12178
REV	TTRQARRNRR	37	10	01	50		12179
REV	GTRQTRKNRR	37	11	01	50		12180
REV	TTRQARRNRR	37	11	01	50		12181
REV	GTETGVGR	103	8	06	19		12182
REV	QGTETGVGR	102	9	06	19		12183
REV	LLKTVRLIK	12	9	10	16		12184
REV	GDSDEELLK	6	9	11	17		12185
REV	PLQLPPIER	76	9	11	17		12186
REV	SGDSDEELLK	5	10	11	17		12187
REV	RSGDSDEELLK	4	11	11	17		12188
REV	PVPLQLPPIER	74	11	11	17		12189
REV	RARQRQIR	50	8	12	19		12190
REV	DSDEELLK	7	8	12	19		12191
REV	ILSTCLGR	63	8	12	19		12192
REV	RILSTCLGR	62	9	12	19		12193
REV	SNPPPSPEGTR	27	11	12	19		12194
REV	AVRIIKILY	17	9	13	20		12195
REV	QLPPLERLII	78	9	13	20		12196
REV	PSPEGTRQAR	31	10	13	20		12197
REV	RNRRRRWRER	43	10	13	20		12198
REV	PSPEGTRQAR	31	11	13	20		12199
REV	PLQLPPLERLII	76	11	13	20		12200
REV	GTRQARKNRR	36	11	14	22		12201
REV	RARQRQIII	50	8	15	24		12202
REV	GTRQARKNR	36	9	15	23		12203
REV	GTRQARKNRR	36	10	15	23		12204
REV	QARKNRRRR	40	9	16	25		12205
REV	QARKNRRRR	40	11	16	25		12206
REV	QARKNRRR	40	8	17	27		12207
REV	IIKILYQSNPY	20	11	18	28		12208
REV	KNRRRRWRA	43	10	19	30		12209
REV	KNRRRRWR	43	8	21	33		12210
REV	RNRRRRWRA	43	10	23	36		12211
REV	KILYQSNPY	22	9	26	41		12212

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
REV	ILYQSNPY	23	8	27	42		12213
REV	EGTRQARR	35	8	27	42		12214
REV	EGTRQARRNR	35	10	27	42		12215
REV	EGTRQARRNR	35	11	27	42		12216
REV	GTRQARRNR	36	9	34	53		12217
REV	GTRQARRNRR	36	10	34	53		12218
REV	GTRQARRNRR	36	11	34	53		12219
REV	PVPLQLPPLER	74	11	34	53		12220
REV	PLQLPPLER	76	9	35	55		12221
REV	QARRNRRRR	40	11	37	58		12222
REV	QARRNRRR	40	8	38	59		12223
REV	QARRNRRRR	40	9	38	59		12224
REV	RNRRRRWR	43	8	40	63		12225
TAT	PGGYPRRK	104	8	01	50		12226
TAT	AGPGGYPRR	102	9	01	50		12227
TAT	TGPSGQPCH	102	9	01	50		12228
TAT	ETGPSGQPCH	101	10	01	50		12229
TAT	KAGPGGYPRR	101	10	01	50		12230
TAT	AGPGGYPRRK	102	10	01	50		12231
TAT	KAGPGGYPRR	101	11	01	50		12232
TAT	GGYPRRKGSC	105	11	01	50		12233
TAT	ACTNCYCK	24	8	10	16		12234
TAT	TACTNCYCK	23	9	10	16		12235
TAT	CNNCYCKK	25	8	11	17		12236
TAT	YCKKCCFH	29	8	11	17		12237
TAT	YCKKCCYH	29	8	11	17		12238
TAT	VDPRLEPWK	4	9	11	17		12239
TAT	ACNNCYCKK	24	9	11	17		12240
TAT	PVDPRLEPWK	3	10	11	17	0.0001	12241
TAT	VDPRLEPWKH	4	10	11	17		12242
TAT	TACNNCYCKK	23	10	11	17		12243
TAT	PVDPRLEPWK	3	11	11	17		12244
TAT	RGDPTGPKES	84	11	11	17		12245
TAT	GDPTGPKESK	85	11	11	17		12246
TAT	ESKKKVESK	93	9	12	19		12247
TAT	GDPTGPKESK	85	10	12	19		12248
TAT	PTGPKESKKK	88	10	12	19		12249
TAT	TGPKESKKK	89	9	13	20		12250
TAT	LNKGLGISY	42	9	14	22		12251
TAT	FLNKGLGISY	41	10	14	22		12252
TAT	PVDPNLEPWN	3	11	14	22		12253
TAT	CFLNKGLGISY	40	11	14	22		12254
TAT	LNKGLGISYGR	42	11	14	22		12255
TAT	WNHPGSQPK	14	9	15	23		12256
TAT	RGDPTGPK	84	8	16	25		12257
TAT	VDPNLEPWNH	4	10	16	25		12258
TAT	PNLEPWNH	9	8	17	27		12259
TAT	ACNNCYCK	24	8	17	27		12260
TAT	TACNNCYCK	23	9	17	27		12261
TAT	PTGPKESKK	88	9	18	28		12262

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
TAT	TGPKESKK	89	8	19	30		12263
TAT	PTGPKESK	88	8	20	31		12264
TAT	YGRKKRRQRR	50	11	22	34		12265
TAT	YGRKKRRQRR	50	10	38	59		12266
TAT	ISYGRKKRRQR	48	11	39	61		12267
TAT	YGRKKRRQR	50	9	41	64		12268
TAT	GISYGRKKRR	47	10	45	70	0.0001	12269
TAT	LGISYGRKKRR	46	11	45	70		12270
TAT	ISYGRKKRR	48	9	46	72	0.0005	12271
TAT	GLGISYGRKKR	45	11	54	86		12272
TAT	GLGISYGR	45	8	55	87		12273
TAT	GLGISYGRK	45	9	55	87	0.0006	12274
TAT	GLGISYGRKK	45	10	55	87		12275
TAT	KGLGISYGR	44	9	55	86	0.0180	12276
TAT	KGLGISYGRK	44	10	55	86	0.0007	12277
TAT	KGLGISYGRKK	44	11	55	86		12278
TAT	GISYGRKKR	47	9	57	89	0.0005	12279
TAT	LGISYGRKKR	46	10	57	89		12280
TAT	LGISYGRK	46	8	58	91		12281
TAT	GISYGRKK	47	8	58	91		12282
TAT	ISYGRKKR	48	8	58	91		12283
TAT	LGISYGRKK	46	9	58	91	0.0005	12284
VIF	LIVWQVDR	8	8	10	16		12285
VIF	RMRINTWK	15	8	10	16		12286
VIF	LIKPKKIK	158	8	10	16		12287
VIF	KGWFYRHHY	36	9	10	16		12288
VIF	ALIKPKKIK	157	9	10	16		12289
VIF	VDRMRINTWK	13	10	10	16		12290
VIF	GVSIEWRLRR	87	10	10	16		12291
VIF	QVDRMRINTW	12	11	10	16		12292
VIF	RLVITTYWGL	65	11	10	16		12293
VIF	QTGERDWHLG	75	11	10	16		12294
VIF	GVSIEWRLRR	87	11	10	16		12295
VIF	IDPDLADQLIH	103	11	10	16		12296
VIF	LVEDRWNKPQ	178	11	10	16		12297
VIF	SIEWRLRR	89	8	11	17		12298
VIF	TALIKPKK	156	8	11	17		12299
VIF	LVEDRWNK	178	8	11	17		12300
VIF	VSIEWRLRR	88	9	11	17		12301
VIF	SIEWRLRRY	89	9	11	17		12302
VIF	LTALIKPKK	155	9	11	17		12303
VIF	KLVEDRWNK	177	9	11	17		12304
VIF	VSIEWRLRRY	88	10	11	17		12305
VIF	GLADQLIHMH	106	10	11	17		12306
VIF	ALTALIKPKK	154	10	11	17		12307
VIF	WNKPQKTRGH	183	10	11	17		12308
VIF	PGLADQLIHMH	105	11	11	17		12309
VIF	GLADQLIHMH	106	11	11	17		12310
VIF	LALTALIKPKK	153	11	11	17		12311
VIF	WNKPQKTRGH	183	11	11	17		12312

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VIF	WFYRHHYESR	38	11	12	19		12313
VIF	KGWFYRHH	36	8	12	19		12314
VIF	WGLQTGER	72	8	12	19		12315
VIF	QTGERDWH	75	8	12	19		12316
VIF	IVWQVDRMK	9	9	12	19		12317
VIF	KIRTWNSLVK	17	10	12	19		12318
VIF	LVKHHMYVSK	24	10	12	19		12319
VIF	GLQTGERDWH	73	10	12	19		12320
VIF	TGERDWHLGH	77	10	12	19		12321
VIF	HGVSIEWRLR	86	10	12	19		12322
VIF	IVWQVDRMKI	9	11	12	19		12323
VIF	KIRTWNSLVK	17	11	12	19		12324
VIF	SLVKHHMYVS	23	11	12	19		12325
VIF	LVKHHMYVSK	24	11	12	19		12326
VIF	WGLQTGERD	72	11	12	19		12327
VIF	WFYRHHYESR	38	10	13	21		12328
VIF	QVDRMKIR	12	8	13	20		12329
VIF	HPLGDAR	56	8	13	20		12330
VIF	ADQLHHMH	108	8	13	20		12331
VIF	CFSDSAIR	119	8	13	20		12332
VIF	FSDSAIRK	120	8	13	20		12333
VIF	SLQYLALK	149	8	13	20		12334
VIF	LTALIKPK	155	8	13	20		12335
VIF	LADQLHHMH	107	9	13	20		12336
VIF	ADQLHHMHY	108	9	13	20		12337
VIF	CFSDSAIRK	119	9	13	20		12338
VIF	GSLQYLALK	148	9	13	20		12339
VIF	ALTALIKPK	154	9	13	20		12340
VIF	SVKKLTEDR	174	9	13	20		12341
VIF	EVHHPLGDAR	54	10	13	20		12342
VIF	LADQLHHMHY	107	10	13	20		12343
VIF	DCFSESAIRK	118	10	13	20		12344
VIF	VGSLQYLALK	147	10	13	20		12345
VIF	LALTALIKPK	153	10	13	20		12346
VIF	PSVKKLTEDR	173	10	13	20		12347
VIF	FDCFSESAIRK	117	11	13	20		12348
VIF	YLALTALIKPK	152	11	13	20		12349
VIF	FSESAIRK	120	8	14	22		12350
VIF	IVSPRCEY	133	8	14	22		12351
VIF	GVSIEWRLR	87	9	14	22		12352
VIF	ADQLHHLYY	108	9	14	22		12353
VIF	CFSESAIRK	119	9	14	22		12354
VIF	VDRMRIRTWK	13	10	14	22		12355
VIF	LADQLHHLYY	107	10	14	22		12356
VIF	RCDYQAGHNK	137	10	14	22		12357
VIF	QVDRMRIRTW	12	11	14	22		12358
VIF	RIRTWNSLVK	17	11	14	22		12359
VIF	RMRIRTWK	15	8	15	23		12360
VIF	RTWKSLVK	19	8	15	23		12361
VIF	VSIEWRLR	88	8	15	23		12362

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VIF	ADQLHHLY	108	8	15	23		12363
VIF	RTWKSLVKH	19	9	15	23		12364
VIF	QGVSIEWRK	86	9	15	23		12365
VIF	LADQLHHLY	107	9	15	23		12366
VIF	AIRKAILGH	124	9	15	23		12367
VIF	CDYQAGHNK	138	9	15	23		12368
VIF	RIRTWKSLVK	17	10	15	23		12369
VIF	RIRTWNSLVK	17	10	15	23		12370
VIF	RTWKSLVKHH	19	10	15	23		12371
VIF	SAIRKAILGH	123	10	15	23		12372
VIF	RIRTWKSLVK	17	11	15	23		12373
VIF	LGQGVSIEWR	84	11	15	23		12374
VIF	VDPGLADQLIH	103	11	15	23		12375
VIF	ITTYWGLH	68	8	16	25		12376
VIF	GVSIEWRK	87	8	16	25		12377
VIF	RCDYQAGH	137	8	16	25		12378
VIF	LALTALIK	153	8	16	25		12379
VIF	VITTYWGLH	67	9	16	25		12380
VIF	YLALTALIK	152	9	16	25		12381
VIF	KTKGHRGSH	188	9	16	25	0.0001	12382
VIF	LVITTYWGLH	66	10	16	25		12383
VIF	WNKPQKTKGH	183	10	16	25		12384
VIF	WNKPQKTKGH	183	11	16	25		12385
VIF	EDRWNKPQKT	180	11	17	27		12386
VIF	WNKPQKTK	183	8	18	28		12387
VIF	KSLVKHHMY	22	9	18	28		12388
VIF	EDRWNKPQKT	180	11	18	28		12389
VIF	RCEYQAGHNK	137	10	19	30		12390
VIF	HIPLGEAR	56	8	20	31		12391
VIF	WNKPQKTR	183	8	20	31		12392
VIF	EVHIPLGEAR	54	10	20	31		12393
VIF	HTGERDWH	75	8	21	33		12394
VIF	DLADQLIH	106	8	21	33		12395
VIF	PDLADQLIH	105	9	21	33		12396
VIF	GLHTGERDWH	73	10	21	33		12397
VIF	WGLHTGERD	72	11	21	33		12398
VIF	VSPRCEYQAG	134	11	21	33		12399
VIF	LTEDRWNKPQ	178	11	21	33	0.0130	12400
VIF	GSHTMNGH	194	8	22	34		12401
VIF	RGSHTMNGH	193	9	22	34		12402
VIF	TTYWGLHTGE	69	11	22	34		12403
VIF	HLGHGVSIEW	83	11	22	34		12404
VIF	NSLVKHHMY	22	9	24	38		12405
VIF	WNSLVKHHM	21	10	24	38		12406
VIF	QGVSIEWR	86	8	25	39		12407
VIF	LGQGVSIEWR	84	10	25	39		12408
VIF	HLGQGVSIEW	83	11	25	39		12409
VIF	RCEYQAGH	137	8	26	41		12410
VIF	RTWNSLVKH	19	9	26	41		12411
VIF	RTWNSLVKHH	19	10	26	41		12412

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VIF	RTWNSLVK	19	8	27	42		12413
VIF	HGVSIEWR	86	8	27	42		12414
VIF	GLADQLIH	106	8	27	42		12415
VIF	PGLADQLIH	105	9	27	42		12416
VIF	LGHGVSIEWR	84	10	27	42		12417
VIF	YFDCFSESAIR	116	11	27	42		12418
VIF	WGLHTGER	72	8	28	44		12419
VIF	DCFSESAIR	118	9	28	44		12420
VIF	FDCFSESAIR	117	10	28	44		12421
VIF	WNSLVKHH	21	8	29	45		12422
VIF	CFSESAIR	119	8	29	45		12423
VIF	KLTEDRWNK	177	9	29	45	0.2700	12424
VIF	LTEDRWNK	178	8	31	48	0.0045	12425
VIF	IVWQVDRMRI	9	11	33	52		12426
VIF	QVDRMRIR	12	8	34	53		12427
VIF	EDRWNKPQK	180	9	39	61		12428
VIF	VMIVWQVDR	7	11	41	64		12429
VIF	QVMIVWQVDR	6	10	43	67		12430
VIF	MIVWQVDRM	8	10	43	67	0.0001	12431
VIF	AGHNKVGSLQ	142	11	43	67		12432
VIF	SLVKHHMY	23	8	44	69		12433
VIF	VMIVWQVDR	7	9	44	69	0.0220	12434
VIF	MIVWQVDR	8	8	46	72		12435
VIF	IVWQVDRMR	9	9	47	73	0.0007	12436
VIF	HNKVGSLQY	144	9	47	73		12437
VPR	#LPGRRGR	85	8	01	50		12438
VPR	NIRGRRVR	85	8	01	50		12439
VPR	WALELLEELK	18	10	09	15		12440
VPR	QLLFVHFR	66	8	10	16		12441
VPR	HSRIGHR	79	8	10	16		12442
VPR	RIGITRQR	81	8	10	16		12443
VPR	IGITRQRR	82	8	10	16		12444
VPR	ALELLEELK	19	9	10	16		12445
VPR	RIGITRQRR	81	9	10	16		12446
VPR	HSRIGITRQR	79	10	10	16		12447
VPR	HSRIGITRQRR	79	11	10	16		12448
VPR	WLHGLGQY	38	8	11	17		12449
VPR	HFRIGCRH	71	8	11	17		12450
VPR	HSRIGITR	79	8	11	17		12451
VPR	FHHFRIGCR	69	9	11	17		12452
VPR	LFHHFRIGCR	68	10	11	17		12453
VPR	FIHFRIGCRH	69	10	11	17		12454
VPR	FVHFRIGCQH	69	10	11	17		12455
VPR	HFRIGCRHSR	71	10	11	17		12456
VPR	LLFHHFRIGCR	67	11	11	17		12457
VPR	LFHHFRIGCRH	68	11	11	17		12458
VPR	LFVHFRIGCQH	68	11	11	17		12459
VPR	RIGCRHSR	74	8	12	19		12460
VPR	LGQHIYNTY	42	9	13	20		12461
VPR	LGQYIYETY	42	9	13	20		12462

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VPR	HFPRIWLH	33	8	14	22		12463
VPR	KSEAVRHFPR	27	10	14	22		12464
VPR	AVRHFPRIWL	30	11	14	22		12465
VPR	ELKSEAVR	25	8	16	25		12466
VPR	AGVEAHR	55	8	16	25		12467
VPR	ELKSEAVRH	25	9	16	25		12468
VPR	WAGVEAHR	54	9	16	25		12469
VPR	LLEELKSEAVR	22	11	16	25		12470
VPR	DTWAGVEAHR	52	11	16	25		12471
VPR	ELKNEAVR	25	8	17	27		12472
VPR	ELKNEAVRH	25	9	17	27		12473
VPR	LGQHIYETY	42	9	17	27		12474
VPR	LLEELKNEAVR	22	11	17	27		12475
VPR	EGVEAHR	55	8	18	28		12476
VPR	DTWEGVEAHR	52	11	18	28		12477
VPR	RARNGASR	93	8	19	30		12478
VPR	KNEAVRHFPR	27	10	19	30		12479
VPR	WLHGLGQH	38	8	20	31		12480
VPR	HGLGQHIY	40	8	20	31		12481
VPR	WLHGLGQHIY	38	10	20	31		12482
VPR	LFIHFRIGCQH	68	11	29	45		12483
VPR	FIHFRIGCQH	69	10	30	47		12484
VPR	HFPRPWLH	33	8	31	49		12485
VPR	AVRHFPRPWL	30	11	31	48		12486
VPR	ILQQLLFIHFR	63	11	35	55		12487
VPR	RILQQLLFIH	62	10	36	56		12488
VPR	ILQQLLFIH	63	9	37	58		12489
VPR	EDQGPQREPY	6	10	37	58		12490
VPR	QAPEDQGPQR	3	10	39	62		12491
VPR	WTLELLEELK	18	10	42	69		12492
VPR	QGPQREPY	8	8	43	68		12493
VPR	QLLFIHFR	66	8	44	69		12494
VPR	HFRIGCQH	71	8	44	69		12495
VPR	TLELLEELK	19	9	44	69		12496
VPR	HFRIGCQHSR	71	10	44	69		12497
VPR	RIGCQHSR	74	8	47	73		12498
VPR	EAVRHFPR	29	8	59	92		12499
VPU	LVQRKQDR	43	8	01	50		12500
VPU	VTLLSSSK	94	8	01	50		12501
VPU	LVQRKQDRR	43	9	01	50		12502
VPU	LVTLLSSSK	91	9	01	50		12503
VPU	RIKEIRDDSDY	64	11	01	50		12504
VPU	RIREIRDDSDY	64	11	01	50		12505
VPU	WTIVFIEYR	34	9	10	16		12506
VPU	TIVFIEYR	35	8	10	16		12507
VPU	IDRLIDRIR	54	9	10	16		12508
VPU	RLIDRIRER	56	9	10	16		12509
VPU	KIDRLIDRIR	52	10	10	16		12510
VPU	VVWTIVFIEYR	31	11	10	16		12511
VPU	WTIVFIEY	34	8	12	19		12512

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VPU	IVFIEYRK	36	8	12	19		12513
VPU	VVWTIVFIEY	31	10	12	19		12514
VPU	IVVWTIVFIEY	30	11	12	19		12515
VPU	LIDRIRER	58	8	14	22		12516
VPU	KIDRLIDR	52	8	15	23		12517
VPU	ILRQRKIDR	46	9	15	23		12518
VPU	KILRQRKIDR	45	10	15	23	0.0001	12519

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
ENV	HMLQLTVW	650	8	10	16		12520
ENV	WFDITNWL	767	8	10	16		12521
ENV	WFDITNWLW	767	9	10	16		12522
ENV	HYCTPAGFAI	262	10	10	16		12523
ENV	IWNNMTWME	717	10	10	16		12524
ENV	WFDITNWLW	767	11	10	16		12525
ENV	SYHRLRDLLLI	864	11	10	16		12526
ENV	HYCTPAGF	262	8	11	17		12527
ENV	FYATGDIIGDI	367	11	11	17		12528
ENV	FYATGDII	367	8	12	19		12529
ENV	WMEWEREI	723	8	12	19		12530
ENV	GWEALKYL	896	8	12	19		12531
ENV	GWEGLKYL	896	8	12	19		12532
ENV	TWMEWEREI	722	9	12	19		12533
ENV	SYHRLRDLLL	864	10	12	19		12534
ENV	NMTWMEWER	720	11	12	19		12535
ENV	YWGQELKNSA	909	11	12	19		12536
ENV	LYKYKVVEI	561	9	13	20		12537
ENV	SYHRLRDFI	864	9	13	20		12538
ENV	SYHRLRDFIL	864	10	13	20		12539
ENV	VMHSFNCGGE	432	11	13	20		12540
ENV	LFSYHRLRDFI	862	11	13	20		12541
ENV	LFSYHRLRDLL	862	11	13	20		12542
ENV	SYHRLRDLL	864	9	14	22		12543
ENV	KYWWNLLQY	901	10	14	22		12544
ENV	WWNLLQYW	903	8	15	23		12545
ENV	YWWNLLQYW	902	9	15	23		12546
ENV	KWASLWNWF	760	11	15	23		12547
ENV	SFNCRGEF	437	8	16	25		12548
ENV	SFNCRGEFF	437	9	16	25		12549
ENV	KWLWYIKIF	772	9	16	25		12550
ENV	KWLWYIKIFI	772	10	16	25		12551
ENV	RYLRDQQLL	671	9	17	27	0.2300	12552
ENV	RYLRDQQLLGI	671	11	17	27		12553
ENV	RYLRDQQL	671	8	18	28		12554
ENV	SYHRLRDF	864	8	18	28		12555
ENV	AYDTEVHNVW	73	10	18	28		12556
ENV	LFSYHRLRDF	862	10	18	28		12557
ENV	KWLWYIKI	772	8	19	30		12558
ENV	AWDDLRSL	853	8	20	31		12559
ENV	NMVEQMHEDI	112	10	20	31	0.0004	12560
ENV	AWDDLRSLCL	853	10	20	31		12561
ENV	NMVEQMHEDII	112	11	20	31		12562
ENV	AWDDLRSLCL	853	11	20	31		12563
ENV	FYCNTSGL	445	8	21	33		12564
ENV	FFYCNTSGL	444	9	21	33		12565
ENV	FYCNTSGLF	445	9	21	33		12566
ENV	EFFYCNTSGL	443	10	21	33		12567
ENV	FFYCNTSGLF	444	10	21	33		12568
ENV	EFFYCNTSGLF	443	11	21	33		12569

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
ENV	VWKEATTTL	55	9	22	34	0.0300	12570
ENV	VWKEATTTLF	55	10	22	34	0.2700	12571
ENV	LFSYHRLRDL	862	10	22	34		12572
ENV	SYHRLRDL	864	8	23	36		12573
ENV	NWLWYIKI	772	8	25	39		12574
ENV	NWLWYIKIF	772	9	25	39		12575
ENV	KYKVVKIEPL	563	10	25	39		12576
ENV	NWLWYIKIFI	772	10	25	39		12577
ENV	GFLALAWDDL	848	10	25	39		12578
ENV	RYLKDQQLLGI	671	11	25	39		12579
ENV	KWASLWNW	760	8	26	41		12580
ENV	KWASLWNWF	760	9	26	41		12581
ENV	HYCAPAGF	262	8	27	42		12582
ENV	HYCAPAGFAI	262	10	27	42		12583
ENV	HYCAPAGFAIL	262	11	27	42		12584
ENV	QMHEDIISL	116	9	29	45		12585
ENV	LYKYKVVKI	561	9	29	45	0.0200	12586
ENV	RYLKDQQLL	671	9	29	45	0.7600	12587
ENV	QMHEDIISLW	116	10	29	45		12588
ENV	GYSPLSFQTL	806	10	29	45		12589
ENV	RYLKDQQL	671	8	30	47		12590
ENV	IFIMIVGGLI	779	10	33	52		12591
ENV	IMIVGGLIGL	781	10	34	54		12592
ENV	IMIVGGLI	781	8	35	56		12593
ENV	SFNCGGEFF	437	9	35	55		12594
ENV	SFNCGGEF	437	8	36	56		12595
ENV	DMRDNWRSEL	552	10	37	58		12596
ENV	TMGAASITL	615	9	39	61		12597
ENV	IFIMIVGGL	779	9	41	64		12598
ENV	WYIKIFIMI	775	9	43	67		12599
ENV	LWYIKIFIMI	774	10	43	67		12600
ENV	IWGCSGKL	681	8	48	75		12601
ENV	IWGCSGKLI	681	9	48	75	0.0270	12602
ENV	LWYIKIFI	774	8	49	77		12603
ENV	VYYGVPVW	49	8	55	86		12604
GAG	LYPLASLKSL	544	10	09	17		12605
GAG	LYPLASLKSLF	544	11	09	17		12606
GAG	KYKLKHIVW	29	9	10	16		12607
GAG	GWMTSNPPI	269	9	10	16		12608
GAG	IMMQKSNF	408	8	11	17		12609
GAG	LYCVHQKI	87	8	13	20		12610
GAG	MYSPTSILDI	300	10	13	20		12611
GAG	RMYSPTSILDI	299	11	13	20		12612
GAG	RMYSPTSI	299	8	14	22		12613
GAG	MYSPTSIL	300	8	14	22		12614
GAG	RMYSPTSIL	299	9	14	22		12615
GAG	RFAVNPGL	45	8	16	25		12616
GAG	LFNTVATL	80	8	16	25		12617
GAG	WMTSNPPI	270	8	16	25		12618
GAG	NWMTDTLL	339	8	16	25		12619

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
GAG	KYRLKHLVW	29	9	16	25		12620
GAG	RFAVNPGLL	45	9	16	25	0.0100	12621
GAG	LYCVHQRI	87	8	18	28		12622
GAG	GWMTNNPPI	269	9	18	28	0.0140	12623
GAG	RFALNPGL	45	8	20	31		12624
GAG	WMTNNPPI	270	8	20	31		12625
GAG	RFALNPGLL	45	9	20	31		12626
GAG	LYNTVATL	80	8	22	34		12627
GAG	AWVKVIEEKA	175	11	24	38		12628
GAG	AMQMLKETI	218	9	26	41		12629
GAG	IMMQRGNF	408	8	27	42		12630
GAG	DYVDRFFKTL	319	10	27	42		12631
GAG	CFNCGKEGHI	425	10	27	42		12632
GAG	CFNCGKEGHL	425	10	27	42		12633
GAG	DYVDRFYKTL	319	10	28	44	0.0010	12634
GAG	AWVKVVEEKA	175	11	28	44		12635
GAG	NYPIVQNL	152	8	31	48		12636
GAG	AMQMLKDTI	218	9	33	52		12637
GAG	PFRDYVDRFF	316	10	35	55		12638
GAG	NWMTETLL	339	8	36	56		12639
GAG	RMYSPVSILDI	299	11	38	59		12640
GAG	RMYSPVSI	299	8	40	63		12641
GAG	RMYSPVSIL	299	9	40	63		12642
GAG	MYSPVSILDI	300	10	40	63		12643
GAG	MYSPVSIL	300	8	42	66		12644
GAG	QMREPRGSDI	248	10	44	69		12645
GAG	VWASRELERF	36	10	45	70		12646
GAG	AFSPEVIPMF	184	10	50	78	0.0078	12647
GAG	IYKRWIIL	285	8	54	84		12648
GAG	IYKRWIILGL	285	10	54	84	0.0140	12649
GAG	RWIILGLNKI	288	10	56	88		12650
GAG	PFRDYVDRF	316	9	63	98		12651
NEF	PMTYKGAF	105	8	12	19		12652
NEF	TYKGAFDL	107	8	12	19		12653
NEF	PMTYKGAFDL	105	10	12	19		12654
NEF	VYHTQGFF	192	8	13	20		12655
NEF	LWVYHTQGF	190	9	13	20		12656
NEF	LWVYHTQGFF	190	10	13	20		12657
NEF	NYTPGPGTRF	206	10	13	20		12658
NEF	VYHTQGFFPD	192	11	13	20		12659
NEF	RFPLTFGWCF	216	10	17	27		12660
NEF	IYSKKRQEI	175	9	18	29		12661
NEF	IYSKKRQEIL	175	10	18	29		12662
NEF	AFDLSFFL	111	8	18	28		12663
NEF	DWQNYTPGPG	203	11	18	28		12664
NEF	RFPLTFGW	216	8	20	32		12665
NEF	NYTPGPGI	206	8	20	31		12666
NEF	KWSKSSIVGW	4	10	20	31		12667
NEF	RYPLTFGWCF	216	10	21	33		12668
NEF	VYHTQGYF	192	8	21	33		12669

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
NEF	LWVYHTQGYF	190	10	21	33		12670
NEF	VYHTQGYFPD	192	11	21	33		12671
NEF	SFFLKEKGGL	115	10	22	34		12672
NEF	FFLKEKGGL	116	9	26	41		12673
NEF	RYPLTFGW	216	8	27	43		12674
NEF	HFLKEKGGL	116	9	29	45		12675
NEF	TFGWCFKL	222	8	40	63		12676
NEF	GFPVRPQVPL	93	10	48	75		12677
POL	AFPQGEAREF	7	10	10	16		12678
POL	NMLTQLGCTL	175	10	10	16		12679
POL	TWETWWTDY	589	10	10	16		12680
POL	TWWTDYWQA	592	11	10	16		12681
POL	CWWAGIQQEF	882	10	11	17		12682
POL	IWGKIPKF	574	8	11	17		12683
POL	WYQLETEPI	618	9	11	17		12684
POL	WWAGIQQEF	883	9	11	17		12685
POL	IYPGIKVKQL	459	10	11	17		12686
POL	LWYQLETEPI	617	10	11	17		12687
POL	WWAGIQQEFG	883	11	11	17		12688
POL	QYDQIPIEI	145	9	12	19		12689
POL	KWTVQPIVL	427	9	12	19		12690
POL	LWQRPLVTVK	92	11	12	19		12691
POL	TWWTEYWQA	592	11	12	19		12692
POL	SFSFPQITLW	84	10	13	20		12693
POL	SFSFPQITL	84	9	14	22		12694
POL	WYQLEKDPI	618	9	14	22		12695
POL	YYRDSRDPL	978	9	14	22		12696
POL	WWTDYWQAT	593	10	14	22		12697
POL	LWYQLEKDPI	617	10	14	22		12698
POL	VYYRDSRDPL	977	10	14	22		12699
POL	YYRDSRDPLW	978	10	14	22		12700
POL	LWQRPLVTIKI	92	11	14	22		12701
POL	PFRKQNPDIVI	359	11	14	22		12702
POL	WWTDYWQAT	593	11	14	22		12703
POL	GYSAGERIVDI	945	11	14	22		12704
POL	VYYRDSRDPL	977	11	14	22		12705
POL	FFREDLAF	1	8	15	23		12706
POL	IYPGIKVRQL	459	10	15	23		12707
POL	PFRKQNPDI	359	9	16	25		12708
POL	RWKPKMIGGI	128	10	17	27		12709
POL	IWGKTPKFKL	574	10	17	27		12710
POL	YFSVPLDKDF	304	10	18	29		12711
POL	LWKGPAKLL	986	9	18	28		12712
POL	NMLTQIGCTL	175	10	18	28		12713
POL	IYAGIKVKQL	459	10	18	28		12714
POL	LWKGPAKLLW	986	10	18	28		12715
POL	AYFSVPLDKDF	303	11	18	28		12716
POL	AMASDFNLPPI	773	11	18	28		12717
POL	LWKGPAKL	986	8	19	30		12718
POL	DYWQATWIPE	596	11	19	30		12719

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	DYWQATWI	596	8	20	31		12720
POL	KFKLPIQKETW	580	11	20	31		12721
POL	CWWAGIKQEF	882	10	21	33		12722
POL	LWQRPLVTI	92	9	21	33	0.0190	12723
POL	WWAGIKQEF	883	9	21	33	0.0120	12724
POL	WWAGIKQEFG	883	11	21	33		12725
POL	NFPQITLW	86	8	22	34		12726
POL	AWVPAHKGI	726	9	22	34		12727
POL	SFPQITLW	86	8	23	36		12728
POL	WWTEYWQAT	593	10	23	36		12729
POL	WWTEYWQAT	593	11	23	36		12730
POL	PYNTPIFAI	244	9	24	38		12731
POL	YFLLKLAGRW	851	10	25	39		12732
POL	AYFLLKLAGR	850	11	25	39		12733
POL	KFRLPIQKETW	580	11	26	41		12734
POL	QYDQILIEI	145	9	27	42		12735
POL	NWASQIYAGI	454	10	27	42		12736
POL	KWTVQPIQL	427	9	28	44		12737
POL	NWASQIYPGI	454	10	29	45		12738
POL	IWGKTPKFRL	574	10	30	47		12739
POL	WYQLEKEPI	618	9	31	48	0.0001	12740
POL	VYYDPSKDLI	509	10	31	48	0.0150	12741
POL	LWYQLEKEPI	617	10	31	48		12742
POL	YFILKLAGRW	851	10	31	48		12743
POL	AYFILKLAGR	850	11	31	48		12744
POL	EMEKEGKISKI	229	11	32	50		12745
POL	EYWQATWIPE	596	11	33	52		12746
POL	YYRDSRDPI	978	9	34	53		12747
POL	VYYRDSRDPI	977	10	34	53		12748
POL	YYRDSRDPIW	978	10	34	53		12749
POL	VYYRDSRDPI	977	11	34	53		12750
POL	YYDPSKDLI	510	9	35	55		12751
POL	IWKGPAKLL	986	9	35	55		12752
POL	IWKGPAKLLW	986	10	35	55		12753
POL	IWKGPAKL	986	8	36	56		12754
POL	EYWQATWI	596	8	37	58		12755
POL	PYNTPVFAI	244	9	37	58	0.0310	12756
POL	SWVPAHKGI	726	9	37	58		12757
POL	KYTAFTIPSI	315	10	37	58		12758
POL	IFQSSMTKI	348	9	38	59	0.0029	12759
POL	IFQSSMTKIL	348	10	38	59	0.0002	12760
POL	VYYDPSKDL	509	9	39	61	0.0004	12761
POL	IYQEPFKNL	533	9	40	63	0.0520	12762
POL	GYSAGERHDI	945	11	40	63		12763
POL	FFRENLAF	1	8	41	64		12764
POL	GYSAGERII	945	9	41	64		12765
POL	GFIKVRQYDQI	139	11	41	64		12766
POL	NWRAMASDF	770	11	41	64		12767
POL	EMEKEGKI	229	8	42	66		12768
POL	DFRKYTAF	312	8	42	66		12769

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	TYQIYQEPF	530	9	42	66	0.3000	12770
POL	KWKPKMIGGI	128	10	42	66		12771
POL	DFRKYTAFTI	312	10	42	66		12772
POL	QWTYQIYQEP	528	11	42	66		12773
POL	YYDPSKDL	510	8	43	67		12774
POL	SMTKILEPF	352	9	43	67	0.0110	12775
POL	NWRAMASDF	770	9	43	67	0.0016	12776
POL	AMASDFNL	773	8	45	70		12777
POL	IWGKTPKF	574	8	48	75		12778
POL	EWEFVNTPPL	605	10	50	78		12779
POL	GMDGPKVKQ	201	10	51	80		12780
POL	TWIPEWEF	601	8	52	81		12781
POL	YWQATWIPE	597	10	52	81	0.0660	12782
POL	SMNKELKKI	905	9	53	83		12783
POL	SMNKELKKII	905	10	53	83		12784
POL	EFVNTPPL	607	8	54	84		12785
POL	GYIEAEVI	834	8	54	84		12786
POL	SWTVNDIQKL	440	10	54	84		12787
POL	EFVNTPPLVKL	607	11	54	84		12788
POL	QWPLTEEKI	210	9	56	88		12789
POL	DFWEVQLGI	275	9	56	88		12790
POL	FWEVQLGI	276	8	57	89		12791
POL	GYSAGERI	945	8	57	89		12792
POL	LYVGSDLEI	376	9	58	91		12793
POL	KWRKLVDF	259	8	59	92		12794
POL	GWKGSPAI	341	8	59	92		12795
POL	GWKGSPAIF	341	9	59	92		12796
POL	IWQLDCTHL	812	9	59	92	0.0095	12797
POL	LWKGEGAVVI	994	10	59	92		12798
POL	KWRKLVDFRE	259	11	59	92		12799
POL	NFKRKGGI	936	8	60	94		12800
POL	GYELHPDKW	420	9	60	94	0.0001	12801
POL	QMAVFIHNF	929	9	60	94	0.0190	12802
POL	WMGYELHPDK	418	11	60	94		12803
POL	IYQYMDDL	369	8	61	95		12804
POL	YMDDLYVGSD	372	11	61	95		12805
POL	KMIGGIGGF	132	9	62	97	0.0011	12806
POL	KMIGGIGGFI	132	10	62	97	0.0001	12807
POL	QYNVLPQGW	334	9	63	98	0.0036	12808
POL	RYQYNVLPQG	332	11	63	98		12809
POL	PFLWMGYEL	415	9	64	100		12810
REV	RWRERQRQI	48	9	11	17		12811
REV	RWRARQRQI	48	9	35	55		12812
TAT	CYCKKCCF	28	8	11	17		12813
TAT	CFHCQVCF	34	8	11	17		12814
TAT	CFLNKGLGI	40	9	14	22		12815
VIF	RWQVLIVW	4	8	10	16		12816
VIF	RYSTQVDPGL	98	10	10	16		12817
VIF	CFSDSAIRKAI	119	11	10	16		12818
VIF	QYLALKAL	151	8	11	17		12819

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
VIF	QYLALAAL	151	8	12	19		12820
VIF	RMKIRTWNSL	15	10	12	19		12821
VIF	YWGLQTGERD	71	11	12	19		12822
VIF	CFSESAIRKAI	119	11	12	19		12823
VIF	CFSESAIRNAI	119	11	12	19		12824
VIF	VWQVDRMKI	10	9	13	20		12825
VIF	HMHYFDCF	113	8	15	23		12826
VIF	RMRIRTWKSL	15	10	15	23		12827
VIF	RMRIRTWNSL	15	10	15	23		12828
VIF	DWHLGQGVSI	81	10	18	28		12829
VIF	YYFDCFSESAI	115	11	20	31		12830
VIF	DWHLGHGVSI	81	10	21	33		12831
VIF	YWGLHTGERD	71	11	22	34		12832
VIF	QYLALTALI	151	9	28	44		12833
VIF	YFDCFSESAI	116	10	28	44		12834
VIF	QYLALTAL	151	8	33	52		12835
VIF	RWQVMIVW	4	8	43	67		12836
VIF	VWQVDRMRI	10	9	48	75		12837
VPR	HFPRIWLHSL	33	10	10	16		12838
VPR	HFRIGCRHSRI	71	11	11	17		12839
VPR	PWLHGLGQHI	37	10	12	19		12840
VPR	QYIYETYGDT	44	11	14	22		12841
VPR	TWEGVEAHRI	53	11	14	22		12842
VPR	TWAGVEAHRI	53	11	15	23		12843
VPR	TWAGVEAI	53	8	16	25		12844
VPR	TWAGVEAH	53	9	16	25		12845
VPR	IYNTYGDTW	46	9	18	28		12846
VPR	TWEGVEAH	53	9	19	30		12847
VPR	TWEGVEAI	53	8	20	31		12848
VPR	HFPRPWLHGL	33	10	24	38		12849
VPR	PYNEWTLEL	14	9	30	47	0.1400	12850
VPR	PYNEWTLELL	14	10	30	47		12851
VPR	IYETYGDTW	46	9	31	48	0.0580	12852
VPR	EWTLELLEEL	17	10	40	63		12853
VPR	HFRIGCQHSRI	71	11	44	69		12854
VPU	NYELAVGAL	5	9	01	25		12855
VPU	NYELAVGALI	5	10	01	25		12856
VPU	DYKLGVGAL	10	9	02	29		12857
VPU	DYKLGVGALI	10	10	02	29		12858
VPU	DYRLGVGAL	10	9	03	43		12859
VPU	DYRLGVGALI	10	10	03	43		12860
VPU	EMGHHAPW	89	8	11	17		12861
VPU	VFIEYRKI	37	8	12	19		12862
VPU	EYRKILRQRKI	41	11	13	21		12863

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	VSTQLLLNG	61	95	KPVVSTQLLLNGSLA	299	29	45	12864
ENV	VVSTQLLLN	60	94	IKPVVSTQLLLNGSL	298	29	45	12865
ENV	LTVWGIKQL	59	92	LLQLTVWGIKQLQAR	651	26	41	12866
ENV	LLSGIVQQQ	58	91	ARQLLSGIVQQQSNL	627	22	34	12867
ENV	WATHACVPT	56	88	HNVWATHACVPTDPN	79	44	69	12868
ENV	LGAAGSTMG	55	86	LGFLGAAGSTMGAAS	605	36	56	12869
ENV	VRQGYSPLS	55	86	VNRVRQGYSPLSFQT	800	36	57	12870
ENV	LLLNGSLAE	54	84	STQLLLNGSLAEEEV	303	16	25	12871
ENV	VKLTPLCVT	53	83	KPCVKLTPLCVTLNC	130	29	45	12872
ENV	LRAIEAQQH	51	80	NNLLRAIEAQQHLLQ	639	18	28	12873
ENV	VSTVQCTHG	51	80	CKNVSTVQCTHGIKP	285	14	22	12874
ENV	LGIWGCSGK	50	78	QQLLGIWGCSGKLIC	676	46	72	12875
ENV	LWDQSLKPC	50	78	IISLWDQSLKPCVKL	121	35	55	12876
ENV	LGFLGAAGS	49	77	AVFLGFLGAAGSTMG	602	19	30	12877
ENV	VWATHACVP	49	77	VHNVWATHACVPTDP	78	34	53	12878
ENV	WGIKQLQAR	49	77	LTVWGIKQLQARVLA	654	39	61	12879
ENV	LWYIKIFIM	43	67	TNWLWYIKIFIMIVG	771	11	17	12880
ENV	FCASDAKAY	42	66	TTLFCASDAKAYDTE	61	18	28	12881
ENV	IVGGLIGLR	42	66	FIMIVGGLIGLRIVF	780	22	34	12882
ENV	IFIMIVGGL	41	64	YIKIFIMIVGGLIGL	776	30	47	12883
ENV	VYYGVPVWK	41	64	WVTVYYGVPVWKEAT	46	22	34	12884
ENV	IKQLQARVL	40	63	VWGIKQLQARVLAVE	656	31	49	12885
ENV	IKIFIMIVG	39	61	LWYIKIFIMIVGGLI	774	31	48	12886
ENV	MGAASITLT	39	61	GSTMGAASITLTVQA	613	28	44	12887
ENV	YIKIFIMIV	39	61	WLWYIKIFIMIVGGL	773	38	59	12888
ENV	ITGLLLTRD	37	58	SSNITGLLLTRDGGK	516	06	9	12889
ENV	IPIHYCAPA	36	56	FEPIPIHYCAPAGFA	255	21	33	12890
ENV	MIVGGLIGL	36	56	IFIMIVGGLIGLRIV	779	22	34	12891
ENV	VQARQLLSG	36	56	TLTVQARQLLSGIVQ	622	35	55	12892
ENV	FEPIPIHYC	35	55	KVSFEPIPIHYCAPA	252	17	27	12893
ENV	LRSLCLFSY	35	55	WDDLRSLCLFSYHRL	854	28	44	12894
ENV	MWKNNMVEQ	35	55	NFNMWKNNMVEQMHE	105	11	17	12895
ENV	VHNVWATHA	35	55	DTEVHNVWATHACVP	75	17	27	12896
ENV	WKNNMVEQM	35	55	FNMWKNNMVEQMHED	106	20	31	12897
ENV	YYGVPVWKE	35	55	VTVYYGVPVWKEATT	47	22	34	12898
ENV	LLQLTVWGI	34	53	QQHLLQLTVWGIKQL	648	34	53	12899
ENV	IEPLGVAPT	33	52	VVKIEPLGVAPTKAK	566	12	19	12900
ENV	IKPVVSTQL	33	52	THGIKPVVSTQLLLN	295	32	50	12901
ENV	LQARVLAVE	33	52	IKQLQARVLAVERYL	659	32	50	12902
ENV	WDDLRSLCL	33	52	ALAWDDLRSLCLFSY	851	18	28	12903
ENV	IINIHTPHR	01	50	SRPIINIHTPHREKR	581	01	2	12904
ENV	INIHTPHRE	01	50	RPIINIHTPHREKRA	582	01	2	12905
ENV	ITQACPKVS	32	50	TSVITQACPKVSFEP	242	08	13	12906
ENV	IVQQQSNLL	32	50	LSGIVQQQSNLLRAI	631	26	41	12907
ENV	LGNNSTNST	01	50	NKTLGNNSTNSTLGN	151	01	2	12908
ENV	VISTRTHRE	01	50	ARPVISTRTHREKRA	580	01	2	12909
ENV	WRWGTLFLG	01	50	QNLWRWGTLFLGMLM	12	01	2	12910
ENV	WRWGTMLLG	01	50	QIILWRWGTMLLGMLM	12	03	5	12911
ENV	FAVLSIVNR	31	48	RIVFAVLSIVNRVRQ	791	14	22	12912
ENV	LLNGSLAEE	31	48	TQLLLNGSLAEEEVV	304	14	22	12913

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	LTPLCVTLN	29	45	CVKLTPLCVTLNCTD	132	11	17	12914
ENV	LYKYKVVKI	29	45	RSELYKYKVVKIEPL	558	23	36	12915
ENV	VPWNSSWSN	29	45	TTNVPWNSSWSNKSL	691	03	5	12916
ENV	YRLINCNTS	28	44	YKEYRLINCNTSAIT	232	01	8	12917
ENV	IHYCAPAGF	27	42	PIPIHYCAPAGFAIL	258	26	41	12918
ENV	LKDQQLLGI	27	42	ERYLKDQQLLGIWGC	670	25	39	12919
ENV	YKYKVVKIE	27	42	SELYKYKVVKIEPLG	559	24	38	12920
ENV	IRPVVSTQL	26	41	THGIRPVVSTQLLLN	295	26	41	12921
ENV	LDKWASLWN	26	41	LLALDKWASLWNWFD	755	08	13	12922
ENV	LRIVFAVLS	26	41	LIGLRIVFAVLSIVN	787	10	16	12923
ENV	LNGSLAEEE	25	39	QLLLNGSLAEEEVVI	305	13	20	12924
ENV	YKVVKIEPL	25	39	LYKYKVVKIEPLGVA	561	23	36	12925
ENV	LKGLRLGWE	11	37	RSSLKGLRLGWEGLK	885	04	7	12926
ENV	FSYHRLRDL	23	36	LCLFSYHRLRDLLLI	860	08	13	12927
ENV	INCTRPNNN	23	36	SVEINCTRPNNNTRK	340	05	8	12928
ENV	VVKIEPLGV	23	36	KYKVVKIEPLGVAPT	563	23	36	12929
ENV	WKEATTTLF	23	36	VPVWKEATTTLFCAS	53	22	34	12930
ENV	IGLRIVFAV	22	34	GGLIGLRIVFAVLSI	785	12	19	12931
ENV	FFYCNTSGL	21	33	GGEFFYCNTSGLFNS	441	07	11	12932
ENV	FGLGALFLG	01	33	RAAFGLGALFLGFLG	594	01	2	12933
ENV	FYCNTSGLF	21	33	GEFFYCNTSGLFNST	442	07	11	12934
ENV	LIGLRIVFA	21	33	VGGLIGLRIVFAVLS	784	17	27	12935
ENV	VGLGAVFLG	01	33	KRAVGLGAVFLGFLG	593	06	9	12936
ENV	VGLGMLFLG	01	33	KRAVGLGMLFLGVLS	594	01	2	12937
ENV	ICTTAVPWN	20	31	GKLICTTAVPWNSSW	686	09	14	12938
ENV	ICTTNVPWN	20	31	GKLICTTNVPWNSSW	686	08	13	12939
ENV	LGVAPTKAK	19	30	IEPLGVAPTKAKRRV	569	15	23	12940
ENV	LICTTAVPW	19	30	SGKLICTTAVPWNSS	685	09	14	12941
ENV	LRDQQLLGI	19	30	ERYLRDQQLLGIWGC	670	17	27	12942
ENV	VFLGFLGAA	19	30	LGAVFLGFLGAAGST	600	09	14	12943
ENV	FSYHRLRDF	18	28	LCLFSYHRLRDFILI	860	08	13	12944
ENV	IPIHYCTPA	18	28	FEPIPIHYCTPAGFA	255	10	16	12945
ENV	IVFAVLSIV	18	28	GLRIVFAVLSIVNRV	789	16	25	12946
ENV	VFAVLSIVN	18	28	LRIVFAVLSIVNRVR	790	16	25	12947
ENV	VPWNASWSN	18	28	TTAVPWNASWSNKSL	691	06	9	12948
ENV	IGLRIIFAV	17	27	GGLIGLRIIFAVLSI	785	11	17	12949
ENV	IRQAHCNIS	17	27	IGDIRQAHCNISRAK	378	02	3	12950
ENV	VAPTKAKRR	17	27	PLGVAPTKAKRRVVQ	571	10	16	12951
ENV	FNGTGPCKN	16	25	DKKFNGTGPCKNVST	276	05	8	12952
ENV	IGPGQTFYA	01	25	SVRIGPGQTFYATGD	355	03	5	12953
ENV	IGSGQAFYV	01	25	RYSIGSGQAFYVTGK	358	01	2	12954
ENV	IRYLNLVNQ	01	25	QTAIRYLNLVNQTEN	400	01	2	12955
ENV	LIGLRIIFA	16	25	VGGLIGLRIIFAVLS	784	12	19	12956
ENV	LLQYWSQEL	16	25	WWNLLQYWSQELKNS	903	09	14	12957
ENV	LRNLCLFSY	16	25	WDDLRNLCLFSYHRL	854	11	17	12958
ENV	LVSGFLALA	16	25	SIRLVSGFLALAWDD	842	09	14	12959
ENV	VSGFLALAW	16	25	IRLVSGFLALAWDDL	843	09	14	12960
ENV	FDPIPIHYC	15	23	KVTFDPIPIHYCTPA	252	03	5	12961
ENV	IIFAVLSIV	15	23	GLRIIFAVLSIVNRV	789	13	20	12962
ENV	LINCNTSAI	15	23	EYRLINCNTSAITQA	234	04	9	12963

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	LLNATAIAV	15	23	AVSLLNATAIAVAEG	918	10	16	12964
ENV	LRIIFAVLS	15	23	LIGLRIIFAVLSIVN	787	11	17	12965
ENV	VITQACPKV	15	23	NTSVITQACPKVSFE	241	08	13	12966
ENV	YWWNLLQYW	15	23	VLKYWWNLLQYWSQE	899	07	11	12967
ENV	FAILKCNDK	14	22	PAGFAILKCNDKKFN	266	09	14	12968
ENV	IFAVLSIVN	14	22	LRIIFAVLSIVNRVR	790	13	20	12969
ENV	INCNTSAIT	14	22	YRLINCNTSAITQAC	235	14	22	12970
ENV	LNATAIAVA	14	22	VSLLNATAIAVAEGT	919	10	16	12971
ENV	WNSSWSNKS	14	22	NVPWNSSWSNKSLDE	693	03	5	12972
ENV	WNASWSNKS	13	21	NVPWNASWSNKSYED	693	02	3	12973
ENV	ICTTTVPWN	13	20	GKLICTTTVPWNASW	686	06	9	12974
ENV	LLKLTVWGI	13	20	QQHLLKLTVWGIKQL	648	13	20	12975
ENV	LYKYKVVEI	13	20	RSELYKYKVVEIKPL	558	05	8	12976
ENV	MFLGFLGAA	13	20	LGAMFLGFLGAAGST	600	07	11	12977
ENV	MHSFNCGGE	13	20	EIVMHSFNCGGEFFY	430	13	20	12978
ENV	YWSQELKNS	13	20	LLQYWSQELKNSAVS	906	10	16	12979
ENV	IGAVFLGFL	12	19	AVGIGAVFLGFLGAA	595	09	14	12980
ENV	LIAARTVEL	12	19	DFILIAARTVELLGH	870	04	6	12981
ENV	LICTTTVPW	12	19	SGKLICTTTVPWNAS	685	06	9	12982
ENV	LLNGSLAEG	12	19	TQLLLNGSLAEGEII	304	03	5	12983
ENV	YWGQELKNS	12	19	LVWYWGQELKNSAIS	906	02	3	12984
ENV	IAARTVELL	11	17	FILIAARTVELLGHS	871	03	5	12985
ENV	LFLGFLGAA	11	17	IGALFLGFLGAAGST	600	06	9	12986
ENV	LKNSAVSLL	11	17	SQELKNSAVSLLNAT	911	08	13	12987
ENV	VGIGAVFLG	11	17	KRAVGIGAVFLGFLG	593	11	17	12988
ENV	VSLLNATAI	11	17	NSAVSLLNATAIAVA	916	09	14	12989
ENV	YATGDIIGD	11	17	QTFYATGDIIGDIRQ	365	04	6	12990
ENV	IAIAVAEGT	10	16	LDIIAIAVAEGTDRI	922	02	3	12991
ENV	IHYCTPAGF	10	16	PIPIHYCTPAGFAIL	258	08	13	12992
ENV	ILGLVIICS	10	16	GTLILGLVIICSASN	19	03	5	12993
ENV	IWNNMTWME	10	16	VDEIWNNMTWMEWER	714	01	2	12994
ENV	LGLVIICSA	10	16	TLILGLVIICSASNN	20	04	6	12995
ENV	LRDFILIAA	10	16	YIIRLRDFILIAARTV	865	06	9	12996
ENV	LTPLCVTLD	10	16	CVKLTPLCVTLDCHN	132	03	5	12997
ENV	MLQLTVWGI	10	16	QQHMLQLTVWGIKQL	648	08	13	12998
ENV	VEINCTRPN	10	16	NESVEINCTRPNNNT	338	02	3	12999
ENV	VRQLLSGIV	10	16	TVQVRQLLSGIVQQQ	624	08	13	13000
ENV	LILGLVIIC	09	15	WGTLILGLVIICSAS	18	07	11	13001
GAG	VGGHQAAMQ	60	94	LNTVGGHQAAMQMLK	209	47	73	13002
GAG	LLVQNANPD	59	92	TETLLVQNANPDCKT	342	26	41	13003
GAG	VQNANPDCK	59	92	TLLVQNANPDCKTIL	344	44	69	13004
GAG	LGLNKIVRM	58	91	WIILGLNKIVRMYSP	289	55	86	13005
GAG	LSEGATPQD	58	91	FSALSEGATPQDLNT	193	29	45	13006
GAG	WIILGLNKI	57	89	YKRWIILGLNKIVRM	286	54	84	13007
GAG	LEEMMTACQ	56	88	GATLEEMMTACQGVG	364	27	42	13008
GAG	YKRWIILGL	55	86	GEIYKRWIILGLNKI	283	37	58	13009
GAG	IYKRWIILG	54	84	VGEIYKRWIILGLNK	282	37	58	13010
GAG	VSQNYPIVQ	48	83	SSQVSQNYPIVQNLQ	145	09	19	13011
GAG	WEKIRLRPG	50	78	LDKWEKIRLRPGGKK	13	16	25	13012
GAG	IAGTTSTLQ	46	72	GSDIAGTTSTLQEQI	254	45	70	13013

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
GAG	WASRELERF	46	72	HLVWASRELERFALN	34	17	27	13014
GAG	IPMFSALSE	45	70	PEVIPMFSALSEGAT	187	44	69	13015
GAG	MFSALSEGA	45	70	VIPMFSALSEGATPQ	189	43	67	13016
GAG	VIPMFSALS	45	70	SPEVIPMFSALSEGA	186	40	63	13017
GAG	MYSPVSILD	41	64	IVRMYSPVSILDIRQ	297	23	36	13018
GAG	IVRMYSPVS	40	63	LNKIVRMYSPVSILD	294	39	61	13019
GAG	VRMYSPVSI	40	63	NKIVRMYSPVSILDI	295	38	59	13020
GAG	YSPVSILDI	40	63	VRMYSPVSILDIRQG	298	23	36	13021
GAG	MTETLLVQN	38	59	KNWMTETLLVQNANP	338	34	53	13022
GAG	WMTETLLVQ	37	58	VKNWMTETLLVQNAN	337	34	53	13023
GAG	ISPRTLNAW	36	56	HQAISPRTLNAWVKV	[illegible]	27	42	13024
GAG	VKNWMTETL	36	56	TQEVKNWMTETLLVQ	334	14	22	13025
GAG	IKCFNCGKE	34	53	QKRIKCFNCGKEGHL	418	05	8	13026
GAG	IPVGEIYKR	34	53	NPPIPVGEIYKRWII	277	32	51	13027
GAG	YTAVFMQRG	02	50	KGGYTAVFMQRGQNP	399	02	3	13028
GAG	VATLYCVHQ	30	47	YNTVATLYCVHQRIE	81	07	11	13029
GAG	WDRLHPVHA	29	45	AAEWDRLHPVHAGPI	230	22	34	13030
GAG	FLQSRPEPT	28	44	PGNFLQSRPEPTAPP	483	27	43	13031
GAG	FKTLRAEQA	27	42	DRFFKTLRAEQATQE	322	16	25	13032
GAG	MVHQAISPR	27	42	QGQMVHQAISPRTLN	160	26	41	13033
GAG	VHQAISPRT	27	42	GQMVHQAISPRTLNA	161	27	42	13034
GAG	YKTLRAEQA	27	42	DRFYKTLRAEQASQE	322	12	19	13035
GAG	VSILDIRQG	25	39	YSPVSILDIRQGPKE	301	24	38	13036
GAG	LAEAMSQVT	23	37	ARVLAEAMSQVTNSA	384	08	13	13037
GAG	LGKIWPSHK	23	36	ANFLGKIWPSHKGRP	467	22	34	13038
GAG	VKCFNCGKE	23	36	RKTVKCFNCGKEGHI	420	07	11	13039
GAG	YNTVATLYC	23	36	RSLYNTVATLYCVHQ	78	11	17	13040
GAG	LHPVHAGPI	22	34	WDRLHPVHAGPIAPG	233	15	23	13041
GAG	LYNTVATLY	22	34	LRSLYNTVATLYCVH	77	13	20	13042
GAG	MTDTLLVQN	22	34	KNWMTDTLLVQNANP	338	16	25	13043
GAG	WMTDTLLVQ	22	34	VKNWMTDTLLVQNAN	337	16	25	13044
GAG	IEVKDTKEA	21	33	HQRIEVKDTKEALDK	91	07	11	13045
GAG	LQGQMVHQA	21	33	VQNLQGQMVHQAISP	156	15	23	13046
GAG	MTNNPPIPV	20	31	IGWMTNNPPIPVGEI	268	16	25	13047
GAG	WMTNNPPIP	20	31	QIGWMTNNPPIPVGE	267	16	25	13048
GAG	IAPGQMREP	19	30	AGPIAPGQMREPRGS	241	19	30	13049
GAG	VHAGPIAPG	19	30	LHPVHAGPIAPGQMR	236	14	22	13050
GAG	LGPGATLEE	18	28	LRALGPGATLEEMMT	358	09	14	13051
GAG	VHAGPIPPG	18	28	VHPVHAGPIPPGQMR	236	10	16	13052
GAG	IPPGQMREP	17	27	AGPIPPGQMREPRGS	241	16	25	13053
GAG	LSPRTLNAW	17	27	HQALSPRTLNAWVKV	165	10	16	13054
GAG	YRLKHLVWA	17	27	KKKYRLKHLVWASRE	27	13	20	13055
GAG	LGPAATLEE	16	25	LKALGPAATLEEMMT	358	16	25	13056
GAG	LKALGPAAT	16	25	KTILKALGPAATLEE	355	16	25	13057
GAG	LKDKEPPLA	01	25	QEQLKDKEPPLASLR	532	01	2	13058
GAG	LSGGKLDAW	16	25	ASVLSGGKLDAWEKI	5	14	22	13059
GAG	MTSNPPIPV	16	25	IGWMTSNPPIPVGEI	268	06	9	13060
GAG	VKNWMTDTL	16	25	TQDVKNWMTDTLLVQ	334	11	17	13061
GAG	VSILDIKQG	16	25	YSPVSILDIKQGPKE	301	16	25	13062
GAG	WMTSNPPIP	16	25	QIGWMTSNPPIPVGE	267	06	10	13063

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
GAG	FNTVATLYC	15	23	KSLFNTVATLYCVHQ	78	07	11	13064
GAG	IPMFTALSE	15	23	PEVIPMFTALSEGAT	187	13	20	13065
GAG	LASLKSLFG	15	23	LYPLASLKSLFGNDP	544	06	11	13066
GAG	LERFAVNPG	15	23	SRELERFAVNPGLLE	39	14	22	13067
GAG	LFNTVATLY	15	23	LRSLFNTVATLYCVH	77	07	11	13068
GAG	MFTALSEGA	15	23	VIPMFTALSEGATPQ	189	14	22	13069
GAG	WDRVHPVHA	15	23	AAEWDRVHPVHAGPI	230	12	19	13070
GAG	IVRMYSPTS	14	22	LNKIVRMYSPTSILD	294	13	20	13071
GAG	LERFALNPG	14	22	SRELERFALNPGLLE	39	14	22	13072
GAG	LQEQIAWMT	14	22	TSTLQEQIAWMTGNP	261	05	8	13073
GAG	VHPVHAGPI	14	22	WDRVHPVHAGPIPPG	233	11	17	13074
GAG	VIPMFTALS	14	22	SPEVIPMFTALSEGA	186	13	20	13075
GAG	VRMYSPTSI	14	22	NKIVRMYSPTSILDI	295	13	20	13076
GAG	LGKIWPSNK	13	20	ANFLGKIWPSNKGRP	467	13	20	13077
GAG	LTSLKSLFG	13	20	LYPLTSLKSLFGNDP	544	04	7	13078
GAG	MYSPTSILD	13	20	IVRMYSPTSILDIRQ	297	12	19	13079
GAG	YKLKHIVWA	13	20	KKKYKLKHIVWASRE	27	08	13	13080
GAG	YSPTSILDI	13	20	VRMYSPTSILDIRQG	298	12	19	13081
GAG	LTSLRSLFG	12	19	LYPLTSLRSLFGNDP	544	04	7	13082
GAG	MMLNIVGGH	12	19	DLNMMLNIVGGHQAA	204	12	19	13083
GAG	IDVKDTKEA	11	17	HQRIDVKDTKEALDK	91	03	5	13084
GAG	IGWMTSNPP	11	17	QEQIGWMTSNPPIPV	265	09	14	13085
GAG	IPVGDIYKR	11	17	NPPIPVGDIYKRWII	277	08	13	13086
GAG	LYPLASLKS	09	17	DKELYPLASLKSLFG	541	06	10	13087
GAG	VHQALSPRT	11	17	GQMVHQALSPRTLNA	161	07	11	13088
GAG	VNPGLLETS	11	17	RFAVNPGLLETSEGC	45	11	17	13089
GAG	YPLASLKSL	08	17	KELYPLASLKSLFGN	542	06	9	13090
GAG	FLQNRPEPT	10	16	PQNFLQNRPEPTAPP	483	10	16	13091
GAG	IMMQKSNFK	10	16	AAAIMMQKSNFKGPR	405	01	25	13092
GAG	LAEAMSQVQ	10	16	ARVLAEAMSQVQQSN	384	02	3	13093
GAG	LGKIWPSSK	10	16	ANFLGKIWPSSKGRP	467	10	16	13094
GAG	LNPGLLETA	10	16	RFALNPGLLETAEGC	45	08	13	13095
GAG	YPLASLRSL	07	15	KELYPLASLRSLFGN	542	04	6	13096
NEF	WQNYTPGPG	52	83	FPDWQNYTPGPGIRY	200	15	23	13097
NEF	VRPQVPLRP	48	75	GFPVRPQVPLRPMTY	93	36	56	13098
NEF	VPLRPMTYK	46	73	RPQVPLRPMTYKGAF	98	07	11	13099
NEF	LTFGWCFKL	39	61	RYPLTFGWCFKLVPV	216	15	24	13100
NEF	ILDLWVYHT	34	53	RQEILDLWVYHTQGY	182	12	19	13101
NEF	WCFKLVPVD	26	41	TFGWCFKLVPVDPRE	222	07	11	13102
NEF	LWVYHTQGY	21	33	ILDLWVYHTQGYFPD	186	21	33	13103
NEF	WSKSSIVGW	20	31	GGKWSKSSIVGWPAI	2	05	8	13104
NEF	ILDLWVYNT	19	30	RQDILDLWVYNTQGY	182	05	8	13105
NEF	LLHPMSQHG	17	27	NNCLLHPMSQHGMDD	254	06	9	13106
NEF	LLHPICQHG	16	25	NNSLLHPICQHGMED	254	04	6	13107
NEF	IRYPLTFGW	13	20	GPGIRYPLTFGWCFK	210	06	9	13108
NEF	ITSSNTAAT	13	20	HGAITSSNTAATNAD	61	10	16	13109
NEF	LEKHGAITS	13	20	SRDLEKHGAITSSNT	50	13	20	13110
NEF	LWVYHTQGF	13	20	ILDLWVYHTQGFFPD	186	13	20	13111
NEF	MTYKGAFDL	12	19	LRPMTYKGAFDLSFF	103	06	9	13112
NEF	LVPVDPREV	11	17	CFKLVPVDPREVEEA	226	08	13	13113

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
NEF	VGWPAIRER	10	17	SSIVGWPAIRERMRR	8	03	5	13114
NEF	WCFKLVPVE	11	17	TFGWCFKLVPVEPEK	222	04	6	13115
NEF	FDSRLAFHH	10	16	EWRFDSRLAFHHVAR	307	02	3	13116
NEF	FKLVPVDPR	10	16	GWCFKLVPVDPREVE	224	10	16	13117
NEF	VPLRPMTFK	10	16	RPQVPLRPMTFKGAF	98	04	6	13118
POL	LLDTGADDT	63	98	KEALLDTGADDTVLE	107	37	58	13119
POL	WMGYELHPD	63	98	PFLWMGYELHPDKWT	415	60	94	13120
POL	YQYNVLPQG	63	98	GIRYQYNVLPQGWKG	330	52	81	13121
POL	FRKYTAFTI	61	97	DKDFRKYTAFTIPSI	310	10	16	13122
POL	WTVNDIQKL	62	97	KDSWTVNDIQKLVGK	438	43	67	13123
POL	LDCTHLEGK	61	95	IWQLDCTHLEGKIIL	812	29	45	13124
POL	LDVGDAYFS	61	95	VTVLDVGDAYFSVPL	295	50	78	13125
POL	MDDLYVGSD	61	95	YQYMDDLYVGSDLEI	370	57	89	13126
POL	VIPAETGQE	61	95	EAEVIPAETGQETAY	837	57	90	13127
POL	WKGEGAVVI	61	95	KLLWKGEGAVVIQDN	992	53	83	13128
POL	WQLDCTHLE	61	95	PGIWQLDCTHLEGKI	810	32	50	13129
POL	VDFRELNKR	60	94	RKLVDFRELNKRTQD	261	57	89	13130
POL	WKPKMIGGI	60	94	PGKWKPKMIGGIGGF	126	39	61	13131
POL	IWQLDCTHL	59	92	SPGIWQLDCTHLEGK	809	56	88	13132
POL	VAVHVASGY	59	92	IILVAVHVASGYIEA	824	26	41	13133
POL	WKGSPAIFQ	59	92	PQGWKGSPAIFQSSM	339	42	66	13134
POL	IGGYSAGER	58	91	KGGIGGYSAGERIID	940	37	59	13135
POL	YALGIIQAQ	58	91	DSQYALGIIQAQPDK	690	39	61	13136
POL	FWEVQLGIP	57	89	TQDFWEVQLGIPHPA	273	52	81	13137
POL	IKKKDSTKW	57	89	VFAIKKKDSTKWRKL	249	36	56	13138
POL	LGIIQAQPD	57	89	QYALGIIQAQPDKSE	692	39	61	13139
POL	LGIPHPAGL	56	89	EVQLGIPHPAGLKKK	278	51	80	13140
POL	VNTPPLVKL	57	89	WEFVNTPPLVKLWYQ	606	50	79	13141
POL	VTVLDVGDA	57	89	KKSVTVLDVGDAYFS	292	49	77	13142
POL	FPISPIETV	56	88	TLNFPISPIETVPVK	183	52	83	13143
POL	ISPIETVPV	56	88	NFPISPIETVPVKLK	185	52	81	13144
POL	FVNTPPLVK	54	86	EWEFVNTPPLVKLWY	605	50	78	13145
POL	LNFPISPIE	55	86	GCTLNFPISPIETVP	181	53	83	13146
POL	WEFVNTPPL	54	86	IPEWEFVNTPPLVKL	603	49	77	13147
POL	IQNFRVYYR	52	84	ITKIQNFRVYYRDSR	969	32	51	13148
POL	LVGPTPVNI	54	84	GTVLVGPTPVNIIGR	160	51	80	13149
POL	VQLGIPHPA	54	84	FWEVQLGIPHPAGLK	276	53	83	13150
POL	WQATWIPEW	54	84	TEYWQATWIPEWEFV	595	19	30	13151
POL	IETVPVKLK	53	83	ISPIETVPVKLKPGM	188	51	80	13152
POL	IGTVLVGPT	53	83	KKAIGTVLVGPTPVN	156	22	34	13153
POL	LVAVHVASG	53	83	KIILVAVHVASGYIE	823	26	41	13154
POL	VLVGPTPVN	53	83	IGTVLVGPTPVNIIG	159	45	70	13155
POL	YIEAEVIPA	53	83	ASGYIEAEVIPAETG	832	52	81	13156
POL	YVGSDLEIG	53	83	DDLYVGSDLEIGQHR	374	52	81	13157
POL	MDGPKVKQW	52	81	KPGMDGPKVKQWPLT	199	47	73	13158
POL	VASGYIEAE	52	81	AVHVASGYIEAEVIP	828	52	81	13159
POL	VGPTPVNII	52	81	TVLVGPTPVNIIGRN	161	51	80	13160
POL	VKQWPLTEE	52	81	GPKVKQWPLTEEKIK	205	45	70	13161
POL	VYYRDSRDP	52	81	NFRVYYRDSRDPIWK	974	29	45	13162
POL	WGFTTPDKK	52	81	LLRWGFTTPDKKHQK	398	23	36	13163

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	VIYQYMDDL	51	80	PEIVIYQYMDDLYVG	365	23	36	13164
POL	LKKKKSVTV	49	78	PAGLKKKKSVTVLDV	286	46	72	13165
POL	VPRRKAKII	50	78	IKVVPRRKAKIIRDY	1010	41	64	13166
POL	FPQITLWQR	49	77	SFSFPQITLWQRPLV	84	09	14	13167
POL	VIWGKTPKF	47	73	ESIVIWGKTPKFRLP	570	23	37	13168
POL	YVDGAANRE	46	72	ETFYVDGAANRETKL	630	24	38	13169
POL	FKNLKTGKY	45	70	QEPFKNLKTGKYAKM	535	15	23	13170
POL	IQTKELQKQ	45	70	ATDIQTKELQKQITK	957	24	38	13171
POL	YGKQMAGDD	45	70	IRDYGKQMAGDDCVA	1021	41	64	13172
POL	WRAMASDFN	43	67	HSNWRAMASDFNLPP	768	31	48	13173
POL	ISKIGPENP	42	66	EGKISKIGPENPYNT	233	40	63	13174
POL	LTQIGCTLN	41	64	RNLLTQIGCTLNFPI	174	21	33	13175
POL	IIQAQPDKS	40	63	ALGIIQAQPDKSESE	694	38	59	13176
POL	LPEKDSWTV	40	63	PIVLPEKDSWTVNDI	432	13	20	13177
POL	FQSSMTKIL	38	59	PAIFQSSMTKILEPF	346	32	50	13178
POL	FTIPSINNE	38	59	YTAFTIPSINNETPG	316	36	56	13179
POL	IFQSSMTKI	38	59	SPAIFQSSMTKILEP	345	33	52	13180
POL	IIEQLIKKE	37	58	VSQIIEQLIKKEKVY	710	19	30	13181
POL	LSWVPAHKG	37	58	KVYLSWVPAHKGIGG	722	23	37	13182
POL	YLSWVPAHK	37	58	EKVYLSWVPAHKGIG	721	15	24	13183
POL	YTAFTIPSI	37	58	FRKYTAFTIPSINNE	313	37	59	13184
POL	IIATDIQTK	35	55	IIDIIATDIQTKELQ	952	22	34	13185
POL	IWKGPAKLL	35	55	RDPIWKGPAKLLWKG	983	34	53	13186
POL	LQKQITKIQ	35	55	TKELQKQITKIQNFR	962	29	46	13187
POL	LKEALLDTG	34	53	GGQLKEALLDTGADD	103	31	48	13188
POL	VYLSWVPAH	33	52	KEKVYLSWVPAHKGI	720	15	23	13189
POL	FILKLAGRW	32	50	TAYFILKLAGRWPVK	849	27	42	13190
POL	LEGKIILVA	31	48	CTHLEGKIILVAVHV	817	30	47	13191
POL	YFILKLAGR	31	48	ETAYFILKLAGRWPV	848	30	47	13192
POL	IILVAVHVA	30	47	EGKIILVAVHVASGY	821	30	47	13193
POL	IWGKTPKFR	30	47	SIVIWGKTPKFRLPI	571	22	34	13194
POL	LAGRWPVKV	30	47	ILKLAGRWPVKVIHT	853	19	30	13195
POL	VVAKEIVAS	30	47	LPPVVAKEIVASCDK	780	21	33	13196
POL	IDIIATDIQ	29	45	ERIIDIIATDIQTKE	950	22	34	13197
POL	IIDIIATDI	29	45	GERIIDIIATDIQTK	949	23	36	13198
POL	IIGRNMLTQ	29	45	PVNIIGRNMLTQIGC	168	11	17	13199
POL	IKVKQLCKL	29	45	YAGIKVKQLCKLLRG	460	18	28	13200
POL	VDKLVSSGI	29	45	NEQVDKLVSSGIRKV	737	26	41	13201
POL	IVGAETFYV	28	44	KEPIVGAETFYVDGA	623	16	25	13202
POL	LPPVVAKEI	28	44	DFNLPPVVAKEIVAS	777	26	41	13203
POL	WTVQPIQLP	28	44	PDKWTVQPIQLPEKD	425	13	20	13204
POL	FNLPPVVAK	27	42	ASDFNLPPVVAKEIV	775	25	39	13205
POL	FTSAAVKAA	27	42	GSNFTSAAVKAACWW	870	25	39	13206
POL	LALQDSGLE	27	42	AIHLALQDSGLEVNI	673	15	23	13207
POL	LPPIVAKEI	27	42	DFNLPPIVAKEIVAS	777	20	31	13208
POL	LQDSGLEVN	27	42	HLALQDSGLEVNIVT	675	13	20	13209
POL	FNLPPIVAK	26	41	ASDFNLPPIVAKEIV	775	21	33	13210
POL	IGQHRAKIE	26	41	DLEIGQHRAKIEELR	381	23	36	13211
POL	IIGRNLLTQ	26	41	PVNIIGRNLLTQIGC	168	21	33	13212
POL	LEVNIVTDS	26	41	DSGLEVNIVTDSQYA	680	26	41	13213

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Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	LRGAKALTD	26	41	CKLLRGAKALTDIVP	469	12	19	13214
POL	LVSSGIRKV	26	41	VDKLVSSGIRKVLFL	740	25	39	13215
POL	FLLKLAGRW	25	39	TAYFLLKLAGRWPVK	849	19	30	13216
POL	LALQDSGSE	25	39	AHILALQDSGSEVNI	673	08	13	13217
POL	LQDSGSEVN	25	39	HLALQDSGSEVNIVT	675	08	13	13218
POL	VKVIHTDNG	25	39	RWPVKVIHTDNGSNF	859	21	33	13219
POL	WPVKVIHTD	25	39	AGRWPVKVIHTDNGS	857	20	31	13220
POL	YFLLKLAGR	25	39	ETAYFLLKLAGRWPV	848	24	38	13221
POL	ICGKKAIGT	24	38	LIEICGKKAIGTVLV	150	12	19	13222
POL	IVAKEIVAS	24	38	LPPIVAKEIVASCDK	780	22	34	13223
POL	LRWGFTTPD	24	38	QHLLRWGFTTPDKKH	396	12	19	13224
POL	LEGKVILVA	23	36	CTHLEGKVILVAVHV	817	23	36	13225
POL	LKWGFTTPD	23	36	EHLLKWGFTTPDKKH	396	13	20	13226
POL	VILVAVHVA	23	36	EGKVILVAVHVASGY	821	21	33	13227
POL	LAWVPAHKG	22	34	KVYLAWVPAHKGIGG	722	20	32	13228
POL	YDQILIEIC	22	34	VRQYDQILIEICGKK	143	08	13	13229
POL	YLAWVPAHK	22	34	EKVYLAWVPAHKGIG	721	20	32	13230
POL	IGQHRTKIE	21	33	DLEIGQHRTKIEELR	381	19	30	13231
POL	IGRNLLTQI	21	33	VNIIGRNLLTQIGCT	169	21	33	13232
POL	LWQRPLVTI	21	33	QITLWQRPLVTIKIG	89	11	17	13233
POL	VSLTETTNQ	21	33	QKVVSLTETTNQKTE	656	10	16	13234
POL	VYLAWVPAH	21	33	KEKVYLAWVPAHKGI	720	20	31	13235
POL	ICGHKAIGT	20	31	LIEICGHKAIGTVLV	150	10	16	13236
POL	LRGTKALTE	19	30	CKLLRGTKALTEVIP	469	11	17	13237
POL	LVNQIIEQL.	19	30	ESELVNQIIEQLIKK	706	13	20	13238
POL	LVSQIIEQL	19	30	ESELVSQIIEQLIKK	706	18	28	13239
POL	YFSVPLDKD	18	29	GDAYFSVPLDKDFRK	301	18	28	13240
POL	IGRNMLTQI	18	28	VNIIGRNMLTQIGCT	169	12	19	13241
POL	IKVRQLCKL	18	28	YPGIKVRQLCKLLRG	460	13	20	13242
POL	LWKGPAKLL	18	28	RDPLWKGPAKLLWKG	983	13	20	13243
POL	LWQRPLVTV	18	28	QITLWQRPLVTVKIG	89	09	14	13244
POL	YAGIKVKQL	18	28	SQIYAGIKVKQLCKL	457	18	28	13245
POL	IWGKTPKFK	17	27	SIVIWGKTPKFKLPI	571	17	27	13246
POL	LREHLLKWG	17	27	IEELREHLLKWGFTT	391	12	19	13247
POL	VQPIQLPEK	17	27	KWTVQPIQLPEKDSW	427	13	20	13248
POL	WQRPLVTIK	17	27	ITLWQRPLVTIKIGG	90	11	17	13249
POL	IIQAQPDRS	16	25	ALGIIQAQPDRSESE	694	12	19	13250
POL	LQAIHLALQ	16	25	KTELQAIHLALQDSG	668	15	23	13251
POL	LVEICTEME	15	24	IKALVEICTEMEKEG	218	15	23	13252
POL	LRQHLLRWG	15	23	IEELRQHLLRWGFTT	391	12	19	13253
POL	LTQLGCTLN	15	23	RNMLTQLGCTLNFPI	174	10	16	13254
POL	LVSAGIRKV	15	23	VDKLVSAGIRKVLFL	740	14	22	13255
POL	VDKLVSAGI	15	23	NEQVDKLVSAGIRKV	737	14	22	13256
POL	YPGIKVRQL	15	23	SQIYPGIKVRQLCKL	457	12	19	13257
POL	FRKQNPDIV	14	22	LEPFRKQNPDIVIYQ	357	14	22	13258
POL	FSFPQITLW	14	22	TVSFSFPQITLWQRP	77	05	10	13259
POL	FTSTTVKAA	14	22	GSNFTSTTVKAACWW	870	11	17	13260
POL	IIASDIQTK	14	22	IIDIIASDIQTKELQ	952	11	17	13261
POL	LAGRWPVKT	14	22	LLKLAGRWPVKTIHT	853	09	14	13262
POL	VQKIATESI	14	22	TEAVQKIATESIVIW	561	10	16	13263

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Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	FTIPSTNNE	13	20	YTAFTIPSTNNETPG	316	13	20	13264
POL	LEDINLPGK	13	20	DTVLEDINLPGKWKP	117	13	20	13265
POL	LTDIVPLTE	13	20	AKALTDIVPLTEEAE	475	08	13	13266
POL	LVTIKIGGQ	13	20	QRPLVTIKIGGQLKE	94	13	20	13267
POL	MRGAIITNDV	13	20	YARMRGAIITNDVKQL	546	12	19	13268
POL	VKTIHTDNG	13	20	RWPVKTIHTDNGSNF	859	09	14	13269
POL	VQPIVLPEK	13	20	KWTVQPIVLPEKDSW	427	12	19	13270
POL	WPVKTIHTD	13	20	AGRWPVKTIHTDNGS	857	09	14	13271
POL	WQRPLVTVK	13	20	ITLWQRPLVTVKIGG	90	09	14	13272
POL	WTVQPIVLP	13	20	PDKWTVQPIVLPEKD	425	12	19	13273
POL	YTAFTIPST	13	20	FRKYTAFTIPSTNNE	313	13	21	13274
POL	IDIIASDIQ	12	19	ERIIDIIASDIQTKE	950	11	17	13275
POL	IIDIIASDI	12	19	GERIIDIIASDIQTK	949	11	17	13276
POL	IVDIIATDI	12	19	GERIVDIIATDIQTK	949	10	16	13277
POL	LEEINLPGK	12	19	DTVLEEINLPGKWKP	117	11	17	13278
POL	LQAIYLALQ	12	19	KTELQAIYLALQDSG	668	11	17	13279
POL	LQKQIIKIQ	12	19	TKELQKQIIKIQNFR	962	09	14	13280
POL	VDIIATDIQ	12	19	ERIVDIIATDIQTKE	950	10	16	13281
POL	YDQIPIEIC	12	19	VRQYDQIPIEICGKK	143	05	8	13282
POL	FNFPQITLW	11	17	VPTFNFPQITLWQRP	79	01	17	13283
POL	IGRNMLTQL	11	17	VNIIGRNMLTQLGCT	169	10	16	13284
POL	ISRIGPENP	11	17	EGKISRIGPENPYNT	233	10	16	13285
POL	LTEVIPLTE	11	17	TKALTEVIPLTEEAE	475	10	16	13286
POL	MESIVIWGK	11	17	KIAMESIVIWGKTPK	566	07	11	13287
POL	VPRRKVKII	11	17	IKVVPRRKVKIIRDY	1010	08	13	13288
POL	VSFSFPQIT	08	17	QGTVSFSFPQITLWQ	75	05	8	13289
POL	WYQLETEPI	11	17	VKLWYQLETEPIVGA	615	04	6	13290
POL	YPGIKVKQL	11	17	SQIYPGIKVKQLCKL	457	09	14	13291
POL	FPQGEAREF	10	16	NLAFPQGEAREFPPE	5	05	8	13292
POL	LIEALLDTG	10	16	GGQLIEALLDTGADD	103	09	14	13293
POL	VSLTDTTNQ	10	16	QKVVSLTDTTNQKTE	656	09	14	13294
POL	WETWWTDYW	10	16	KETWETWWTDYWQAT	587	09	14	13295
POL	YAKMRTAHT	10	16	TGKYAKMRTAHTNDV	543	09	14	13296
POL	YKNLKTGKY	10	16	QEPYKNLKTGKYARM	535	03	5	13297
REV	LQLPPLERL	36	56	PVPLQLPPLERLTLD	74	13	20	13298
REV	VPLQLPPLE	36	56	AEPVPLQLPPLERLT	72	10	16	13299
REV	LYQSNPPPS	18	28	IKFLYQSNPPPSPEG	21	04	6	13300
REV	VRIIKILYQ	16	25	LKAVRIIKILYQSNP	13	06	9	13301
REV	YQSNPPPSP	12	19	KFLYQSNPPPSPEGT	22	05	8	13302
REV	LQLPPIERL	11	17	PVPLQLPPIERLRLD	74	04	6	13303
REV	VPLQLPPIE	11	17	AEPVPLQLPPIERLR	72	04	6	13304
TAT	WNHPGSQPK	15	23	LEPWNHPGSQPKTAC	11	11	17	13305
TAT	FLNKGLGIS	14	22	QVCFLNKGLGISYGR	38	04	6	13306
TAT	WKHPGSQPK	13	20	LEPWKHPGSQPKTAC	11	11	17	13307
TAT	YCKKCCFHC	11	17	NNCYCKKCCFHCQVC	26	04	6	13308
TAT	YCKKCCYHC	11	17	TNCYCKKCCYHCQVC	26	02	3	13309
TAT	WNHPGSQPT	10	16	LEPWNHPGSQPTTAC	11	07	11	13310
VIF	MIVWQVDRM	46	72	WQVMIVWQVDRMRIR	5	28	44	13311
VIF	WQVMIVWQV	43	67	ENRWQVMIVWQVDRM	2	41	64	13312
VIF	WQVDRMRIR	34	53	MIVWQVDRMRIRTWK	8	14	22	13313

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Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VIF	LQYLALTAL	33	52	VGSLQYLALTALIKP	147	14	22	13314
VIF	LGHGVSIEW	31	48	DWHLGHGVSIEWRLR	81	11	17	13315
VIF	VDRMRIRTW	31	48	VWQVDRMRIRTWNSL	10	15	23	13316
VIF	YFDCFSESA	28	44	HLYYFDCFSESAIRN	113	08	13	13317
VIF	YWGLHTGER	28	44	ITTYWGLHTGERDWH	68	14	22	13318
VIF	IRTWNSLVK	27	42	RMRIRTWNSLVKHHM	15	12	19	13319
VIF	LGQGVSIEW	26	41	DWHLGQGVSIEWRKK	81	07	11	13320
VIF	LVKHHMYVS	21	33	WNSLVKHHMYVSKKA	21	07	11	13321
VIF	IPLGEARLV	19	30	EVHIPLGEARLVVRT	54	05	8	13322
VIF	LVKHHMYIS	19	30	WKSLVKHHMYISGKA	21	05	8	13323
VIF	YLALTALIK	16	25	SLQYLALTALIKPKK	[illegible]	11	17	13324
VIF	IRTWKSLVK	15	23	RMRIRTWKSLVKHHM	15	14	22	13325
VIF	LADQLIHLY	15	23	DPDLADQLIHLYYFD	104	07	11	13326
VIF	LALTALIKP	15	23	LQYLALTALIKPKKI	150	08	13	13327
VIF	VDPGLADQL	15	23	STQVDPGLADQLIHL	100	04	6	13328
VIF	LYYFDCFSE	14	22	LIHLYYFDCFSESAI	111	14	22	13329
VIF	FSESAIRKA	13	20	FDCFSESAIRKAILG	117	10	16	13330
VIF	LADQLIHMH	13	20	EPGLADQLIHMHYFD	104	08	13	13331
VIF	WQVDRMKIR	13	20	LIVWQVDRMKIRTWN	8	09	14	13332
VIF	FSDSAIRKA	12	19	FDCFSDSAIRKAILG	117	05	8	13333
VIF	FSESAIRNA	12	19	FDCFSESAIRNAILG	117	12	19	13334
VIF	IVSPRCEYQ	12	19	LGHIVSPRCEYQAGH	130	06	9	13335
VIF	LQYLALAAL	12	19	VGSLQYLALAALITP	147	04	6	13336
VIF	VDRMKIRTW	12	19	VWQVDRMKIRTWNSL	10	12	19	13337
VIF	YWGLQTGER	12	19	IKTYWGLQTGERDWH	68	08	13	13338
VIF	IPLGDARLV	11	17	EVHIPLGDARLVITT	54	06	9	13339
VIF	LQYLALKAL	11	17	VGSLQYLALKALVTP	147	08	13	13340
VIF	WQVDRMRIN	11	17	MIVWQVDRMRINTWK	8	08	13	13341
VIF	IKPKKIKPP	10	16	TALIKPKKIKPPLPS	156	08	13	13342
VIF	VDRMRINTW	10	16	VWQVDRMRINTWKSL	10	09	14	13343
VPR	IGCQHSRIG	46	72	HFRIGCQHSRIGITR	71	08	13	13344
VPR	WTLELLEEL	42	69	YNEWTLELLEELKSE	15	12	19	13345
VPR	ILQQLLFIH	37	58	HRILQQLLFIHFRI	60	31	48	13346
VPR	FIHFRIGCQ	30	47	QLLFIHFRIGCQHSR	66	29	45	13347
VPR	YNEWTLELL	30	47	REPYNEWTLELLEEL	12	27	42	13348
VPR	FPRPWLHGL	24	38	VRHFPRPWLHGLGQH	31	12	19	13349
VPR	WEGVEAIIR	18	28	GDTWEGVEAIIRILQ	51	14	22	13350
VPR	LEELKSEAV	16	25	LELLEELKSEAVRHF	20	15	23	13351
VPR	WAGVEAIIR	16	25	GDTWAGVEAIIRILQ	51	15	23	13352
VPR	YGDTWAGVE	16	25	YETYGDTWAGVEAII	47	16	25	13353
VPR	IGCRHSRIG	12	19	HFRIGCRHSRIGITR	71	03	5	13354
VPR	FIHFRIGCR	11	17	QLLFIHFRIGCRHSR	66	11	17	13355
VPR	FVHFRIGCQ	11	17	QLLFVHFRIGCQHSR	66	10	16	13356
VPR	YGDTWTGVE	11	17	YETYGDTWTGVEAII	47	04	6	13357
VPR	FPRIWLHSL	10	16	VRHFPRIWLHSLGQH	31	05	8	13358
VPR	WALELLEEL	09	15	YNEWALELLEELKNE	15	03	5	13359
VPU	LVTLLSSSK	01	50	EEWLVTLLSSSKLDQ	87	01	2	13360
VPU	VTLLSSSKL	01	50	EWLVTLLSSSKLDQG	89	01	2	13361
VPU	IIAIVVWTI	23	36	VVAIIAIVVWTIVFI	20	02	3	13362
VPU	VDYRIVIVA	01	33	LAKVDYRIVIVAFIV	5	01	25	13363

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VPU	LRQRKIDRL	17	27	RKILRQRKIDRLIDR	44	11	17	13364
VPU	IVVWTIVFI	15	23	IIAIVVWTIVFIEYR	27	07	11	13365
VPU	VVWTIVFIE	14	22	IAIVVWTIVFIEYRK	28	06	9	13366
VPU	IEYRKILRQ	13	21	IVFIEYRKILRQRKI	36	07	11	13367
VPU	ILAIVALVV	11	17	SLYILAIVALVVAII	3	01	2	13368
VPU	WTIVFIEYR	10	16	IVVWTIVFIEYRKIL	30	05	8	13369
VPU	LAIVALVVA	09	15	LQILAIVALVVAGII	4	02	3	13370

Table XIXb

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w81	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
VSTQLLLNG	KPVVSTQLLLNGSLA									12864
VVSTQLLLN	IKPVVSTQLLLNGSL									12865
LTVWGIKQL	LLQLTVWGIKQLQAR	0.0840		0.0096		0.0190		0.0750		12866
LLSGIVQQQ	ARQLLSGIVQQQSNL									12867
WATHACVPT	HNVWATHACVPTDPN									12868
LGAAGSTMG	LGFLGAAGSTMGAAS									12869
VRQGYSPLS	VNRVRQGYSPLSFQT	0.0032		-0.0014		0.0230		-0.0010		12870
LLLNGSLAE	STQLLLNGSLAEEEV									12871
VKLTPLCVT	KPCVKLTPLCVTLNC									12872
LRAIEAQQH	NNLLRAIEAQQHLLQ	0.0280				0.0150				12873
VSTVQCTHG	CKNVSTVQCTHGIKP									12874
LGIWGCSGK	QQLLGIWGCSGKLIC									12875
LWDQSLKPC	IISLWDQSLKPCVKL	0.0057		0.0061		0.0096		0.0059		12876
LGFLGAAGS	AVFLGFLGAAGSTMG									12877
VWATHACVP	VHNVWATHACVPTDP									12878
WGIKQLQAR	LTVWGIKQLQARVLA									12879
LWYIKIFIM	TNWLWYIKIFIMIVG									12880
FCASDAKAY	TTLFCASDAKAYDTE									12881
IVGGLIGLR	FIMIVGGLIGLRIVF									12882
IFIMIVGGL	YIKIFIMIVGGLIGL									12883
VYYGVPVWK	WVTVYYGVPVWKEAT	0.0790	6.1000	0.0700	0.0043	0.0180	8.2000	-0.0010	0.0098	12884
IKQLQARVL	VWGIKQLQARVLAVE									12885
IKIFIMIVG	LWYIKIFIMIVGGLI									12886
MGAASITLT	GSTMGAASITLTVQA									12887
YIKIFIMIV	WLWYIKIFIMIVGGL									12888
ITGLLLTRD	SSNITGLLLTRDGGK									12889
IPIHYCAPA	FEPIPIHYCAPAGFA									12890
MIVGGLIGL	IFIMIVGGLIGLRIV									12891
VQARQLLSG	TLTVQARQLLSGIVQ									12892
FEPIPIHYC	KVSFEPIPIHYCAPA									12893
LRSLCLFSY	WDDLRSLCLFSYHRL									12894
MWKNNMVEQ	NFNMWKNNMVEQMHE									12895
VHNVWATHA	DTEVHNVWATHACVP									12896
WKNNMVEQM	FNMWKNNMVEQMHED									12897
YYGVPVWKE	VTVYYGVPVWKEATT	0.0087		0.0270		0.0071		0.0021		12898
LLQLTVWGI	QQHLLQLTVWGIKQL	1.1000	0.7500	0.0580	-0.0043	0.0330	0.2700	0.0036	0.4900	12899
IEPLGVAPT	VVKIEPLGVAPTKAK									12900
IKPVVSTQL	THGIKPVVSTQLLLN									12901
LQARVLAVE	IKQLQARVLAVERYL									12902
WDDLRSLCL	ALAWDDLRSLCLFSY									12903
IINIHTPHR	SRPIINIHTPHREKR									12904
INIHTPHRE	RPIINIHTPHREKRA									12905
ITQACPKVS	TSVITQACPKVSFEP									12906
IVQQQSNLL	LSGIVQQQSNLLRAI									12907
LGNNSTNST	NKTLGNNSTNSTLGN									12908
VISTRTHRE	ARPVISTRTHREKRA									12909
WRWGTLFLG	QNLWRWGTLFLGMLM									12910
WRWGTMLLG	QHLWRWGTMLLGMLM									12911
FAVLSIVNR	RIVFAVLSIVNRVRQ									12912
LLNGSLAEE	TQLLLNGSLAEEEVV									12913

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VSTQLLLNG	KPVVSTQLLLNGSLA						12864
VVSTQLLLN	IKPVVSTQLLLNGSL						12865
LTVWGIKQL	LLQLTVWGIKQLQAR		0.0180				12866
LLSGIVQQQ	ARQLLSGIVQQQSNL						12867
WATHACVPT	IINVWATHACVPTDPN						12868
LGAAGSTMG	LGFLGAAGSTMGAAS						12869
VRQGYSPLS	VNRVRQGYSPLSFQT		-0.0007				12870
LLLNGSLAE	STQLLLNGSLAEEEV						12871
VKLTPLCVT	KPCVKLTPLCVTLNC						12872
LRAIEAQQH	NNLLRAIEAQQHLLQ		0.0150				12873
VSTVQCTHG	CKNVSTVQCTHGIKP						12874
LGIWGCSGK	QQLLGIWGCSGKLIC						12875
LWDQSLKPC	IISLWDQSLKPCVKL		0.0012				12876
LGFLGAAGS	AVFLGFLGAAGSTMG						12877
VWATHACVP	VHNVWATHACVPTDP						12878
WGIKQLQAR	LTVWGIKQLQARVLA						12879
LWYIKIFIM	TNWLWYIKIFIMIVG						12880
FCASDAKAY	TTLFCASDAKAYDTE						12881
IVGGLIGLR	FIMIVGGLIGLRIVF						12882
IFIMIVGGL	YIKIFIMIVGGLIGL						12883
VYYGVPVWK	WVTVYYGVPVWKEAT	-0.0004	0.0310	0.0049	0.4600		12884
IKQLQARVL	VWGIKQLQARVLAVE						12885
IKIFIMIVG	LWYIKIFIMIVGGLI						12886
MGAASITLT	GSTMGAASITLTVQA						12887
YIKIFIMIV	WLWYIKIFIMIVGGL						12888
ITGLLLTRD	SSNITGLLLTRDGGK						12889
IPIHYCAPA	FEPIPIHYCAPAGFA						12890
MIVGGLIGL	IFIMIVGGLIGLRIV						12891
VQARQLLSG	TLTVQARQLLSGIVQ						12892
FEPIPIHYC	KVSFEPIPIHYCAPA						12893
LRSLCLFSY	WDDLRSLCLFSYHRL						12894
MWKNNMVEQ	NFNMWKNNMVEQMHE						12895
VHNVWATHA	DTEVHNVWATHACVP						12896
WKNNMVEQM	FNMWKNNMVEQMHED						12897
YYGVPVWKE	VTVYYGVPVWKEATT		0.0160				12898
LLQLTVWGI	QQHLLQLTVWGIKQL	0.0180	0.3900	0.0210	0.5100		12899
IEPLGVAPT	VVKIEPLGVAPTKAK						12900
IKPVVSTQL	THGIKPVVSTQLLLN						12901
LQARVLAVE	IKQLQARVLAVERYL						12902
WDDLRSLCL	ALAWDDLRSLCLFSY						12903
IINIHTPHR	SRPIINIHTPHREKR						12904
INIHTPHRE	RPIINIHTPHREKRA						12905
ITQACPKVS	TSVITQACPKVSFEP						12906
IVQQQSNLL	LSGIVQQQSNLLRAI						12907
LGNNSTNST	NKTLGNNSTNSTLGN						12908
VISTRTHRE	ARPVISTRTHREKRA						12909
WRWGTLFLG	QNLWRWGTLFLGMLM						12910
WRWGTMLLG	QHLWRWGTMLLGMLM						12911
FAVLSIVNR	RIVFAVLSIVNRVRQ						12912
LLNGSLAEE	TQLLLNGSLAEEEVV						12913

Table XIXb

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w81	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LTPLCVTLN	CVKLTPLCVTLNCTD									12914
LYKYKVVKI	RSELYKYKVVKIEPL	0.0066	0.0320	0.0014		0.0011	0.0190	0.0042		12915
VPWNSSWSN	TTNVPWNSSWSNKSL									12916
YRLINCNTS	YKEYRLINCNTSAIT									12917
IIYCAPAGF	PIPIHYCAPAGFAIL									12918
LKDQQLLGI	ERYLKDQQLLGIWGC									12919
YKYKVVKIE	SELYKYKVVKIEPLG									12920
IRPVVSTQL	TIIGIRPVVSTQLLLN									12921
LDKWASLWN	LLALDKWASLWNWFD									12922
LRIVFAVLS	LIGLRIVFAVLSIVN									12923
LNGSLAEEE	QLLLNGSLAEEEVVI									12924
YKVVKIEPL	LYKYKVVKIEPLGVA									12925
LKGLRLGWE	RSSLKGLRLGWEGLK									12926
FSYHRLRDL	LCLFSYHRLRDLLLI									12927
INCTRPNNN	SVEINCTRPNNNTRK									12928
VVKIEPLGV	KYKVVKIEPLGVAPT									12929
WKEATTTLF	VPVWKEATTTLFCAS	0.0260	-0.0002	0.0520	-0.0030	0.1100	0.0900	0.0021	-0.0045	12930
IGLRIVFAV	GGLIGLRIVFAVLSI									12931
FFYCNTSGL	GGEFFYCNTSGLFNS									12932
FGLGALFLG	RAAFGLGALFLGFLG									12933
FYCNTSGLF	GEFFYCNTSGLFNST									12934
LIGLRIVFA	VGGLIGLRIVFAVLS									12935
VGLGAVFLG	KRAVGLGAVFLGFLG									12936
VGLGMLFLG	KRAVGLGMLFLGVLS									12937
ICTTAVPWN	GKLICTTAVPWNSSW									12938
ICTTNVPWN	GKLICTTNVPWNSSW									12939
LGVAPTKAK	IEPLGVAPTKAKRRV									12940
LICTTAVPW	SGKLICTTAVPWNSS									12941
LRDQQLLGI	ERYLRDQQLLGIWGC									12942
VFLGFLGAA	LGAVFLGFLGAAGST									12943
FSYHRLRDF	LCLFSYHRLRDFILI									12944
IPIIYCTPA	FEPIPIHYCTPAGFA									12945
IVFAVLSIV	GLRIVFAVLSIVNRV									12946
VFAVLSIVN	LRIVFAVLSIVNRVK									12947
YPWNASWSN	TTAVPWNASWSNKSL									12948
IGLRIIFAV	GGLIGLRIIFAVLSI									12949
IRQAHCNIS	IGDIRQAHCNISRAK									12950
VAPTKAKRR	PLGVAPTKAKRRVVQ									12951
FNGTGPCKN	DKKFNGTGPCKNVST									12952
IGPGQTFYA	SVRIGPGQTFYATGD									12953
IGSGQAFYV	RYSIGSGQAFYVTGK									12954
IRYLNLVNQ	QTAIRYLNLVNQTEN									12955
LIGLRIIFA	VGGLIGLRIIFAVLS									12956
LLQYWSQEL	WWNLLQYWSQELKNS									12957
LRNLCLFSY	WDDLRNLCLFSYHRL									12958
LVSGFLALA	SIRLVSGFLALAWDD									12959
VSGFLALAW	IRLVSGFLALAWDDL									12960
FDPIPIIYC	KVTFDPIPIHYCTPA									12961
IIFAVLSIV	GLRIIFAVLSIVNRV									12962
LINCNTSAI	EYRLINCNTSAITQA									12963

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LTPLCVTLN	CVKLTPLCVTLNCTD						12914
LYKYKVVKI	RSELYKYKVVKIEPL	0.0100	0.1800	0.1100	0.1700		12915
VPWNSSWSN	TTNVPWNSSWSNKSL						12916
YRLINCNTS	YKEYRLINCNTSAIT						12917
IHYCAPAGF	PIPIHYCAPAGFAIL						12918
LKDQQLLGI	ERYLKDQQLLGIWGC						12919
YKYKVVKIE	SELYKYKVVKIEPLG						12920
IRPVVSTQL	THGIRPVVSTQLLLN						12921
LDKWASLWN	LLALDKWASLWNWFD						12922
LRIVFAVLS	LIGLRIVFAVLSIVN						12923
LNGSLAEEE	QLLLNGSLAEEEVVI						12924
YKVVKIEPL	LYKYKVVKIEPLGVA						12925
LKGLRLGWE	RSSLKGLRLGWEGLK						12926
FSYHRLRDL	LCLFSYHRLRDLLLI						12927
INCTRPNNN	SVEINCTRPNNNTRK						12928
VVKIEPLGV	KYKVVKIEPLGVAPT						12929
WKEATTTLF	VPVWKEATTTLFCAS	0.0004	0.0630	0.0086	0.4700		12930
IGLRIVFAV	GGLIGLRIVFAVLSI						12931
FFYCNTSGL	GGEFFYCNTSGLFNS						12932
FGLGALFLG	RAAFGLGALFLGFLG						12933
FYCNTSGLF	GEFFYCNTSGLFNST						12934
LIGLRIVFA	VGGLIGLRIVFAVLS						12935
VGLGAVFLG	KRAVGLGAVFLGFLG						12936
VGLGMLFLG	KRAVGLGMLFLGVLS						12937
ICTTAVPWN	GKLICTTAVPWNSSW						12938
ICTTNVPWN	GKLICTTNVPWNSSW						12939
LGVAPTKAK	IEPLGVAPTKAKRRV						12940
LICTTAVPW	SGKLICTTAVPWNSS						12941
LRDQQLLGI	ERYLRDQQLLGIWGC						12942
VFLGFLGAA	LGAVFLGFLGAAGST						12943
FSYHRLRDF	LCLFSYHRLRDFILI						12944
IPIHYCTPA	FEPIPIHYCTPAGFA						12945
IVFAVLSIV	GLRIVFAVLSIVNRV						12946
VFAVLSIVN	LRIVFAVLSIVNRVR						12947
VPWNASWSN	TTAVPWNASWSNKSL						12948
IGLRIIFAV	GGLIGLRIIFAVLSI						12949
IRQAHCNIS	IGDIRQAHCNISRAK						12950
VAPTKAKRR	PLGVAPTKAKRRVVQ						12951
FNGTGPCKN	DKKFNGTGPCKNVST						12952
IGPGQTFYA	SVRIGPGQTFYATGD						12953
IGSGQAFYV	RYSIGSGQAFYVTGK						12954
IRYLNLVNQ	QTAIRYLNLVNQTEN						12955
LIGLRIIFA	VGGLIGLRIIFAVLS						12956
LLQYWSQEL	WWNLLQYWSQELKNS						12957
LRNLCLFSY	WDDLRNLCLFSYHRL						12958
LVSGFLALA	SIRLVSGFLALAWDD						12959
VSGFLALAW	IRLVSGFLALAWDDL						12960
FDPIPIHYC	KVTFDPIPIHYCTPA						12961
IIFAVLSIV	GLRIIFAVLSIVNRV						12962
LINCNTSAI	EYRLINCNTSAITQA						12963

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2wB1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LLNATAIAV	AVSLLNATAIAVAEG									12964
LRIIFAVLS	LIGLRIIFAVLSIVN									12965
VITQACPKV	NTSVITQACPKVSFE									12966
YWWNLLQYW	VLKYWWNLLQYWSQE									12967
FAILKCNDK	PAGFAILKCNDKKFN									12968
IFAVLSIVN	LRIIFAVLSIVNRVR									12969
INCNTSAIT	YRLINCNTSAITQAC									12970
LNATAIAVA	VSLLNATAIAVAEGT									12971
WNSSWSNKS	NVPWNSSWSNKSLDE									12972
WNASWSNKS	NVPWNASWSNKSYED									12973
ICTTTVPWN	GKLICTTTVPWNASW									12974
LLKLTVWGI	QQHLLKLTVWGIKQL									12975
LYKYKVVEI	RSELYKYKVVEIKPL									12976
MFLGFLGAA	LGAMFLGFLGAAGST									12977
MHSFNCGGE	EIVMHSFNCGGEFFY									12978
YWSQELKNS	LLQYWSQELKNSAVS									12979
IGAVFLGFL	AVGIGAVFLGFLGAA									12980
LIAARTVEL	DFILIAARTVELLGH									12981
LICTTTVPW	SGKLICTTTVPWNAS									12982
LLNGSLAEG	TQLLLNGSLAEGEII									12983
YWGQELKNS	LVWYWGQELKNSAIS									12984
IAARTVELL	FILIAARTVELLGHS									12985
LFLGFLGAA	IGALFLGFLGAAGST									12986
LKNSAVSLL	SQELKNSAVSLLNAT									12987
VGIGAVFLG	KRAVGIGAVFLGFLG									12988
VSLLNATAI	NSAVSLLNATAIAVA									12989
YATGDIIGD	QTFYATGDIIGDIRQ									12990
IAIAVAEGT	LDIIAIAVAEGTDRI									12991
IHYCTPAGF	PIPIHYCTPAGFAIL									12992
ILGLVIICS	GTLILGLVIICSASN									12993
IWNNMTWME	VDEIWNNMTWMEWER									12994
LGLVIICSA	TLILGLVIICSASNN									12995
LRDFILIAA	YHRLRDFILIAARTV									12996
LTPLCVTLD	CVKLTPLCVTLDCHN									12997
MLQLTVWGI	QQIIMLQLTVWGIKQL									12998
VEINCTRPN	NESVEINCTRPNNNT									12999
VRQLLSGIV	TVQVRQLLSGIVQQQ									13000
LILGLVIIC	WGTLILGLVIICSAS									13001
VGGHQAAMQ	LNTVGGHQAAMQMLK									13002
LLVQNANPD	TETLLVQNANPDCKT									13003
VQNANPDCK	TLLVQNANPDCKTIL									13004
LGLNKIVRM	WIILGLNKIVRMYSP	0.0400	0.3300	0.1100	1.1000	0.0310	0.0290	0.3700	0.2400	13005
LSEGATPQD	FSALSEGATPQDLNT									13006
WIILGLNKI	YKRWIILGLNKIVRM	1.2000	1.6000	0.7800	1.1000	0.0740	0.2400	0.3100	1.5000	13007
LEEMMTACQ	GATLEEMMTACQGVG									13008
YKRWIILGL	GEIYKRWIILGLNKI	0.0610	0.0660	0.0890	-0.0043	0.0300	0.1000	0.0940	0.1800	13009
IYKRWIILG	VGEIYKRWIILGLNK									13010
VSQNYPIVQ	SSQVSQNYPIVQNLQ									13011
WEKIRLRPG	LDKWEKIRLRPGGKK									13012
IAGTTSTLQ	GSDIAGTTSTLQEQI									13013

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LLNATAIAV	AVSLLNATAIAVAEG						12964
LRIIFAVLS	LIGLRIIFAVLSIVN						12965
VITQACPKV	NTSVITQACPKVSFE						12966
YWWNLLQYW	VLKYWWNLLQYWSQE						12967
FAILKCNDK	PAGFAILKCNDKKFN						12968
IFAVLSIVN	LRIIFAVLSIVNRVR						12969
INCNTSAIT	YRLINCNTSAITQAC						12970
LNATAIAVA	VSLLNATAIAVAEGT						12971
WNSSWSNKS	NVPWNSSWSNKSLDE						12972
WNASWSNKS	NVPWNASWSNKSYED						12973
ICTTTVPWN	GKLICTTTVPWNASW						12974
LLKLTVWGI	QQHLLKLTVWGIKQL						12975
LYKYKVVEI	RSELYKYKVVEIKPL						12976
MFLGFLGAA	LGAMFLGFLGAAGST						12977
MHSFNCGGE	EIVMHSFNCGGEFFY						12978
YWSQELKNS	LLQYWSQELKNSAVS						12979
IGAVFLGFL	AVGIGAVFLGFLGAA						12980
LIAARTVEL	DFILIAARTVELLGH						12981
LICTTTVPW	SGKLICTTTVPWNAS						12982
LLNGSLAEG	TQLLLNGSLAEGEII						12983
YWGQELKNS	LVWYWGQELKNSAIS						12984
IAARTVELL	FILIAARTVELLGHS						12985
LFLGFLGAA	IGALFLGFLGAAGST						12986
LKNSAVSLL	SQELKNSAVSLLNAT						12987
VGIGAVFLG	KRAVGIGAVFLGFLG						12988
VSLLNATAI	NSAVSLLNATAIAVA						12989
YATGDIIGD	QTFYATGDIIGDIRQ						12990
IAIAVAEGT	LDIIAIAVAEGTDRI						12991
IHYCTPAGF	PIPIHYCTPAGFAIL						12992
ILGLVIICS	GTLILGLVIICSASN						12993
IWNNMTWME	VDEIWNNMTWMEWER						12994
LGLVIICSA	TLILGLVIICSASNN						12995
LRDFILIAA	YHRLRDFILIAARTV						12996
LTPLCVTLD	CVKLTPLCVTLDCHN						12997
MLQLTVWGI	QQHMLQLTVWGIKQL						12998
VEINCTRPN	NESVEINCTRPNNNT						12999
VRQLLSGIV	TVQVRQLLSGIVQQQ						13000
LILGLVIIC	WGTLILGLVIICSAS						13001
VGGHQAAMQ	LNTVGGHQAAMQMLK						13002
LLVQNANPD	TETLLVQNANPDCKT						13003
VQNANPDCK	TLLVQNANPDCKTIL						13004
LGLNKIVRM	WIILGLNKIVRMYSP	1.8000	0.0088	0.2800	0.0024		13005
LSEGATPQD	FSALSEGATPQDLNT						13006
WIILGLNKI	YKRWIILGLNKIVRM	4.0000	0.1200	0.5400	0.6200		13007
LEEMMTACQ	GATLEEMMTACQGVG						13008
YKRWIILGL	GEIYKRWIILGLNKI	0.0356	0.1300	0.7800	0.1400		13009
IYKRWIILG	VGEIYKRWIILGLNK						13010
VSQNYPIVQ	SSQVSQNYPIVQNLQ						13011
WEKIRLRPG	LDKWEKIRLRPGGKK						13012
IAGTTSTLQ	GSDIAGTTSTLQEQI						13013

Table XIXb

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
WASRELERF	HLVWASRELERFALN									13014
IPMFSALSE	PEVIPMFSALSEGAT									13015
MFSALSEGA	VIPMFSALSEGATPQ	0.0085		-0.0014		0.0058		-0.0010		13016
VIPMFSALS	SPEVIPMFSALSEGA	0.0160	0.0280	0.0034	-0.0043	0.1600		0.0075	-0.0045	13017
MYSPVSILD	IVRMYSPVSILDIRQ									13018
IVRMYSPVS	LNKIVRMYSPVSILD									13019
VRMYSPVSI	NKIVRMYSPVSILDI									13020
YSPVSILDI	VRMYSPVSILDIRQG									13021
MTETLLVQN	KNWMTETLLVQNANP									13022
WMTETLLVQ	VKNWMTETLLVQNAN	0.0033	0.0130	0.0077	-0.0043	0.0480		-0.0010	-0.0045	13023
ISPRTLNAW	HQAISPRTLNAWVKV									13024
VKNWMTETL	TQEVKNWMTETLLVQ									13025
IKCFNCGKE	QKRIKCFNCGKEGHL									13026
IPVGEIYKR	NPPIPVGEIYKRWII									13027
YTAVFMQRG	KGGYTAVFMQRGQNP									13028
VATLYCVHQ	YNTVATLYCVHQRIE									13029
WDRLHPVHA	AAEWDRLHPVHAGPI									13030
FLQSRPEPT	PGNFLQSRPEPTAPP	0.0970		0.0170		0.0190		0.0015		13031
FKTLRAEQA	DRFFKTLRAEQATQE									13032
MVHQAISPR	QGQMVHQAISPRTLN	0.0690	0.1400	1.5000	0.0170	0.8300	0.0950	-0.0010	0.0048	13033
VHQAISPRT	GQMVHQAISPRTLNA	0.0003		0.0023		0.0034		-0.0010		13034
YKTLRAEQA	DRFYKTLRAEQASQE	0.0530	0.0016	0.0500		0.1500		0.0430		13035
VSILDIRQG	YSPVSILDIRQGPKE									13036
LAEAMSQVT	ARVLAEAMSQVTNSA									13037
LGKIWPSHK	ANFLGKIWPSHKGRP									13038
VKCFNCGKE	RKTVKCFNCGKEGHI									13039
YNTVATLYC	RSLYNTVATLYCVHQ									13040
LHPVHAGPI	WDRLHPVHAGPIAPG									13041
LYNTVATLY	LRSLYNTVATLYCVH									13042
MTDTLLVQN	KNWMTDTLLVQNANP									13043
WMTDTLLVQ	VKNWMTDTLLVQNAN									13044
IEVKDTKEA	HQRIEVKDTKEALDK									13045
LQGQMVHQA	VQNLQGQMVHQAISP									13046
MTNNPPIPV	IGWMTNNPPIPVGEI									13047
WMTNNPPIP	QIGWMTNNPPIPVGE									13048
IAPGQMREP	AGPIAPGQMREPRGS									13049
VHAGPIAPG	LHPVHAGPIAPGQMR									13050
LGPGATLEE	LRALGPGATLEEMMT									13051
VHAGPIPPG	VHPVHAGPIPPGQMR									13052
IPPGQMREP	AGPIPPGQMREPRGS									13053
LSPRTLNAW	HQALSPRTLNAWVKV									13054
YRLKHLVWA	KKKYRLKHLVWASRE									13055
LGPAATLEE	LKALGPAATLEEMMT									13056
LKALGPAAT	KTILKALGPAATLEE	0.0760		0.0100		-0.0023		-0.0010		13057
LKDKEPPLA	QEQLKDKEPPLASLR									13058
LSGGKLDAW	ASVLSGGKLDAWEKI									13059
MTSNPPIPV	IGWMTSNPPIPVGEI									13060
VKNWMTDTL	TQDVKNWMTDTLLVQ									13061
VSILDIKQG	YSPVSILDIKQGPKE									13062
WMTSNPPIP	QIGWMTSNPPIPVGE									13063

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
WASRELERF	HLVWASRELERFALN						13014
IPMFSALSE	PEVIPMFSALSEGAT						13015
MFSALSEGA	VIPMFSALSEGATPQ		-0.0007				13016
VIPMFSALS	SPEVIPMFSALSEGA	0.0007	-0.0007	0.0130	0.0130		13017
MYSPVSILD	IVRMYSPVSILDIRQ						13018
IVRMYSPVS	LNKIVRMYSPVSILD						13019
VRMYSPVSI	NKIVRMYSPVSILDI						13020
YSPVSILDI	VRMYSPVSILDIRQG						13021
MTETLLVQN	KNWMTETLLVQNANP						13022
WMTETLLVQ	VKNWMTETLLVQNAN	0.0032	0.0280	0.0008	0.0053		13023
ISPRTLNAW	HQAISPRTLNAWVKV						13024
VKNWMTETL	TQEVKNWMTETLLVQ						13025
IKCFNCGKE	QKRIKCFNCGKEGHL						13026
IPVGEIYKR	NPPIPVGEIYKRWII						13027
YTAVFMQRG	KGGYTAVFMQRGQNP						13028
VATLYCVHQ	YNTVATLYCVHQRIE						13029
WDRLHPVHA	AAEWDRLHPVHAGPI						13030
FLQSRPEPT	PGNFLQSRPEPTAPP		0.0130				13031
FKTLRAEQA	DRFFKTLRAEQATQE						13032
MVHQAISPR	QGQMVHQAISPRTLN	0.0085	0.0550	0.0067	0.6400		13033
VHQAISPRT	GQMVHQAISPRTLNA		-0.0007				13034
YKTLRAEQA	DRFYKTLRAEQASQE	-0.0001	0.0028		-0.0015		13035
VSILDIRQG	YSPVSILDIRQGPKE						13036
LAEAMSQVT	ARVLAEAMSQVTNSA						13037
LGKIWPSHK	ANFLGKIWPSHKGRP						13038
VKCFNCGKE	RKTVKCFNCGKEGHI						13039
YNTVATLYC	RSLYNTVATLYCVHQ						13040
LHPVHAGPI	WDRLHPVHAGPIAPG						13041
LYNTVATLY	LRSLYNTVATLYCVH						13042
MTDTLLVQN	KNWMTDTLLVQNANP						13043
WMTDTLLVQ	VKNWMTDTLLVQNAN						13044
IEVKDTKEA	HQRIEVKDTKEALDK						13045
LQGQMVHQA	VQNLQGQMVHQAISP						13046
MTNNPPIPV	IGWMTNNPPIPVGEI						13047
WMTNNPPIP	QIGWMTNNPPIPVGE						13048
IAPGQMREP	AGPIAPGQMREPRGS						13049
VHAGPIAPG	LHPVHAGPIAPGQMR						13050
LGPGATLEE	LRALGPGATLEEMMT						13051
VHAGPIPPG	VHPVHAGPIPPGQMR						13052
IPPGQMREP	AGPIPPGQMREPRGS						13053
LSPRTLNAW	HQALSPRTLNAWVKV						13054
YRLKHLVWA	KKKYRLKHLVWASRE						13055
LGPAATLEE	LKALGPAATLEEMMT						13056
LKALGPAAT	KTILKALGPAATLEE		0.0006				13057
LKDKEPPLA	QEQLKDKEPPLASLR						13058
LSGGKLDAW	ASVLSGGKLDAWEKI						13059
MTSNPPIPV	IGWMTSNPPIPVGEI						13060
VKNWMTDTL	TQDVKNWMTDTLLVQ						13061
VSILDIKQG	YSPVSILDIKQGPKE						13062
WMTSNPPIP	QIGWMTSNPPIPVGE						13063

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
FNTVATLYC	KSLFNTVATLYCVHQ									13064
IPMFTALSE	PEVIPMFTALSEGAT									13065
LASLKSLFG	LYPLASLKSLFGNDP									13066
LERFAVNPG	SRELERFAVNPGLLE									13067
LFNTVATLY	LRSLFNTVATLYCVH									13068
MFTALSEGA	VIPMFTALSEGATPQ									13069
WDRVHPVHA	AAEWDRVHPVHAGPI									13070
IVRMYSPTS	LNKIVRMYSPTSILD									13071
LERFALNPG	SRELERFALNPGLLE									13072
LQEQIAWMT	TSTLQEQIAWMTGNP									13073
VHPVHAGPI	WDRVHPVHAGPIPPG									13074
VIPMFTALS	SPEVIPMFTALSEGA									13075
VRMYSPTSI	NKIVRMYSPTSILDI									13076
LGKIWPSNK	ANFLGKIWPSNKGRP									13077
LTSLKSLFG	LYPLTSLKSLFGNDP									13078
MYSPTSILD	IVRMYSPTSILDIRQ									13079
YKLKHIVWA	KKKYKLKHIVWASRE									13080
YSPTSILDI	VRMYSPTSILDIRQG									13081
LTSLRSLFG	LYPLTSLRSLFGNDP									13082
MMLNIVGGH	DLNMMLNIVGGHQAA									13083
IDVKDTKEA	HQRIDVKDTKEALDK									13084
IGWMTSNPP	QEQIGWMTSNPPIPV									13085
IPVGDIYKR	NPPIPVGDIYKRWII									13086
LYPLASLKS	DKELYPLASLKSLFG									13087
VHQALSPRT	GQMVHQALSPRTLNA									13088
VNPGLLETS	RFAVNPGLLETSEGC									13089
YPLASLKSL	KELYPLASLKSLFGN									13090
FLQNRPEPT	PGNFLQNRPEPTAPP									13091
IMMQKSNFK	AAAIMMQKSNFKGPR									13092
LAEAMSQVQ	ARVLAEAMSQVQQSN									13093
LGKIWPSSK	ANFLGKIWPSSKGRP									13094
LNPGLLETA	RFALNPGLLETAEGC									13095
YPLASLRSL	KELYPLASLRSLFGN									13096
WQNYTPGPG	FPDWQNYTPGPGIRY									13097
VRPQVPLRP	GFPVRPQVPLRPMTY									13098
VPLRPMTYK	RPQVPLRPMTYKGAF									13099
LTFGWCFKL	RYPLTFGWCFKLVPV									13100
ILDLWVYHT	RQEILDLWVYHTQGY									13101
WCFKLVPVD	TFGWCFKLVPVDPRE									13102
LWVYHTQGY	ILDLWVYHTQGYFPD									13103
WSKSSIVGW	GGKWSKSSIVGWPAI									13104
ILDLWVYNT	RQDILDLWVYNTQGY									13105
LLHPMSQHG	NNCLLHPMSQHGMDD									13106
LLHPICQHG	NNSLLHPICQHGMED									13107
IRYPLTFGW	GPGIRYPLTFGWCFK									13108
ITSSNTAAT	HGAITSSNTAATNAD									13109
LEKHGAITS	SRDLEKHGAITSSNT									13110
LWVYHTQGF	ILDLWVYHTQGFFPD									13111
MTYKGAFDL	LRPMTYKGAFDLSFF									13112
LVPVDPREV	CFKLVPVDPREVEEA									13113

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
FNTVATLYC	KSLFNTVATLYCVHQ						13064
IPMFTALSE	PEVIPMFTALSEGAT						13065
LASLKSLFG	LYPLASLKSLFGNDP						13066
LERFAVNPG	SRELERFAVNPGLLE						13067
LFNTVATLY	LRSLFNTVATLYCVH						13068
MFTALSEGA	VIPMFTALSEGATPQ						13069
WDRVHPVHA	AAEWDRVHPVHAGPI						13070
IVRMYSPTS	LNKIVRMYSPTSILD						13071
LERFALNPG	SRELERFALNPGLLE						13072
LQEQIAWMT	TSTLQEQIAWMTGNP						13073
VHPVHAGPI	WDRVHPVHAGPIPPG						13074
VIPMFTALS	SPEVIPMFTALSEGA						13075
VRMYSPTSI	NKIVRMYSPTSILDI						13076
LGKIWPSNK	ANFLGKIWPSNKGRP						13077
LTSLKSLFG	LYPLTSLKSLFGNDP						13078
MYSPTSILD	IVRMYSPTSILDIRQ						13079
YKLKHIVWA	KKKYKLKHIVWASRE						13080
YSPTSILDI	VRMYSPTSILDIRQG						13081
LTSLRSLFG	LYPLTSLRSLFGNDP						13082
MMLNIVGGH	DLNMMLNIVGGHQAA						13083
IDVKDTKEA	HQRIDVKDTKEALDK						13084
IGWMTSNPP	QEQIGWMTSNPPIPV						13085
IPVGDIYKR	NPPIPVGDIYKRWII						13086
LYPLASLKS	DKELYPLASLKSLFG						13087
VHQALSPRT	GQMVHQALSPRTLNA						13088
VNPGLLETS	RFAVNPGLLETSEGC						13089
YPLASLKSL	KELYPLASLKSLFGN						13090
FLQNRPEPT	PGNFLQNRPEPTAPP						13091
IMMQKSNFK	AAAIMMQKSNFKGPR						13092
LAEAMSQVQ	ARVLAEAMSQVQQSN						13093
LGKIWPSSK	ANFLGKIWPSSKGRP						13094
LNPGLLETA	RFALNPGLLETAEGC						13095
YPLASLRSL	KELYPLASLRSLFGN						13096
WQNYTPGPG	FPDWQNYTPGPGIRY						13097
VRPQVPLRP	GFPVRPQVPLRPMTY						13098
VPLRPMTYK	RPQVPLRPMTYKGAF						13099
LTFGWCFKL	RYPLTFGWCFKLVPV						13100
ILDLWVYHT	RQEILDLWVYHTQGY						13101
WCFKLVPVD	TFGWCFKLVPVDPRE						13102
LWVYHTQGY	ILDLWVYHTQGYFPD						13103
WSKSSIVGW	GGKWSKSSIVGWPAI						13104
ILDLWVYNT	RQDILDLWVYNTQGY						13105
LLHPMSQHG	NNCLLHPMSQHGMDD						13106
LLHPICQHG	NNSLLHPICQHGMED						13107
IRYPLTFGW	GPGIRYPLTFGWCFK						13108
ITSSNTAAT	HGAITSSNTAATNAD						13109
LEKHGAITS	SRDLEKHGAITSSNT						13110
LWVYHTQGF	ILDLWVYHTQGFFPD						13111
MTYKGAFDL	LRPMTYKGAFDLSFF						13112
LVPVDPREV	CFKLVPVDPREVEEA						13113

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
VGWPAIRER	SSIVGWPAIRERMRR									13114
WCFKLVPVE	TFGWCFKLVPVEPEK									13115
FDSRLAFHH	EWRFDSRLAFHHVAR									13116
FKLVPVDPR	GWCFKLVPVDPREVE									13117
VPLRPMTFK	RPQVPLRPMTFKGAF									13118
LLDTGADDT	KEALLDTGADDTVLE	0.0001		-0.0015		-0.0023		-0.0010		13119
WMGYELHPD	PFLWMGYELHPDKWT									13120
YQYNVLPQG	GIRYQYNVLPQGWKG									13121
FRKYTAFTI	DKDFRKYTAFTIPSI									13122
WTVNDIQKL	KDSWTVNDIQKLVGK	0.0027		-0.0014		-0.0026		0.1200		13123
LDCTHLEGK	IWQLDCTHLEGKIIL									13124
LDVGDAYFS	VTVLDVGDAYFSVPL	0.0003		-0.0014		-0.0026		-0.0007		13125
MDDLYVGSD	YQYMDDLYVGSDLEI	0.0006		-0.0014	-0.0160	0.0036		-0.0006		13126
VIPAETGQE	EAEVIPAETGQETAY									13127
WKGEGAVVI	KLLWKGEGAVVIQDN	0.4600	0.0011	0.0058	-0.0043	0.0750	0.0200	0.0060	-0.0045	13128
WQLDCTHLE	PGIWQLDCTHLEGKI									13129
VDFRELNKR	RKLVDFRELNKRTQD									13130
WKPKMIGGI	PGKWKPKMIGGIGGF									13131
IWQLDCTHL	SPGIWQLDCTHLEGK	0.0013		-0.0021		0.0990		-0.0006		13132
VAVHVASGY	IILVAVHVASGYIEA									13133
WKGSPAIFQ	PQGWKGSPAIFQSSM	0.0010		-0.0014		-0.0026		-0.0007		13134
IGGYSAGER	KGGIGGYSAGERIID									13135
YALGIIQAQ	DSQYALGIIQAQPDK									13136
FWEVQLGIP	TQDFWEVQLGIPHPA									13137
IKKKDSTKW	VFAIKKKDSTKWRKL									13138
LGIIQAQPD	QYALGIIQAQPDKSE									13139
LGIPHPAGL	EVQLGIPHPAGLKKK	0.0020		0.1300		-0.0026		-0.0007		13140
VNTPPLVKL	WEFVNTPPLVKLWYQ	0.6900	0.0410	9.5000	0.0220	1.8000	1.9000	0.0630	0.2200	13141
VTVLDVGDA	KKSVTVLDVGDAYFS	0.0019		-0.0014		0.0065		0.0030		13142
FPISPIETV	TLNFPISPIETVPVK	0.0190	0.0003	-0.0014	-0.0043	0.0350		-0.0007	0.0370	13143
ISPIETVPV	NFPISPIETVPVKLK	0.0480	0.0013	0.0022	-0.0043	0.0810	0.0095	-0.0007	0.0460	13144
FVNTPPLVK	EWEFVNTPPLVKLWY									13145
LNFPISPIE	GCTLNFPISPIETVP	0.0014		-0.0014		-0.0026		-0.0006		13146
WEFVNTPPL	IPEWEFVNTPPLVKL	1.1000	0.0089	1.8000	0.0920	0.6600	1.6000	0.0830	0.0540	13147
IQNFRVYYR	ITKIQNFRVYYRDSR									13148
LVGPTPVNI	GTVLVGPTPVNIIGR	0.0066	0.0061	-0.0014	-0.0043	-0.0026		0.0043	-0.0045	13149
VQLGIPHPA	FWEVQLGIPHPAGLK	0.0240		-0.0014		0.0033		-0.0006		13150
WQATWIPEW	TEYWQATWIPEWEFV									13151
IETVPVKLK	ISPIETVPVKLKPGM	0.0019		0.0140		-0.0026		-0.0007		13152
IGTVLVGPT	KKAIGTVLVGPTPVN									13153
LVAVHVASG	KIILVAVHVASGYIE									13154
VLVGPTPVN	IGTVLVGPTPVNIIG	0.0120	0.0170	-0.0003		0.0008	0.0030	-0.0004		13155
YIEAEVIPA	ASGYIEAEVIPAETG	0.0230	-0.0003	-0.0021	-0.0043	0.2300		0.0020	-0.0045	13156
YVGSDLEIG	DDLYVGSDLEIGQHR									13157
MDGPKVKQW	KPGMDGPKVKQWPLT									13158
VASGYIEAE	AVIIVASGYIEAEVIP									13159
VGPTPVNII	TVLVGPTPVNIIGRN	0.0010		-0.0014		-0.0026		0.0035		13160
VKQWPLTEE	GPKVKQWPLTEEKIK									13161
VYYRDSRDP	NFRVYYRDSRDPIWK									13162
WGFTTPDKK	LLRWGFTTPDKKHQK									13163

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VGWPAIRER	SSIVGWPAIRERMRR						13114
WCFKLVPVE	TFGWCFKLVPVEPEK						13115
FDSRLAFHH	EWRFDSRLAFHHVAR						13116
FKLVPVDPR	GWCFKLVPVDPREVE						13117
VPLRPMTFK	RPQVPLRPMTFKGAF						13118
LLDTGADDT	KEALLDTGADDTVLE		-0.0003				13119
WMGYELHPD	PFLWMGYELHPDKWT						13120
YQYNVLPQG	GIRYQYNVLPQGWKG						13121
FRKYTAFTI	DKDFRKYTAFTIPSI						13122
WTVNDIQKL	KDSWTVNDIQKLVGK		-0.0005				13123
LDCTHLEGK	IWQLDCTHLEGKIIL						13124
LDVGDAYFS	VTVLDVGDAYFSVPL		-0.0005				13125
MDDLYVGSD	YQYMDDLYVGSDLEI		-0.0005				13126
VIPAETGQE	EAEVIPAETGQETAY						13127
WKGEGAVVI	KLLWKGEGAVVIQDN	0.0450	0.2400	0.0450	0.2100		13128
WQLDCTHLE	PGIWQLDCTHLEGKI						13129
VDFRELNKR	RKLVDFRELNKRTQD						13130
WKPKMIGGI	PGKWKPKMIGGIGGF						13131
IWQLDCTHL	SPGIWQLDCTHLEGK		-0.0009				13132
VAVHVASGY	IILVAVHVASGYIEA						13133
WKGSPAIFQ	PQGWKGSPAIFQSSM		0.0087				13134
IGGYSAGER	KGGIGGYSAGERIID						13135
YALGIIQAQ	DSQYALGIIQAQPDK						13136
FWEVQLGIP	TQDFWEVQLGIPHPA						13137
IKKKDSTKW	VFAIKKKDSTKWRKL						13138
LGIIQAQPD	QYALGIIQAQPDKSE						13139
LGIPHPAGL	EVQLGIPHPAGLKKK		-0.0005				13140
VNTPPLVKL	WEFVNTPPLVKLWYQ	0.0390	1.7000	0.1400	1.9000		13141
VTVLDVGDA	KKSVTVLDVGDAYFS		-0.0005				13142
FPISPIETV	TLNFPISPIETVPVK	0.0150	0.0640	-0.0005	0.0016		13143
ISPIETVPV	NFPISPIETVPVKLK	0.0190	0.1500	0.0008	0.0046		13144
FVNTPPLVK	EWEFVNTPPLVKLWY						13145
LNFPISPIE	GCTLNFPISPIETVP		0.0380				13146
WEFVNTPPL	IPEWEFVNTPPLVKL	0.0230	1.4000	0.2600	2.6000		13147
IQNFRVYYR	ITKIQNFRVYYRDSR						13148
LVGPTPVNI	GTVLVGPTPVNIIGR	0.0290	0.0820	-0.0005	0.0180		13149
VQLGIPHPA	FWEVQLGIPHPAGLK		0.0024				13150
WQATWIPEW	TEYWQATWIPEWEFV						13151
IETVPVKLK	ISPIETVPVKLKPGM		0.0150				13152
IGTVLVGPT	KKAIGTVLVGPTPVN						13153
LVAVHVASG	KIILVAVHVASGYIE						13154
VLVGPTPVN	IGTVLVGPTPVNIIG	0.0400	0.0710	-0.0003	0.0320		13155
YIEAEVIPA	ASGYIEAEVIPAETG	0.0006	0.0120	0.0097	0.0480		13156
YVGSDLEIG	DDLYVGSDLEIGQHR						13157
MDGPKVKQW	KPGMDGPKVKQWPLT						13158
VASGYIEAE	AVHVASGYIEAEVIP						13159
VGPTPVNII	TVLVGPTPVNIIGRN		0.0150				13160
VKQWPLTEE	GPKVKQWPLTEEKIK						13161
VYYRDSRDP	NFRVYYRDSRDPIWK						13162
WGFTTPDKK	LLRWGFTTPDKKIQK						13163

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w81	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
VIYQYMDDL	PEIVIYQYMDDLYVG									13164
LKKKKSVTV	PAGLKKKKSVTVLDV	0.0060		-0.0014		-0.0026		-0.0006		13165
VPRRKAKII	IKVVPRRKAKIIRDY	0.0003		0.0700		-0.0024		2.5000		13166
FPQITLWQR	SFSFPQITLWQRPLV	0.0027				0.0130				13167
VIWGKTPKF	ESIVIWGKTPKFRLP									13168
YVDGAANRE	ETFYVDGAANRETKL									13169
FKNLKTGKY	QEPFKNLKTGKYAKM									13170
IQTKELQKQ	ATDIQTKELQKQITK									13171
YGKQMAGDD	IRDYGKQMAGDDCVA									13172
WRAMASDFN	HSNWRAMASDFNLPP	0.1500	0.0004	0.1600	-0.0030	4.7000	2.6000	0.2100	-0.0045	13173
ISKIGPENP	EGKISKIGPENPYNT									13174
LTQIGCTLN	RNLLTQIGCTLNFPI									13175
IIQAQPDKS	ALGIIQAQPDKSESE	0.0001		-0.0014		-0.0026		-0.0007		13176
LPEKDSWTV	PIVLPEKDSWTVNDI									13177
FQSSMTKIL	PAIFQSSMTKILEPF	0.0320	0.0320	0.0200	-0.0043	0.0058	0.6500	0.0660	-0.0045	13178
FTIPSINNE	YTAFTIPSINNETPG									13179
IFQSSMTKI	SPAIFQSSMTKILEP	0.0140	0.0420	0.0300	-0.0043	0.0140	0.3500	0.0270	0.0122	13180
IIEQLIKKE	VSQIIEQLIKKEKVY									13181
LSWVPAHKG	KVYLSWVPAHKGIGG									13182
YLSWVPAHK	EKVYLSWVPAHKGIG									13183
YTAFTIPSI	FRKYTAFTIPSINNE	0.0270	0.1300	0.0048	-0.0043	0.1700	0.2800	0.0110	0.0089	13184
IIATDIQTK	IIDIIATDIQTKELQ									13185
IWKGPAKLL	RDPIWKGPAKLLWKG									13186
LQKQITKIQ	TKELQKQITKIQNFR	0.0071	0.0210	0.0350		0.0540	0.0200	0.0530		13187
LKEALLDTG	GGQLKEALLDTGADD	0.0001		-0.0021		-0.0024		-0.0005		13188
VYLSWVPAH	KEKVYLSWVPAHKGI									13189
FILKLAGRW	TAYFILKLAGRWPVK									13190
LEGKIILVA	CTHLEGKIILVAVHV									13191
YFILKLAGR	ETAYFILKLAGRWPV									13192
IILVAVHVA	EGKIILVAVHVASGY									13193
IWGKTPKFR	SIVIWGKTPKFRLPI									13194
LAGRWPVKV	ILKLAGRWPVKVIHT									13195
VVAKEIVAS	LPPVVAKEIVASCDK	0.0001		-0.0021		0.0043		-0.0010		13196
IDIIATDIQ	ERIIDIIATDIQTKE									13197
. IIDIIATDI	GERIIDIIATDIQTK									13198
IIGRNMLTQ	PVNIIGRNMLTQIGC									13199
IKVKQLCKL	YAGIKVKQLCKLLRG									13200
VDKLVSSGI	NEQVDKLVSSGIRKV									13201
IVGAETFYV	KEPIVGAETFYVDGA									13202
LPPVVAKEI	DFNLPPVVAKEIVAS	0.0042		-0.0021		-0.0024		0.0036		13203
WTVQPIQLP	PDKWTVQPIQLPEKD									13204
FNLPPVVAK	ASDFNLPPVVAKEIV	0.0026		-0.0021		-0.0028		-0.0006		13205
FTSAAVKAA	GSNFTSAAVKAACWW									13206
LALQDSGLE	AIHLALQDSGLEVNI									13207
LPPIVAKEI	DFNLPPIVAKEIVAS									13208
LQDSGLEVN	HLALQDSGLEVNIVT									13209
FNLPPIVAK	ASDFNLPPIVAKEIV									13210
IGQHRAKIE	DLEIGQHRAKIEELR									13211
IIGRNLLTQ	PVNIIGRNLLTQIGC	0.0059		-0.0014		0.0043		0.0990		13212
LEVNIVTDS	DSGLEVNIVTDSQYA	0.0001		-0.0014		0.0350		-0.0007		13213

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VTYQYMDDL	PEIVIYQYMDDLYVG						13164
LKKKKSVTV	PAGLKKKKSVTVLDV		0.0140				13165
VPRRKAKII	IKVVPRRKAKIIRDY		0.0030				13166
FPQITLWQR	SFSFPQITLWQRPLV		0.0006				13167
VIWGKTPKF	ESIVIWGKTPKFRLP						13168
YVDGAANRE	ETFYVDGAANRETKL						13169
FKNLKTGKY	QEPFKNLKTGKYAKM						13170
IQTKELQKQ	ATDIQTKELQKQITK						13171
YGKQMAGDD	IRDYGKQMAGDDCVA						13172
WRAMASDFN	HSNWRAMASDFNLPP	0.0008	0.0530	0.0250	0.0860		13173
ISKIGPENP	EGKISKIGPENPYNT						13174
LTQIGCTLN	RNLLTQIGCTLNFPI						13175
IIQAQPDKS	ALGIIQAQPDKSESE		-0.0005				13176
LPEKDSWTV	PIVLPEKDSWTVNDI						13177
FQSSMTKIL	PAIFQSSMTKILEPF	0.1100	0.7300	0.0140	0.9100		13178
FTIPSINNE	YTAFTIPSINNETPG						13179
IFQSSMTKI	SPAIFQSSMTKILEP	0.2800	0.3700	0.0150	2.3000		13180
IIEQLIKKE	VSQIIEQLIKKEKVY						13181
LSWVPAHKG	KVYLSWVPAHKGIGG						13182
YLSWVPAHK	EKVYLSWVPAHKGIG						13183
YTAFTIPSI	FRKYTAFTIPSINNE	-0.0004	0.8400	0.0610	1.9000		13184
IIATDIQTK	IIDIIATDIQTKELQ						13185
IWKGPAKLL	RDPIWKGPAKLLWKG						13186
LQKQITKIQ	TKELQKQITKIQNFR	0.0050	0.0055	0.0250	0.0028		13187
LKEALLDTG	GGQLKEALLDTGADD		-0.0009				13188
VYLSWVPAH	KEKVYLSWVPAHKGI						13189
FILKLAGRW	TAYFILKLAGRWPVK						13190
LEGKIILVA	CTHLEGKIILVAVHV						13191
YFILKLAGR	ETAYFILKLAGRWPV						13192
IILVAVHVA	EGKIILVAVHVASGY						13193
IWGKTPKFR	SIVIWGKTPKFRLPI						13194
LAGRWPVKV	ILKLAGRWPVKVIHT						13195
VVAKEIVAS	LPPVVAKEIVASCDK		-0.0009				13196
IDIIATDIQ	ERIIDIIATDIQTKE						13197
IIDIIATDI	GERIIDIIATDIQTK						13198
IIGRNMLTQ	PVNIIGRNMLTQIGC						13199
IKVKQLCKL	YAGIKVKQLCKLLRG						13200
VDKLVSSGI	NEQVDKLVSSGIRKV						13201
IVGAETFYV	KEPIVGAETFYVDGA						13202
LPPVVAKEI	DFNLPPVVAKEIVAS		0.0530				13203
WTVQPIQLP	PDKWTVQPIQLPEKD						13204
FNLPPVVAK	ASDFNLPPVVAKEIV		0.0840				13205
FTSAAVKAA	GSNFTSAAVKAACWW						13206
LALQDSGLE	AIHLALQDSGLEVNI						13207
LPPIVAKEI	DFNLPPIVAKEIVAS						13208
LQDSGLEVN	IILALQDSGLEVNIVT						13209
FNLPPIVAK	ASDFNLPPIVAKEIV						13210
IGQHRAKIE	DLEIGQHRAKIEELR						13211
IIGRNLLTQ	PVNIIGRNLLTQIGC		-0.0005				13212
LEVNIVTDS	DSGLEVNIVTDSQYA		-0.0005				13213

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LRGAKALTD	CKLLRGAKALTDIVP									13214
LVSSGIRKV	VDKLVSSGIRKVLFL									13215
FLLKLAGRW	TAYFLLKLAGRWPVK									13216
LALQDSGSE	AIHLALQDSGSEVNI									13217
LQDSGSEVN	HLALQDSGSEVNIVT									13218
VKVIITDNG	RWPVKVIHTDNGSNF									13219
WPVKVIHTD	AGRWPVKVIHTDNGS									13220
YFLLKLAGR	ETAYFLLKLAGRWPV	0.0610				0.0210				13221
ICGKKAIGT	LIEICGKKAIGTVLV									13222
IVAKEIVAS	LPPIVAKEIVASCDK									13223
LRWGFTTPD	QHLLRWGFTTPDKKH									13224
LEGKVILVA	CTHLEGKVILVAVHV									13225
LKWGFTTPD	EHLLKWGFTTPDKKH									13226
VILVAVHVA	EGKVILVAVHVASGY									13227
LAWVPAHKG	KVYLAWVPAHKGIGG	0.6000	0.3700	0.8200	0.0049	0.3200	0.2300	0.2800	0.0240	13228
YDQILIEIC	VRQYDQILIEICGKK									13229
YLAWVPAHK	EKVYLAWVPAHKGIG	1.4000	0.4400	4.1000	0.0930	5.4000	1.4000	0.5400	0.0460	13230
IGQHRTKIE	DLEIGQHRTKIEELR									13231
IGRNLLTQI	VNIIGRNLLTQIGCT	0.0027		-0.0014		0.0620		0.0067		13232
LWQRPLVTI	QITLWQRPLVTIKIG									13233
VSLTETTNQ	QKVVSLTETTNQKTE									13234
VYLAWVPAH	KEKVYLAWVPAHKGI									13235
ICGHKAIGT	LIEICGHKAIGTVLV									13236
LRGTKALTE	CKLLRGTKALTEVIP									13237
LVNQIIEQL	ESELVNQIIEQLIKK									13238
LVSQIIEQL	ESELVSQIIEQLIKK	0.0059		0.0210		0.0095		0.0009		13239
YFSVPLDKD	GDAYFSVPLDKDFRK									13240
IGRNMLTQI	VNIIGRNMLTQIGCT									13241
IKVRQLCKL	YPGIKVRQLCKLLRG									13242
LWKGPAKLL	RDPLWKGPAKLLWKG									13243
LWQRPLVTV	QITLWQRPLVTVKIG									13244
YAGIKVKQL	SQIYAGIKVKQLCKL									13245
IWGKTPKFK	SIVIWGKTPKFKLPI									13246
LREHLLKWG	IEELREHLLKWGFTT									13247
.VQPIQLPEK	KWTVQPIQLPEKDSW									13248
WQRPLVTIK	ITLWQRPLVTIKIGG									13249
IIQAQPDRS	ALGIIQAQPDRSESE									13250
LQAIHLALQ	KTELQAIHLALQDSG									13251
LVEICTEME	IKALVEICTEMEKEG									13252
LRQHLLRWG	IEELRQHLLRWGFTT									13253
LTQLGCTLN	RNMLTQLGCTLNFPI									13254
LVSAGIRKV	VDKLVSAGIRKVLFL	0.0039		0.1500		-0.0026		0.0045		13255
VDKLVSAGI	NEQVDKLVSAGIRKV	0.0024		0.5900		-0.0026		-0.0006		13256
YPGIKVRQL	SQIYPGIKVRQLCKL									13257
FRKQNPDIV	. LEPFRKQNPDIVIYQ									13258
FSFPQITLW	TVSFSFPQITLWQRP									13259
FTSTTVKAA	GSNFTSTTVKAACWW									13260
IIASDIQTK	IIDIIASDIQTKELQ									13261
LAGRWPVKT	LLKLAGRWPVKTIHT									13262
VQKIATESI	TEAVQKIATESIVIW									13263

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LRGAKALTD	CKLLRGAKALTDIVP						13214
LVSSGIRKV	VDKLVSSGIRKVLFL						13215
FLLKLAGRW	TAYFLLKLAGRWPVK						13216
LALQDSGSE	AIHLALQDSGSEVNI						13217
LQDSGSEVN	HLALQDSGSEVNIVT						13218
VKVIIITDNG	RWPVKVIHTDNGSNF						13219
WPVKVIHTD	AGRWPVKVIHTDNGS						13220
YFLLKLAGR	ETAYFLLKLAGRWPV		0.0041				13221
ICGKKAIGT	LIEICGKKAIGTVLV						13222
IVAKEIVAS	LPPIVAKEIVASCDK						13223
LRWGFTTPD	QHLLRWGFTTPDKKH						13224
LEGKVILVA	CTHLEGKVILVAVHV						13225
LKWGFTTPD	EHLLKWGFTTPDKKH						13226
VILVAVHVA	EGKVILVAVHVASGY						13227
LAWVPAHKG	KVYLAWVPAHKGIGG	0.0014	0.1400	0.2500	0.3000		13228
YDQILIEIC	VRQYDQILIEICGKK						13229
YLAWVPAHK	EKVYLAWVPAHKGIG	0.0010	1.4000	1.6000	0.5200		13230
IGQHRTKIE	DLEIGQHRTKIEELR						13231
IGRNLLTQI	VNIIGRNLLTQIGCT		0.0012				13232
LWQRPLVTI	QITLWQRPLVTIKIG						13233
VSLTETTNQ	QKVVSLTETTNQKTE						13234
VYLAWVPAH	KEKVYLAWVPAHKGI						13235
ICGHKAIGT	LIEICGHKAIGTVLV						13236
LRGTKALTE	CKLLRGTKALTEVIP						13237
LVNQIIEQL	ESELVNQIIEQLIKK						13238
LVSQIIEQL	ESELVSQIIEQLIKK		0.0040				13239
YFSVPLDKD	GDAYFSVPLDKDFRK						13240
IGRNMLTQI	VNIIGRNMLTQIGCT						13241
IKVRQLCKL	YPGIKVRQLCKLLRG						13242
LWKGPAKLL	RDPLWKGPAKLLWKG						13243
LWQRPLVTV	QITLWQRPLVTVKIG						13244
YAGIKVKQL	SQIYAGIKVKQLCKL						13245
IWGKTPKFK	SIVIWGKTPKFKLPI						13246
LREHLLKWG	IEELREHLLKWGFTT						13247
VQPIQLPEK	KWTVQPIQLPEKDSW						13248
WQRPLVTIK	ITLWQRPLVTIKIGG						13249
IIQAQPDRS	ALGIIQAQPDRSESE						13250
LQAIHLALQ	KTELQAIHLALQDSG						13251
LVEICTEME	IKALVEICTEMEKEG						13252
LRQHLLRWG	IEELRQHLLRWGFTT						13253
LTQLGCTLN	RNMLTQLGCTLNFPI						13254
LVSAGIRKV	VDKLVSAGIRKVLFL		0.0120				13255
VDKLVSAGI	NEQVDKLVSAGIRKV		0.0028				13256
YPGIKVRQL	SQIYPGIKVRQLCKL						13257
FRKQNPDIV	LEPFRKQNPDIVIYQ						13258
FSFPQITLW	TVSFSFPQITLWQRP						13259
FTSTTVKAA	GSNFTSTTVKAACWW						13260
IIASDIQTK	IIDIIASDIQTKELQ						13261
LAGRWPVKT	LLKLAGRWPVKTIHT						13262
VQKIATESI	TEAVQKIATESIVIW						13263

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w81	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
FTIPSTNNE	YTAFTIPSTNNETPG									13264
LEDINLPGK	DTVLEDINLPGKWKP									13265
LTDIVPLTE	AKALTDIVPLTEEAE									13266
LVTIKIGGQ	QRPLVTIKIGGQLKE									13267
MRGAHTNDV	YARMRGAHTNDVKQL									13268
VKTIHTDNG	RWPVKTIHTDNGSNF									13269
VQPIVLPEK	KWTVQPIVLPEKDSW									13270
WPVKTIHTD	AGRWPVKTIHTDNGS									13271
WQRPLVTVK	ITLWQRPLVTVKIGG									13272
WTVQPIVLP	PDKWTVQPIVLPEKD									13273
YTAFTIPST	FRKYTAFTIPSTNNE									13274
IDIIASDIQ	ERIIDIIASDIQTKE									13275
IIDIIASDI	GERIIDIIASDIQTK									13276
IVDIIATDI	GERIVDIIATDIQTK	0.0031				0.0320				13277
LEEINLPGK	DTVLEEINLPGKWKP									13278
LQAIYLALQ	KTELQAIYLALQDSG									13279
LQKQIIKIQ	TKELQKQIIKIQNFR									13280
VDIIATDIQ	ERIVDIIATDIQTKE									13281
YDQIPIEIC	VRQYDQIPIEICGKK									13282
FNFPQITLW	VPTFNFPQITLWQRP									13283
IGRNMLTQL	VNIIGRNMLTQLGCT									13284
ISRIGPENP	EGKISRIGPENPYNT									13285
LTEVIPLTE	TKALTEVIPLTEEAE									13286
MESIVIWGK	KIAMESIVIWGKTPK									13287
VPRRKVKII	IKVVPRRKVKIIRDY									13288
VSFSFPQIT	QGTVSFSFPQITLWQ									13289
WYQLETEPI	VKLWYQLETEPIVGA									13290
YPGIKVKQL	SQIYPGIKVKQLCKL									13291
FPQGEAREF	NLAFPQGEAREFPPE									13292
LIEALLDTG	GGQLIEALLDTGADD									13293
VSLTDTTNQ	QKVVSLTDTTNQKTE									13294
WETWWTDYW	KETWETWWTDYWQAT									13295
YAKMRTAHT	TGKYAKMRTAHTNDV									13296
YKNLKTGKY	QEPYKNLKTGKYARM									13297
LQLPPLERL	PVPLQLPPLERLTLD									13298
VPLQLPPLE	AEPVPLQLPPLERLT									13299
LYQSNPPPS	IKFLYQSNPPPSPEG									13300
VRIIKILYQ	LKAVRIIKILYQSNP									13301
YQSNPPPSP	KFLYQSNPPPSPEGT									13302
LQLPPIERL	PVPLQLPPIERLRLD									13303
VPLQLPPIE	AEPVPLQLPPIERLR									13304
WNHPGSQPK	LEPWNHPGSQPKTAC									13305
FLNKGLGIS	QVCFLNKGLGISYGR									13306
WKHPGSQPK	LEPWKHPGSQPKTAC									13307
YCKKCCFHC	NNCYCKKCCFHCQVC									13308
YCKKCCYHC	TNCYCKKCCYHCQVC									13309
WNHPGSQPT	LEPWNIIPGSQPTTAC									13310
MIVWQVDRM	WQVMIVWQVDRMRIR									13311
WQVMIVWQV	ENRWQVMIVWQVDRM	3.3000	0.0059	0.0036	-0.0043	0.0690	1.9000	0.0032	-0.0045	13312
WQVDRMRIR	MIVWQVDRMRIRTWK									13313

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
FTIPSTNNE	YTAFTIPSTNNETPG						13264
LEDINLPGK	DTVLEDINLPGKWKP						13265
LTDIVPLTE	AKALTDIVPLTEEAE						13266
LVTIKIGGQ	QRPLVTIKIGGQLKE						13267
MRGAHTNDV	YARMRGAHTNDVKQL						13268
VKTIHTDNG	RWPVKTIHTDNGSNF						13269
VQPIVLPEK	KWTVQPIVLPEKDSW						13270
WPVKTIHTD	AGRWPVKTIHTDNGS						13271
WQRPLVTVK	ITLWQRPLVTVKIGG						13272
WTVQPIVLP	PDKWTVQPIVLPEKD						13273
YTAFTIPST	FRKYTAFTIPSTNNE						13274
IDIIASDIQ	ERIIDIIASDIQTKE						13275
IIDIIASDI	GERIIDIIASDIQTK						13276
IVDIIATDI	GERIVDIIATDIQTK		0.0026				13277
LEEINLPGK	DTVLEEINLPGKWKP						13278
LQAIYLALQ	KTELQAIYLALQDSG						13279
LQKQIIKIQ	TKELQKQIIKIQNFR						13280
VDIIATDIQ	ERIVDIIATDIQTKE						13281
YDQIPIEIC	VRQYDQIPIEICGKK						13282
FNFPQITLW	VPTFNFPQITLWQRP						13283
IGRNMLTQL	VNIIGRNMLTQLGCT						13284
ISRIGPENP	EGKISRIGPENPYNT						13285
LTEVIPLTE	TKALTEVIPLTEEAE						13286
MESIVIWGK	KIAMESIVIWGKTPK						13287
VPRRKVKII	IKVVPRRKVKIIRDY						13288
VSFSFPQIT	QGTVSFSFPQITLWQ						13289
WYQLETEPI	VKLWYQLETEPIVGA						13290
YPGIKVKQL	SQIYPGIKVKQLCKL						13291
FPQGEAREF	NLAFPQGEAREFPPE						13292
LIEALLDTG	GGQLIEALLDTGADD						13293
VSLTDTTNQ	QKVVSLTDTTNQKTE						13294
WETWWTDYW	KETWETWWTDYWQAT						13295
YAKMRTAHT	TGKYAKMRTAHTNDV						13296
YKNLKTGKY	QEPYKNLKTGKYARM						13297
LQLPPLERL	PVPLQLPPLERLTLD						13298
VPLQLPPLE	AEPVPLQLPPLERLT						13299
LYQSNPPPS	IKFLYQSNPPPSPEG						13300
VRIIKILYQ	LKAVRIIKILYQSNP						13301
YQSNPPPSP	KFLYQSNPPPSPEGT						13302
LQLPPIERL	PVPLQLPPIERLRLD						13303
VPLQLPPIE	AEPVPLQLPPIERLR						13304
WNHPGSQPK	LEPWNHPGSQPKTAC						13305
FLNKGLGIS	QVCFLNKGLGISYGR						13306
WKHPGSQPK	LEPWKHPGSQPKTAC						13307
YCKKCCFHC	NNCYCKKCCFHCQVC						13308
YCKKCCYHC	TNCYCKKCCYHCQVC						13309
WNHPGSQPT	LEPWNHPGSQPTTAC						13310
MIVWQVDRM	WQVMIVWQVDRMRIR						13311
WQVMIVWQV	ENRWQVMIVWQVDRM	0.0018	0.1200	0.1500	0.2900		13312
WQVDRMRIR	MIVWQVDRMRIRTWK						13313

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LQYLALTAL	VGSLQYLALTALIKP									13314
LGHGVSIEW	DWHLGHGVSIEWRLR									13315
VDRMRIRTW	VWQVDRMRIRTWNSL									13316
YFDCFSESA	HLYYFDCFSESAIRN									13317
YWGLHTGER	ITTYWGLHTGERDWH									13318
IRTWNSLVK	RMRIRTWNSLVKHHM									13319
LGQGVSIEW	DWHLGQGVSIEWRKK									13320
LVKHHMYVS	WNSLVKHHMYVSKKA									13321
IPLGEARLV	EVHIPLGEARLVVRT									13322
LVKHHMYIS	WKSLVKHHMYISGKA									13323
YLALTALIK	SLQYLALTALIKPKK									13324
IRTWKSLVK	RMRIRTWKSLVKHHM									13325
LADQLIHLY	DPDLADQLIHLYYFD									13326
LALTALIKP	LQYLALTALIKPKKI									13327
VDPGLADQL	STQVDPGLADQLIHL									13328
LYYFDCFSE	LIHLYYFDCFSESAI									13329
FSESAIRKA	FDCFSESAIRKAILG									13330
LADQLIHMH	EPGLADQLIHMHYFD									13331
WQVDRMKIR	LIVWQVDRMKIRTWN									13332
FSDSAIRKA	FDCFSDSAIRKAILG									13333
FSESAIRNA	FDCFSESAIRNAILG									13334
IVSPRCEYQ	LGHIVSPRCEYQAGH									13335
LQYLALAAL	VGSLQYLALAALITP									13336
VDRMKIRTW	VWQVDRMKIRTWNSL									13337
YWGLQTGER	IKTYWGLQTGERDWH									13338
IPLGDARLV	EVHIPLGDARLVITT									13339
LQYLALKAL	VGSLQYLALKALVTP									13340
WQVDRMRIN	MIVWQVDRMRINTWK									13341
IKPKKIKPP	TALIKPKKIKPPLPS									13342
VDRMRINTW	VWQVDRMRINTWKSL									13343
IGCQHSRIG	HFRIGCQHSRIGITR									13344
WTLELLEEL	YNEWTLELLEELKSE									13345
ILQQLLFIH	HRILQQLLFIHFRI	0.0054				0.0200				13346
FIHFRIGCQ	QLLFIHFRIGCQHSR									13347
YNEWTLELL	REPYNEWTLELLEEL									13348
FPRPWLHGL	VRHFPRPWLHGLGQH									13349
WEGVEAIIR	GDTWEGVEAIIRILQ									13350
LEELKSEAV	LELLEELKSEAVRHF									13351
WAGVEAIIR	GDTWAGVEAIIRILQ									13352
YGDTWAGVE	YETYGDTWAGVEAII									13353
IGCRHSRIG	HFRIGCRHSRIGITR									13354
FIHFRIGCR	QLLFIHFRIGCRHSR									13355
FVHFRIGCQ	QLLFVHFRIGCQHSR									13356
YGDTWTGVE	YETYGDTWTGVEAII									13357
FPRIWLHSL	VRHFPRIWLHSLGQH									13358
WALELLEEL	YNEWALELLEELKNE									13359
LVTLLSSSK	EEWLVTLLSSSKLDQ									13360
VTLLSSSKL	EWLVTLLSSSKLDQG									13361
IIAIVVWTI	VVAIIAIVVWTIVFI									13362
VDYRIVIVA	LAKVDYRIVIVAFIV									13363

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LQYLALTAL	VGSLQYLALTALIKP						13314
LGHGVSIEW	DWHLGHGVSIEWRLR						13315
VDRMRIRTW	VWQVDRMRIRTWNSL						13316
YFDCFSESA	HLYYFDCFSESAIRN						13317
YWGLHTGER	ITTYWGLHTGERDWH						13318
IRTWNSLVK	RMRIRTWNSLVKHHM						13319
LGQGVSIEW	DWHLGQGVSIEWRKK						13320
LVKHHMYVS	WNSLVKHHMYVSKKA						13321
IPLGEARLV	EVHIPLGEARLVVRT						13322
LVKHHMYIS	WKSLVKHHMYISGKA						13323
YLALTALIK	SLQYLALTALIKPKK						13324
IRTWKSLVK	RMRIRTWKSLVKHHM						13325
LADQLIHLY	DPDLADQLIHLYYFD						13326
LALTALIKP	LQYLALTALIKPKKI						13327
VDPGLADQL	STQVDPGLADQLIHL						13328
LYYFDCFSE	LIHLYYFDCFSESAI						13329
FSESAIRKA	FDCFSESAIRKAILG						13330
LADQLIHMH	EPGLADQLIHMHYFD						13331
WQVDRMKIR	LIVWQVDRMKIRTWN						13332
FSDSAIRKA	FDCFSDSAIRKAILG						13333
FSESAIRNA	FDCFSESAIRNAILG						13334
IVSPRCEYQ	LGHIVSPRCEYQAGH						13335
LQYLALAAL	VGSLQYLALAALITP						13336
VDRMKIRTW	VWQVDRMKIRTWNSL						13337
YWGLQTGER	IKTYWGLQTGERDWH						13338
IPLGDARLV	EVHIPLGDARLVITT						13339
LQYLALKAL	VGSLQYLALKALVTP						13340
WQVDRMRIN	MIVWQVDRMRINTWK						13341
IKPKKIKPP	TALIKPKKIKPPLPS						13342
VDRMRINTW	VWQVDRMRINTWKSL						13343
IGCQHSRIG	HFRIGCQHSRIGITR						13344
WTLELLEEL	YNEWTLELLEELKSE						13345
ILQQLLFIH	HRILQQLLFIHFRI		0.0084				13346
FIHFRIGCQ	QLLFIHFRIGCQHSR						13347
YNEWTLELL	REPYNEWTLELLEEL						13348
FPRPWLHGL	VRHFPRPWLHGLGQH						13349
WEGVEAIIR	GDTWEGVEAIIRILQ						13350
LEELKSEAV	LELLEELKSEAVRHF						13351
WAGVEAIIR	GDTWAGVEAIIRILQ						13352
YGDTWAGVE	YETYGDTWAGVEAII						13353
IGCRHSRIG	HFRIGCRHSRIGITR						13354
FIHFRIGCR	QLLFIHFRIGCRHSR						13355
FVHFRIGCQ	QLLFVHFRIGCQHSR						13356
YGDTWTGVE	YETYGDTWTGVEAII						13357
FPRIWLHSL	VRHFPRIWLHSLGQH						13358
WALELLEEL	YNEWALELLEELKNE						13359
LVTLLSSSK	EEWLVTLLSSSKLDQ						13360
VTLLSSSKL	EWLVTLLSSSKLDQQ						13361
IIAIVVWTI	VVAIIAIVVWTIVFI						13362
VDYRIVIVA	LAKVDYRIVIVAFIV						13363

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LRQRKIDRL	RKILRQRKIDRLIDR									13364
IVVWTIVFI	IIAIVVWTIVFIEYR									13365
VVWTIVFIE	IAIVVWTIVFIEYRK									13366
IEYRKILRQ	IVFIEYRKILRQRKI									13367
ILAIVALVV	SLYILAIVALVVAII									13368
WTIVFIEYR	IVVWTIVFIEYRKIL									13369
LAIVALVVA	LQILAIVALVVAGII									13370

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LRQRKIDRL	RKILRQRKIDRLIDR						13364
IVVWTIVFI	IIAIVVWTIVFIEYR						13365
VVWTIVFIE	IAIVVWTIVFIEYRK						13366
IEYRKILRQ	IVFIEYRKILRQRKI						13367
ILAIVALVV	SLYILAIVALVVAII						13368
WTIVFIEYR	IVVWTIVFIEYRKIL						13369
LAIVALVVA	LQILAIVALVVAGII						13370

Table XXa
HIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	VPTDPNPQE	53	83	HACVPTDPNPQEVVL	85	12	19	13371
ENV	YLKDQQLLG	31	48	VERYLKDQQLLGIWG	669	18	28	13372
ENV	MHEDIISLW	29	45	VEQMHEDIISLWDQS	114	17	27	13373
ENV	VSFEPIPIH	29	45	CPKVSFEPIPIHYCA	250	18	28	13374
ENV	LAVERYLKD	26	41	ARVLAVERYLKDQQL	664	15	23	13375
ENV	VKIEPLGVA	23	36	YKVVKIEPLGVAPTK	564	15	23	13376
ENV	VWKEATTTL	22	34	GVPVWKEATTTLFCA	52	22	34	13377
ENV	LAWDDLRSL	20	31	FLALAWDDLRSLCLF	849	19	30	13378
ENV	LIEESQNQQ	20	31	IYTLIEESQNQQEKN	737	07	11	13379
ENV	LGWEGLKYL	09	29	GLRLGWEGLKYLWNL	892	07	23	13380
ENV	LELDKWASL	18	28	QELLELDKWASLWNW	733	07	11	13381
ENV	YLRDQQLLG	18	28	VERYLRDQQLLGIWG	669	11	17	13382
ENV	MWQEVGKAM	15	23	IINMWQEVGKAMYAP	492	12	19	13383
ENV	IEEEGGERD	13	20	PEGIEEEGGERDRDR	827	08	13	13384
ENV	MNNENNGTN	01	20	INEMNNENNGTNSTW	212	01	2	13385
ENV	IEEEGGEQD	12	19	LGRIEEEGGEQDKNR	827	02	3	13386
ENV	LAEEEVVIR	12	19	NGSLAEEEVVIRSEN	309	04	6	13387
ENV	LALDKWASL	11	17	QDLLALDKWASLWNW	753	05	8	13388
ENV	LAVERYLRD	11	17	ARVLAVERYLRDQQL	664	10	16	13389
ENV	IRSENLTNN	10	16	EIIRSENLTNNVKT	317	03	5	13390
ENV	MEWEREIDN	10	16	MTWMEWEREIDNYTS	721	03	5	13391
GAG	INEEAAEWD	55	86	KETINEEAAEWDRLH	223	18	28	13392
GAG	FSPEVIPMF	54	84	EKAFSPEVIPMFSAL	182	36	56	13393
GAG	VLAEAMSQV	33	52	KARVLAEAMSQVTNS	383	09	14	13394
GAG	MLKDTINEE	32	50	AMQMLKDTINEEAAE	218	30	47	13395
GAG	VVEEKAFSP	28	44	WVKVVEEKAFSPEVI	176	28	44	13396
GAG	LRAEQATQE	27	42	FKTLRAEQATQEVKN	325	09	14	13397
GAG	MLKETINEE	23	36	AMQMLKETINEEAAE	218	22	34	13398
GAG	VIEEKAFSP	21	33	WVKVIEEKAFSPEVI	176	20	31	13399
GAG	VLAEAMSQA	16	25	KARVLAEAMSQASGA	383	03	5	13400
GAG	IEEEQNKSK	15	23	LDKIEEEQNKSKKKA	103	09	14	13401
GAG	LRAEQATQD	14	22	FKTLRAEQATQDVKN	325	10	16	13402
GAG	LRAEQASQE	12	19	YKTLRAEQASQEVKN	325	12	19	13403
NEF	YFPDWQNYT	36	56	TQGYFPDWQNYTPGP	195	33	52	13404
NEF	FLKEKGGLE	30	47	LSHFLKEKGGLEGLI	114	15	23	13405
NEF	FLKEKGGLD	26	41	LSFFLKEKGGLDGLI	114	14	22	13406
NEF	FFPDWQNYT	17	27	TQGFFPDWQNYTPGP	195	17	27	13407
NEF	VSRDLEKHG	11	17	VGAVSRDLEKHGAIT	46	11	17	13408
POL	YMDDLYVGS	62	97	IYQYMDDLYVGSDLE	369	59	92	13409
POL	IGPENPYNT	60	94	ISKIGPENPYNTPVF	236	28	44	13410
POL	LHPDKWTVQ	60	94	GYELHPDKWTVQPIQ	420	29	45	13411
POL	IVTDSQYAL	59	92	EVNIVTDSQYALGII	684	58	91	13412
POL	IPAETGQET	58	91	AEVIPAETGQETAYF	838	55	86	13413
POL	LTEEKIKAL	56	88	QWPLTEEKIKALTEI	210	26	41	13414
POL	IEAEVIPAE	55	86	SGYIEAEVIPAETGQ	833	51	80	13415
POL	LFLDGIDKA	55	86	RKVLFLDGIDKAQEE	749	32	50	13416
POL	VAKEIVASC	54	86	PPVVAKEIVASCDKC	781	22	34	13417
POL	LKGEAMHGQ	53	83	KCQLKGEAMHGQVDC	794	47	73	13418
POL	VGSDLEIGQ	53	83	DLYVGSDLEIGQHRA	375	28	44	13419
POL	IIRDYGKQM	50	78	KAKIIRDYGKQMAGD	1017	36	56	13420

Table XXa
HIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	MASDFNLPP	47	73	WRAMASDFNLPPVVA	771	24	38	13421
POL	FYVDGAANR	43	67	AETFYVDGAANRETK	629	33	52	13422
POL	IHTDNGSNF	42	66	VKVIHTDNGSNFTSA	862	17	27	13423
POL	ILKEPVHGV	41	64	NREILKEPVHGVYYD	495	36	56	13424
POL	IYQEPFKNL	40	63	TYQIYQEPFKNLKTG	530	39	61	13425
POL	VYYDPSKDL	39	61	VHGVYYDPSKDLIAE	506	26	41	13426
POL	YVTDRGRQK	39	61	KAGYVTDRGRQKVVS	646	19	30	13427
POL	LTEEAELEL	37	58	IVPLTEEAELELAEN	481	12	19	13428
POL	VIQDNSDIK	37	58	GAVVIQDNSDIKVVP	999	37	58	13429
POL	IATDIQTKE	35	55	IDIIATDIQTKELQK	953	22	34	13430
POL	INNETPGIR	32	51	IPSINNETPGIRYQY	321	31	48	13431
POL	LIAEIQKQG	30	47	SKDLIAEIQKQGQGQ	514	09	14	13432
POL	ICTEMEKEG	28	44	LVEICTEMEKEGKIS	221	14	22	13433
POL	VGAETFYVD	28	44	EPIVGAETFYVDGAA	624	20	31	13434
POL	IQKETWETW	27	42	RLPIQKETWETWWTD	582	09	14	13435
POL	IKQEFGIPY	26	41	WAGIKQEFGIPYNPQ	884	21	33	13436
POL	MAGDDCVAG	25	39	GKQMAGDDCVAGRQD	1025	23	36	13437
POL	IKKEKVYLA	20	31	EQLIKKEKVYLAWVP	715	19	30	13438
POL	MAGDDCVAS	19	30	GKQMAGDDCVASRQD	1025	19	30	13439
POL	VPLDKDFRK	18	28	YFSVPLDKDFRKYTA	304	18	29	13440
POL	IQQEFGIPY	16	25	WAGIQQEFGIPYNPQ	884	11	17	13441
POL	LEKEPIVGA	16	25	WYQLEKEPIVGAETF	618	16	25	13442
POL	YQLEKEPIV	16	25	KLWYQLEKEPIVGAE	616	16	25	13443
POL	IQKETWEAW	15	23	KLPIQKETWEAWWTE	582	05	8	13444
POL	FSSEQTRAN	14	22	AREFSSEQTRANSPT	14	10	16	13445
POL	IASDIQTKE	14	22	IDIIASDIQTKELQK	953	09	14	13446
POL	IATESIVIW	14	22	VQKIATESIVIWGKT	564	11	17	13447
POL	ILIEICGKK	14	22	YDQILIEICGKKAIG	146	13	20	13448
POL	VLEEINLPG	14	22	DDTVLEEINLPGKWK	116	11	17	13449
POL	IKKEKVYLS	13	20	EQLIKKEKVYLSWVP	715	07	11	13450
POL	VLEDINLPG	13	20	DDTVLEDINLPGKWK	116	13	20	13451
POL	VLPEKDSWT	13	20	QPIVLPEKDSWTVND	431	13	20	13452
POL	VIQDNSEIK	12	19	GAVVIQDNSEIKVVP	999	12	19	13453
POL	IIKDYGKQM	11	17	KAKIIKDYGKQMAGA	1017	06	9	13454
TAT	VERETETDP	11	17	KEKVERETETDPAVQ	95	01	2	13455
VIF	LTEDRWNKP	28	44	VKKLTEDRWNKPQKT	175	09	14	13456
VIF	YYFDCFSES	20	31	IIILYYFDCFSESAIR	112	14	22	13457
VIF	LVEDRWNKP	11	17	VQKLVEDRWNKPQKT	175	04	6	13458
VIF	IDPDLADQL	10	16	STQIDPDLADQLIHL	100	10	16	13459
VPR	LKNEAVRHF	18	28	LEELKNEAVRHFPRP	23	10	16	13460
VPR	LKSEAVRHF	15	23	LEELKSEAVRHFPRI	23	07	11	13461
VPR	YIYETYGDT	14	22	LGQYIYETYGDTWAG	42	07	11	13462
VPR	LKQEAVRHF	11	17	LEELKQEAVRHFPRP	23	06	9	13463

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2wβ1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
VPTDPNPQE	HACVPTDPNPQEVVL									13371
YLKDQQLLG	VERYLKDQQLLGIWG									13372
MHEDIISLW	VEQMHEDIISLWDQS									13373
VSFEPIPIH	CPKVSFEPIPIHYCA									13374
LAVERYLKD	ARVLAVERYLKDQQL									13375
VKIEPLGVA	YKVVKIEPLGVAPTK									13376
VWKEATTTL	GVPVWKEATTTLFCA									13377
LAWDDLRSL	FLALAWDDLRSLCLF									13378
LIEESQNQQ	IYTLIEESQNQQEKN									13379
LGWEGLKYL	GLRLGWEGLKYLWNL									13380
LELDKWASL	QELLELDKWASLWNW									13381
YLRDQQLLG	VERYLRDQQLLGIWG									13382
MWQEVGKAM	INMWQEVGKAMYAP									13383
IEEEGGERD	PEGIEEEGGERDRDR									13384
MNNENNGTN	INEMNNENNGTNSTW									13385
IEEEGGEQD	LGRIEEEGGEQDKNR									13386
LAEEEVVIR	NGSLAEEEVVIRSEN									13387
LALDKWASL	QDLLALDKWASLWNW									13388
LAVERYLRD	ARVLAVERYLRDQQL									13389
IRSENLTNN	EIIRSENLTNNVKT									13390
MEWEREIDN	MTWMEWEREIDNYTS									13391
INEEAAEWD	KETINEEAAEWDRLH									13392
FSPEVIPMF	EKAFSPEVIPMFSAL	0.0086		0.0015	-0.0130	0.0340		-0.0010		13393
VLAEAMSQV	KARVLAEAMSQVTNS	0.0080				0.0120				13394
MLKDTINEE	AMQMLKDTINEEAAE									13395
VVEEKAFSP	WVKVVEEKAFSPEVI	0.0006				0.0016				13396
LRAEQATQE	FKTLRAEQATQEVKN									13397
MLKETINEE	AMQMLKETINEEAAE									13398
VIEEKAFSP	WVKVIEEKAFSPEVI									13399
VLAEAMSQA	KARVLAEAMSQASGA									13400
IEEEQNKSK	LDKIEEEQNKSKKKA									13401
LRAEQATQD	FKTLRAEQATQDVKN									13402
LRAEQASQE	YKTLRAEQASQEVKN									13403
YFPDWQNYT	TQGYFPDWQNYTPGP				-0.0017					13404
FLKEKGGLE	LSHFLKEKGGLEGLI									13405
FLKEKGGLD	LSFFLKEKGGLDGLI									13406
FFPDWQNYT	TQGFFPDWQNYTPGP									13407
VSRDLEKHG	VGAVSRDLEKHGAIT									13408
YMDDLYVGS	IYQYMDDLYVGSDLE									13409
IGPENPYNT	ISKIGPENPYNTPVF	0.0001		-0.0014	-0.0130	-0.0026		-0.0006		13410
LIIPDKWTVQ	GYELHPDKWTVQPIQ									13411
IVTDSQYAL	EVNIVTDSQYALGII	0.0002	0.0034	-0.0010	0.4100	-0.0055		-0.0006		13412
IPAETGQET	AEVIPAETGQETAYF				-0.0033					13413
LTEEKIKAL	QWPLTEEKIKALTEI									13414
IEAEVIPAE	SQYIEAEVIPAETGQ									13415
LFLDGIDKA	RKVLFLDGIDKAQEE									13416
VAKEIVASC	PPVVAKEIVASCDKC	0.0001		-0.0021	-0.0130	0.0085		-0.0006		13417
LKGEAMHGQ	KCQLKGEAMHGQVDC				-0.0017					13418
VGSDLEIGQ	DLYVGSDLEIGQHRA									13419
IIRDYGKQM	KAKIIRDYGKQMAGD									13420

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VPTDPNPQE	HACVPTDPNPQEVVL						13371
YLKDQQLLG	VERYLKDQQLLGIWG						13372
MIIEDIISLW	VEQMHEDIISLWDQS						13373
VSFEPIPIH	CPKVSFEPIPIHYCA						13374
LAVERYLKD	ARVLAVERYLKDQQL						13375
VKIEPLGVA	YKVVKIEPLGVAPTK						13376
VWKEATTTL	GVPVWKEATTTLFCA						13377
LAWDDLRSL	FLALAWDDLRSLCLF						13378
LIEESQNQQ	IYTLIEESQNQQEKN						13379
LGWEGLKYL	GLRLGWEGLKYLWNL						13380
LELDKWASL	QELLELDKWASLWNW						13381
YLRDQQLLG	VERYLRDQQLLGIWG						13382
MWQEVGKAM	IINMWQEVGKAMYAP						13383
IEEEGGERD	PEGIEEEGGERDRDR						13384
MNNENNGTN	INEMNNENNGTNSTW						13385
IEEEGGEQD	LGRIEEEGGEQDKNR						13386
LAEEEVVIR	NGSLAEEEVVIRSEN						13387
LALDKWASL	QDLLALDKWASLWNW						13388
LAVERYLRD	ARVLAVERYLRDQQL						13389
IRSENLTNN	EIIIRSENLTNNVKT						13390
MEWEREIDN	MTWMEWEREIDNYTS						13391
INEEAAEWD	KETINEEAAEWDRLH						13392
FSPEVIPMF	EKAFSPEVIPMFSAL		0.0023				13393
VLAEAMSQV	KARVLAEAMSQVTNS		0.0025				13394
MLKDTINEE	AMQMLKDTINEEAAE						13395
VVEEKAFSP	WVKVVEEKAFSPEVI		0.0003				13396
LRAEQATQE	FKTLRAEQATQEVKN						13397
MLKETINEE	AMQMLKETINEEAAE						13398
VIEEKAFSP	WVKVIEEKAFSPEVI						13399
VLAEAMSQA	KARVLAEAMSQASGA						13400
IEEEQNKSK	LDKIEEEQNKSKKKA						13401
LRAEQATQD	FKTLRAEQATQDVKN						13402
LRAEQASQE	YKTLRAEQASQEVKN						13403
YFPDWQNYT	TQGYFPDWQNYTPGP						13404
FLKEKGGLE	LSIIFLKEKGGLEGLI						13405
FLKEKGGLD	LSFFLKEKGGLDGLI						13406
FFPDWQNYT	TQGFFPDWQNYTPGP						13407
VSRDLEKHG	VGAVSRDLEKHGAIT						13408
YMDDLYVGS	IYQYMDDLYVGSDLE						13409
IGPENPYNT	ISKIGPENPYNTPVF		-0.0005				13410
LHPDKWTVQ	GYELHPDKWTVQPIQ						13411
IVTDSQYAL	EVNIVTDSQYALGII	0.0108	-0.0014	-0.0009			13412
IPAETGQET	AEVIPAETGQETAYF						13413
LTEEKIKAL	QWPLTEEKIKALTEI						13414
IEAEVIPAE	SQYIEAEVIPAETGQ						13415
LFLDGIDKA	RKVLFLDGIDKAQEE						13416
VAKEIVASC	PPVVAKEIVASCDKC		0.0015				13417
LKGEAMHGQ	KCQLKGEAMHGQVDC						13418
VGSDLEIGQ	DLYVGSDLEIGQHRA						13419
IIRDYGKQM	KAKIIRDYGKQMAGD						13420

Table XXb

HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w81	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
MASDFNLPP	WRAMASDFNLPPVVA									13421
FYVDGAANR	AETFYVDGAANRETK	0.0021	-0.0005	0.0046	0.3900	0.0150		-0.0006		13422
IITDNGSNF	VKVIHTDNGSNFTSA									13423
ILKEPVHGV	NREILKEPVHGVYYD	0.3000	0.1500	-0.0014	0.1000	0.1900	0.0300	-0.0007	0.0230	13424
IYQEPFKNL	TYQIYQEPFKNLKTG				-0.0017					13425
VYYDPSKDL	VHGVYYDPSKDLIAE									13426
YVTDRGRQK	KAGYVTDRGRQKVVS									13427
LTEEAELEL	IVPLTEEAELELAEN									13428
VIQDNSDIK	GAVVIQDNSDIKVVP	0.0033	0.0280	0.0014	0.3000	-0.0055		-0.0006		13429
IATDIQTKE	IDIIATDIQTKELQK									13430
INNETPGIR	IPSINNETPGIRYQY									13431
LIAEIQKQG	SKDLIAEIQKQGQGQ									13432
ICTEMEKEG	LVEICTEMEKEGKIS				-0.0017					13433
VGAETFYVD	EPIVGAETFYVDGAA									13434
IQKETWETW	RLPIQKETWETWWTD									13435
IKQEFGIPY	WAGIKQEFGIPYNPQ	0.0018	0.0018	0.1600	1.0000	0.0140		-0.0006		13436
MAGDDCVAG	GKQMAGDDCVAGRQD									13437
IKKEKVYLA	EQLIKKEKVYLAWVP	0.6400	0.0800	0.0059	0.0300	4.1000		0.0058	-0.0045	13438
MAGDDCVAS	GKQMAGDDCVASRQD									13439
VPLDKDFRK	YFSVPLDKDFRKYTA									13440
IQQEFGIPY	WAGIQQEFGIPYNPQ									13441
LEKEPIVGA	WYQLEKEPIVGAETF									13442
YQLEKEPIV	KLWYQLEKEPIVGAE									13443
IQKETWEAW	KLPIQKETWEAWWTE									13444
FSSEQTRAN	AREFSSEQTRANSPT									13445
IASDIQTKE	IDIIASDIQTKELQK									13446
IATESIVIW	VQKIATESIVIWGKT									13447
ILIEICGKK	YDQILIEICGKKAIG									13448
VLEEINLPG	DDTVLEEINLPGKWK									13449
IKKEKVYLS	EQLIKKEKVYLSWVP									13450
VLEDINLPG	DDTVLEDINLPGKWK									13451
VLPEKDSWT	QPIVLPEKDSWTVND									13452
VIQDNSEIK	GAVVIQDNSEIKVVP									13453
IIKDYGKQM	KAKIIKDYGKQMAGA									13454
VERETETDP	KEKVERETETDPAVQ									13455
LTEDRWNKP	VKKLTEDRWNKPQKT									13456
YYFDCFSES	IHLYYFDCFSESAIR									13457
LVEDRWNKP	VQKLVEDRWNKPQKT									13458
IDPDLADQL	STQIDPDLADQLIHL									13459
LKNEAVRHF	LEELKNEAVRHFPRP									13460
LKSEAVRHF	LEELKSEAVRHFPRI									13461
YIYETYGDT	LGQYIYETYGDTWAG									13462
LKQEAVRHF	LEELKQEAVRHFPRP									13463

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MASDFNLPP	WRAMASDFNLPPVVA						13421
FYVDGAANR	AETFYVDGAANRETK	-0.0002	-0.0014	0.0035			13422
IHTDNGSNF	VKVIHTDNGSNFTSA						13423
ILKEPVHGV	NREILKEPVHGVYYD	0.0120	0.0033	0.0010	0.0210		13424
IYQEPFKNL	TYQIYQEPFKNLKTG						13425
VYYDPSKDL	VHGVYYDPSKDLIAE						13426
YVTDRGRQK	KAGYVTDRGRQKVVS						13427
LTEEAELEL	IVPLTEEAELELAEN						13428
VIQDNSDIK	GAVVIQDNSDIKVVP	0.0447	-0.0014	-0.0009			13429
IATDIQTKE	IDIIATDIQTKELQK						13430
INNETPGIR	IPSINNETPGIRYQY						13431
LIAEIQKQG	SKDLIAEIQKQGQGQ						13432
ICTEMEKEG	LVEICTEMEKEGKIS						13433
VGAETFYVD	EPIVGAETFYVDGAA						13434
IQKETWETW	RLPIQKETWETWWTD						13435
IKQEFGIPY	WAGIKQEFGIPYNPQ	0.0123	-0.0014	-0.0009			13436
MAGDDCVAG	GKQMAGDDCVAGRQD						13437
IKKEKVYLA	EQLIKKEKVYLAWVP	-0.0003	-0.0005	-0.0015	0.0011		13438
MAGDDCVAS	GKQMAGDDCVASRQD						13439
VPLDKDFRK	YFSVPLDKDFRKYTA						13440
IQQEFGIPY	WAGIQQEFGIPYNPQ						13441
LEKEPIVGA	WYQLEKEPIVGAETF						13442
YQLEKEPIV	KLWYQLEKEPIVGAE						13443
IQKETWEAW	KLPIQKETWEAWWTE						13444
FSSEQTRAN	AREFSSEQTRANSPT						13445
IASDIQTKE	IDIIASDIQTKELQK						13446
IATESIVIW	VQKIATESIVIWGKT						13447
ILIEICGKK	YDQILIEICGKKAIG						13448
VLEEINLPG	DDTVLEEINLPGKWK						13449
IKKEKVYLS	EQLIKKEKVYLSWVP						13450
VLEDINLPG	DDTVLEDINLPGKWK						13451
VLPEKDSWT	QPIVLPEKDSWTVND						13452
VIQDNSEIK	GAVVIQDNSEIKVVP						13453
IIKDYGKQM	KAKIIKDYGKQMAGA						13454
VERETETDP	KEKVERETETDPAVQ						13455
LTEDRWNKP	VKKLTEDRWNKPQKT						13456
YYFDCFSES	IHLYYFDCFSESAIR						13457
LVEDRWNKP	VQKLVEDRWNKPQKT						13458
IDPDLADQL	STQIDPDLADQLIHL						13459
LKNEAVRHF	LEELKNEAVRHFPRP						13460
LKSEAVRHF	LEELKSEAVRHFPRI						13461
YIYETYGDT	LGQYIYETYGDTWAG						13462
LKQEAVRHF	LEELKQEAVRHFPRP						13463

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	MRDNWRSEL	40	63	GGDMRDNWRSELYKY	550	37	58	13464
ENV	LTVQARQLL	36	56	SITLTVQARQLLSGI	620	27	42	13465
ENV	IEAQQHLLQ	35	55	LRAIEAQQHLLQLTV	642	34	53	13466
ENV	IIGDIRQAH	27	44	TGEIIGDIRQAHCNI	370	07	11	13467
ENV	VEREKRAVG	23	37	RRVVEREKRAVGIGA	582	11	17	13468
ENV	MVEQMHEDI	23	36	KNNMVEQMHEDIISL	110	19	30	13469
ENV	AWDDLRSLC	20	31	LALAWDDLRSLCLFS	850	18	28	13470
ENV	LEITTHSFN	20	31	GGDLEITTHSFNCRG	426	10	16	13471
ENV	YDTEVHNVW	18	28	AKAYDTEVHNVWATH	71	15	23	13472
ENV	AEGTDRIIE	17	27	IAVAEGTDRIIEVVQ	927	02	3	13473
ENV	VQREKRAVG	17	27	RRVVQREKRAVGIGA	582	05	8	13474
ENV	AEGTDRVIE	15	23	IAVAEGTDRVIEVVQ	927	07	11	13475
ENV	IEAQQHLLK	12	19	LRAIEAQQHLLKLTV	642	08	13	13476
ENV	LKCNDKKFN	12	19	FAILKCNDKKFNGTG	269	05	8	13477
GAG	ANPDCKTIL	45	70	VQNANPDCKTILKAL	347	27	42	13478
GAG	FYKTLRAEQ	28	44	VDRFYKTLRAEQASQ	321	19	30	13479
GAG	APGQMREPR	27	42	GPIAPGQMREPRGSD	242	19	30	13480
GAG	FFKTLRAEQ	27	42	VDRFFKTLRAEQATQ	321	26	41	13481
GAG	IWPSHKGRP	23	36	LGKIWPSHKGRPGNF	470	22	34	13482
GAG	LARNCRAPR	20	32	EGHLARNCRAPRKKG	431	19	30	13483
GAG	IAKNCRAPR	18	29	EGHIAKNCRAPRKKG	431	10	16	13484
GAG	ATQEVKNWM	18	28	AEQATQEVKNWMTET	330	14	22	13485
GAG	ATQDVKNWM	15	23	AEQATQDVKNWMTDT	330	11	17	13486
GAG	IARNCRAPR	13	21	EGHIARNCRAPRKKG	431	13	20	13487
GAG	IWPSNKGRP	13	20	LGKIWPSNKGRPGNF	470	13	20	13488
GAG	ANPDCKSIL	11	17	VQNANPDCKSILRAL	347	06	9	13489
GAG	ASQEVKNWM	11	17	AEQASQEVKNWMTET	330	11	17	13490
GAG	IWPSSKGRP	10	16	LGKIWPSSKGRPGNF	470	10	16	13491
NEF	LIYSKKRQE	18	28	LDGLIYSKKRQEILD	171	11	17	13492
NEF	VPVDPREVE	11	17	FKLVPVDPREVEEAN	227	06	9	13493
NEF	MARELHPEY	10	16	FHHMARELHPEYYKD	316	04	6	13494
POL	MGYELHPDK	60	94	FLWMGYELHPDKWTV	416	60	94	13495
POL	FIHNFKRKG	58	91	MAVFIHNFKRKGGIG	930	57	89	13496
POL	MNKELKKII	56	89	VESMNKELKKIIGQV	903	45	70	13497
POL	IIGQVRDQA	44	69	LKKIIGQVRDQAEHL	910	43	67	13498
POL	YHSNWRAMA	39	61	HEKYHSNWRAMASDF	764	23	36	13499
POL	MEKEGKISK	36	56	CTEMEKEGKISKIGP	225	22	34	13500
POL	YYRDSRDPI	34	53	FRVYYRDSRDPIWKG	975	34	54	13501
POL	ANRETKLGK	30	47	DGAANRETKLGKAGY	635	28	44	13502
POL	IGGQLKEAL	25	39	TIKIGGQLKEALLDT	99	17	27	13503
POL	LDKDFRKYT	19	30	SVPLDKDFRKYTAFT	306	17	27	13504
POL	YYRDSRDPL	14	22	FRVYYRDSRDPLWKG	975	13	21	13505
POL	IIGQVREQA	13	20	LKKIIGQVREQAEHL	910	13	20	13506
POL	YHNNWRAMA	10	16	HEKYHNNWRAMASDF	764	06	9	13507
REV	ARRNRRRRW	39	61	TRQARRNRRRRWRAR	38	18	28	13508
REV	ARKNRRRRW	18	28	TRQARKNRRRRWRAR	38	13	20	13509
REV	LLKTVRLIK	10	16	DEELLKTVRLIKFLY	9	04	6	13510
VIF	ISSEVHIPL	27	42	HPRISSEVHIPLGDA	48	08	13	13511
VIF	VSSEVHIPL	27	42	HPKVSSEVHIPLGEA	48	11	17	13512
VIF	VSIEWRLRR	11	17	GHGVSIEWRLRRYST	85	05	8	13513

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VPR	LPSNTRGRG	01	50	IGILPSNTRGRGRRN	82	01	2	13514
VPR	LLEELKNEA	17	27	TLELLEELKNEAVRH	19	12	19	13515
VPR	LLEELKSEA	16	25	TLELLEELKSEAVRH	19	15	23	13516
VPU	AKVDYRIVI	01	33	DLLAKVDYRIVIVAF	3	01	2	13517
VPU	AKVDYRLGV	01	33	NFLAKVDYRLGVGAL	3	01	2	13518
VPU	ILRQRKIDR	15	23	YRKILRQRKIDRLID	42	12	19	13519

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
MRDNWRSEL	GGDMRDNWRSELYKY									13464
LTVQARQLL	SITLTVQARQLLSGI									13465
IEAQQHLLQ	LRAIEAQQHLLQLTV									13466
IIGDIRQAH	TGEIIGDIRQAHCNI									13467
VEREKRAVG	RRVVEREKRAVGIGA									13468
MVEQMHEDI	KNNMVEQMHEDIISL									13469
AWDDLRSLC	LALAWDDLRSLCLFS									13470
LEITTHSFN	GGDLEITTHSFNCRG									13471
YDTEVHNVW	AKAYDTEVHNVWATH									13472
AEGTDRIIE	IAVAEGTDRIIEVVQ									13473
VQREKRAVG	RRVVQREKRAVGIGA									13474
AEGTDRVIE	IAVAEGTDRVIEVVQ									13475
IEAQQHLLK	LRAIEAQQHLLKLTV									13476
LKCNDKKFN	FAILKCNDKKFNGTG									13477
ANPDCKTIL	VQNANPDCKTILKAL				0.0031					13478
FYKTLRAEQ	VDRFYKTLRAEQASQ				0.0049					13479
APGQMREPR	GPIAPGQMREPRGSD				-0.0017					13480
FFKTLRAEQ	VDRFFKTLRAEQATQ									13481
IWPSHKGRP	LGKIWPSHKGRPGNF									13482
LARNCRAPR	EGHLARNCRAPRKKG									13483
IAKNCRAPR	EGHIAKNCRAPRKKG									13484
ATQEVKNWM	AEQATQEVKNWMTET									13485
ATQDVKNWM	AEQATQDVKNWMTDT									13486
IARNCRAPR	EGHIARNCRAPRKKG									13487
IWPSNKGRP	LGKIWPSNKGRPGNF									13488
ANPDCKSIL	VQNANPDCKSILRAL									13489
ASQEVKNWM	AEQASQEVKNWMTET									13490
IWPSSKGRP	LGKIWPSSKGRPGNF									13491
LIYSKKRQE	LDGLIYSKKRQEILD									13492
VPVDPREVE	FKLVPVDPREVEEAN									13493
MARELHPEY	FHHMARELHPEYYKD									13494
MGYELHPDK	FLWMGYELHPDKWTV				-0.0017					13495
FIHNFKRKG	MAVFIHNFKRKGGIG	0.0009		1.3000	0.0470	0.0085		6.9000		13496
MNKELKKII	VESMNKELKKIIGQV									13497
IIGQVRDQA	LKKIIGQVRDQAEHL				0.0700					13498
YHSNWRAMA	HEKYHSNWRAMASDF				0.0022					13499
MEKEGKISK	CTEMEKEGKISKIGP				0.0110					13500
YYRDSRDPI	FRVYYRDSRDPIWKG									13501
ANRETKLGK	DGAANRETKLGKAGY				-0.0017					13502
IGGQLKEAL	TIKIGGQLKEALLDT				0.0090					13503
LDKDFRKYT	SVPLDKDFRKYTAFT									13504
YYRDSRDPL	FRVYYRDSRDPLWKG									13505
IIGQVREQA	LKKIIGQVREQAEHL									13506
YHNNWRAMA	HEKYHNNWRAMASDF									13507
ARRNRRRRW	TRQARRNRRRRWRAR									13508
ARKNRRRRW	TRQARKNRRRRWRAR									13509
LLKTVRLIK	DEELLKTVRLIKFLY									13510
ISSEVHIPL	HPRISSEVHIPLGDA									13511
VSSEVHIPL	HPKVSSEVHIPLGEA									13512
VSIEWRLRR	GHGVSIEWRLRRYST									13513

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MRDNWRSEL	GGDMRDNWRSELYKY						13464
LTVQARQLL	SITLTVQARQLLSGI						13465
IEAQQHLLQ	LRAIEAQQHLLQLTV						13466
IIGDIRQAH	TGEIIGDIRQAHCNI						13467
VEREKRAVG	RRVVEREKRAVGIGA						13468
MVEQMHEDI	KNNMVEQMHEDIISL						13469
AWDDLRSLC	LALAWDDLRSLCLFS						13470
LEITTHSFN	GGDLEITTHSFNCRG						13471
YDTEVHNVW	AKAYDTEVHNVWATH						13472
AEGTDRIIE	IAVAEGTDRIIEVVQ						13473
VQREKRAVG	RRVVQREKRAVGIGA						13474
AEGTDRVIE	IAVAEGTDRVIEVVQ						13475
IEAQQHLLK	LRAIEAQQHLLKLTV						13476
LKCNDKKFN	FAILKCNDKKFNGTG						13477
ANPDCKTIL	VQNANPDCKTILKAL						13478
FYKTLRAEQ	VDRFYKTLRAEQASQ						13479
APGQMREPR	GPIAPGQMREPRGSD						13480
FFKTLRAEQ	VDRFFKTLRAEQATQ						13481
IWPSHKGRP	LGKIWPSHKGRPGNF						13482
LARNCRAPR	EGHLARNCRAPRKKG						13483
IAKNCRAPR	EGHIAKNCRAPRKKG						13484
ATQEVKNWM	AEQATQEVKNWMTET						13485
ATQDVKNWM	AEQATQDVKNWMTDT						13486
IARNCRAPR	EGHIARNCRAPRKKG						13487
IWPSNKGRP	LGKIWPSNKGRPGNF						13488
ANPDCKSIL	VQNANPDCKSILRAL						13489
ASQEVKNWM	AEQASQEVKNWMTET						13490
IWPSSKGRP	LGKIWPSSKGRPGNF						13491
LIYSKKRQE	LDGLIYSKKRQEILD						13492
VPVDPREVE	FKLVPVDPREVEEAN						13493
MARELHPEY	FHHMARELHPEYYKD						13494
MGYELHPDK	FLWMGYELHPDKWTV						13495
FIHNFKRKG	MAVFIHNFKRKGGIG		0.0048				13496
MNKELKKII	VESMNKELKKIIGQV						13497
IIGQVRDQA	LKKIIGQVRDQAEHL						13498
YHSNWRAMA	HEKYHSNWRAMASDF						13499
MEKEGKISK	CTEMEKEGKISKIGP						13500
YYRDSRDPI	FRVYYRDSRDPIWKG						13501
ANRETKLGK	DGAANRETKLGKAGY						13502
IGGQLKEAL	TIKIGGQLKEALLDT						13503
LDKDFRKYT	SVPLDKDFRKYTAFT						13504
YYRDSRDPL	FRVYYRDSRDPLWKG						13505
IIGQVREQA	LKKIIGQVREQAEHL						13506
YHNNWRAMA	HEKYHNNWRAMASDF						13507
ARRNRRRRW	TRQARRNRRRRWRAR						13508
ARKNRRRRW	TRQARKNRRRRWRAR						13509
LLKTVRLIK	DEELLKTVRLIKFLY						13510
ISSEVHIPL	HPRISSEVHIPLGDA						13511
VSSEVHIPL	HPKVSSEVHIPLGEA						13512
VSIEWRLRR	GHGVSIEWRLRRYST						13513

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LPSNTRGRG	IGILPSNTRGRGRRN									13514
LLEELKNEA	TLELLEELKNEAVRH									13515
LLEELKSEA	TLELLEELKSEAVRH									13516
AKVDYRIVI	DLLAKVDYRIVIVAF									13517
AKVDYRLQV	NFLAKVDYRLQVGAL									13518
ILRQRKIDR	YRKILRQRKIDRLID	0.0024	0.0740	0.0410	13.0000	-0.0055		0.1500		13519

Table XXd

HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LPSNTRGRG	IGILPSNTRGRGRRN						13514
LLEELKNEA	TLELLEELKNEAVRII						13515
LLEELKSEA	TLELLEELKSEAVRII						13516
AKVDYRIVI	DLLAKVDYRIVIVAF						13517
AKVDYRLGV	NFLAKVDYRLGVGAL						13518
ILRQRKIDR	YRKILRQRKIDRLID	0.0016	-0.0014	0.0270			13519

TABLE XXI. Population coverage with combined HLA Supertypes

HLA-SUPERTYPES	PHENOTYPIC FREQUENCY Caucasian	North American Black	Japanese	Chinese	Hispanic	Average
a. Individual Supertypes						
A2	45.8	39.0	42.4	45.9	43.0	43.2
A3	37.5	42.1	45.8	52.7	43.1	44.2
B7	38.6	52.7	48.8	35.5	47.1	44.7
A1	47.1	16.1	21.8	14.7	26.3	25.2
A24	23.9	38.9	58.6	40.1	38.3	40.0
B44	43.0	21.2	42.9	39.1	39.0	37.0
B27	28.4	26.1	13.3	13.9	35.3	23.4
B62	12.6	4.8	36.5	25.4	11.1	18.1
B58	10.0	25.1	1.6	9.0	5.9	10.3
b. Combined Supertypes						
A2, A3, B7	83.0	86.1	87.5	88.4	86.3	86.2
A2, A3, B7, A24, B44, A1	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44, A1, B27, B62, B58	99.9	99.6	100.0	99.8	99.9	99.8

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Table XXIII: Immunogenicity of HIV peptides

	Peptide	Sequence	Protein	Immunogenicity patients	Immunogenicity transgenic
A2 Supermotif	1261.04	LTFGWCFKL	HIV nef 221	4/12	3/3
	1261.15	MASDFNLPPV	hiv pol 774	1/15	2/6
	1069.32	VLAEAMSQV	hiv gag 386	6/19	3/3
	1261.16	CTLNFPISPI	hiv pol 182	0/1	1/6
	1261.02	LLQLTVWGI	HIV env 651	2/8	1/6
	1261.13	KLVGKLNWA	HIV pol 448	3/15	3/3
	1211.04	KLTPLCVTL	HIV env 134	2/12	2/6
	1261.08	ALVEICTEM	HIV pol 220	0/2	1/6
	1261.11	AIIRILQQL	HIV vpr 59	5/9	0/6
	1261.09	LVGPTPVNI	HIV pol 163	1/9	1/6
	1261.12	RILQQLLFI	HIV vpr 62	6/20	2/6
	1261.05	TLNFPISPI	HIV pol 183	1/7	0/6
	1261.03	MTNNPPIPV	HIV gag 271	2/17	4/6
	1261.17	KMIGGIGGFI	HIV pol 132	2/7	0/6
	941.03	ILKEPVHGV	HIV pol 498	8/19	3/6
	1261.10	RAMASDFNL	HIV pol 772	2/9	0/6
	1261.07	KAACWWAGI	HIV pol 879	1/8	0/6
A3 Supermotif	1211.32	KIQNFRVYYR	HIV pol 971	4/6	
	1193.03	AVFIHNFKR	HIV pol 931	3/6	
	1069.49	QMAVFIHNFK	HIV pol 929	3/6	
	1150.14	MAVFIHNFK	HIV pol 930	6/6	
	1069.42	KVYLAWVPAHK	HIV pol 722	6/6	
	966.01	AIFQSSMTK	HIV pol 347	5/6	1/6
	940.03	QVPLRPMTYK	HIV nef 100	0/6	6/10
	1273.07	TTLFCASDAK	HIV env 61	3/6	
	1273.09	VTIKIGGQLK	HIV pol 98	6/6	
	1069.43	TVYYGVPVWK	HIV env 48		28/33
	1069.47	VTVYYGVPVWK	HIV env 47	6/6	
DR Supermotif	27.0313	KRWILGLNKIVRMY	HIV gag 298	3/13	
	27.0311	GEIYKRWILGLNKI	HIV gag 294	2/13	
	27.0354	WEFVNTPPLVKLWYQ	HIV pol 596	2/13	
	27.0377	QKQITKIQNFRVYYR	HIV pol 956	3/13	
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712	3/13	
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711	1/13	
	27.0304	QGQMVHQAISPRTLN	HIV gag 171	4/13	
	27.0344	SPAIFQSSMTKILEP	HIV pol 335	3/13	
	27.0341	FRKYTAFTIPSINNE	HIV pol 303	3/13	
	27.0364	HSNWRAMASDFNLPP	HIV pol 758	3/13	
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915	4/13	

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide Source	Radiolabeled peptide Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0207	21.221 (transfecte	HBVc 18-27 F6->Y	FLPSDYFPSV
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK
	A11		BVR	non-natural (A3CON1)	KVFPYALINK
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVRR
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVYLL
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL
	B27	B*2705	LG2	R 60s	FRYNGLIHR
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL
	Cw6	Cw*0602	'21.221 transfecte	non-natural (C6CON1)	YRHDGGNVL
	Cw7	Cw*0702	'21.221 transfecte	non-natural (C6CON1)	YRHDGGNVL
Mouse	D^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI
	K^b		EL4	VSV NP 52-59	RGYVFQGL
	D^d		P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI
	K^d		P815	non-natural (KdCON1)	KFNPMKTYI
	L^d		P815	HBVs 28-39	IPQSLDSYWTSL

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide: Source	Radiolabeled peptide: Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAAAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	3M3107 or L416.:	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*03(	PF	non-natural (ROIV)	AHAAHAAHAAHAAHAA
Mouse	IA^b		DB27.4	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IA^d		A20	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IA^k		CH-12	HEL 46-61	YNTDGSTDYGILQINSR
	IA^s		LS102.9	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IA^u		91.7	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IE^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

Table XXV. Monoclonal antibodies used in MHC purification.

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	H-2 D^b and L^d
34-5-8S	H-2 D^d
B8-24-3	H-2 K^b
SF1-1.1.1	H-2 K^d
Y-3	H-2 K^b
10.3.6	H-2 IA^k
14.4.4	H-2 IE^d, IE^K
MKD6	H-2 IA^d
Y3JP	H-2 IA^b, IA^s, IA^u

Table XXVI. The table lists the 64 fully represented aligned amino acid sequences that were identified for Motif analysis. Included are the aligned amino acid sequence ID number, the complete nucleotide sequence name it was derived from, the accession numbers for the sequence, the subtype, country and the total length of all nine sequences.

	ID Number	Name	Accession Numbers	Subtype	Country	Length
1	A.KE.Q23-CxC-CG	HIVQ2317	AF004885	A	KE	3584
2	A.SE.UGSE8891	AUGSE8891	AF069673	A	SE	3584
3	A.UG.92UG037	H92UG037	U51190	A	UG	3584
4	A.UG.U455	HIVU455A	M62320	A	UG	3584
5	AC.IN.21301	21301	AF067156	AC	IN	3584
6	AC.RW.92RW009	92RW009	U88823	AC	RW	3584
7	AC.ZM.ZAM184	ZAM184	U86780	AC	ZM	3584
8	ADI.ZR.MAL	HIVMALCG	K03456, X04415	ADI	ZR	3584
9	AE.CF.90CR402	HIV90CF4O2	U51188	AE	CF	3584
10	AE.TH.93TH253	H93TH253	U51 189	AE	TH	3584
11	AE.TH.CM240	HIV1CM240	U54771	AE	TH	3584
12	AG.DJ.DJ263	DJ263	AF063223	AG	DJ	3584
13	AG.DJ.DJ264	HDJ264	AF063224	AG	DJ	3584
14	AG.NG.92NG003	92NG003	U88825	AG	NG	3584
15	AG.NG.92NG083	H92NG083	U88826	AG	NG	3584
16	AG.NG.IBNG	HIVIBNG	L39106	AG	NG	3584
17	AGI.CY.94CY0323	94CY032-3	AF049337	AGI	CY	3584
18	AGI.ZR.Z321	HIVU76035, Z321B	U76035	AGI	ZR	3584
19	AGJ.AU.BFP90	HIVBFP9O	AF064699	AGJ	AU	3584
20	B.CN.RL42	HCHRL42CG	U71182	B	CN	3584
21	B.DE.D31	HIV1D31	U43096	B	DE	3584
22	B.DE.HAN	HIVHAN2	U43141	B	DE	3584
23	B.FR.HXB2R	HIVHXB2	AF033819, K03455, M38432	B	FR	3584
24	B.GA.OYI	HIVOYI	M26727	B	GA	3584
25	B.GB.CAM1	HIVCAM1	D00917, D10112	B	GB	3584
26	B.GB.MANC	HIV1MANC	U23487	B	GB	3584
27	B.NL.ACH32OA	HIV1ACH32OA	U34604	B	NL	3584
28	B.US.ADA	HIV1AD8	AF004394	B	US	3584
29	B.US.DH123	HIV1DH123	AF069140	B	US	3584
30	B.US.JRCSF	HIVJRCSF	M38429	B	US	3584
31	B.US.JRFL	HIVJRFL	U63632	B	US	3584
32	B.US.MN	HIVMN	M17449	B	US	3584
33	B.US.P896	HIV1896	M96155, U39362	B	US	3584
34	B.US.RF	HIVRF	M12508	B	US	3584
35	B.US.SF2	HIVSF2CG	K02007	B	US	3584
36	B.US.WEAU16O	HIVWEAU160	U21135	B	US	3584
37	B.US.WR27	HIV1WR27	U26546	B	US	3584
38	B.US.YU2	HIVYU2	M93258	B	US	3584
39	BF.BR.93BR029.4	93BR029	AF005495	BF	BR	3584
40	C.BR.92BR025	H92BR025	U52953	C	BR	3584
41	C.BW.BW96BW0502	96BW0502	AF110967	C	BW	3584
42	C.ET.ETH2220	HIVETH2220	U46016	C	ET	3584
43	C.IN.11246	1N11246	AF067159	C	IN	3584
44	C.IN.21068	C1N21068	AF067155	C	IN	3584
45	C.IN.301904	301904	AF067157	C	IN	3584
46	C.IN.301905	CIN301905	AF067158	C	IN	3584
47	C.IN.301999	CIN301999	AF067154	C	IN	3584
48	D.UG.94UG1141	94UG114	U88824	D	UG	3584
49	D.ZR.84ZR085	84ZR085	U88822	D	ZR	3584
50	D.ZR.ELI	HIVELICG	K03454, X04414	D	ZR	3584
51	D.ZR.NDK	HIVNDK	M27323	D	ZR	3584
52	F.BR.93BR0201	93BR020	AF005494	F	BR	3584
53	F.FN.FIN9363	FIN9363	AF075703	F	FN	3584
54	G.BE.DRCBL	DRCBL	AF084936	G	BE	3584
55	G.FI.HH87931	HH8793	AF061640, AF061641	G	FI	3584
56	G.SE.SE6165	SE6165	AF061642	G	SE	3584
57	H.BE.VI991	VI991	VI991	H	BE	3584
58	H.BE.VI997	VI997	VI997	H	BE	3584

.. . .	ID Number	Name	Accession Numbers	Subtype	Country	Length
59	H.CF.90CF056	90CF056	AF005496	H	CF	3584
60	J.SE.SE91733	SE91733	AF082395	J	SE	3584
61	J.SE.SE92809	SE92809	AF082394	J	SE	3584
62	N.CM.YBF3O	NCMYBF3O	AJ006022	N	CM	3584
63	O.CM.ANT7OC	HIVANT7OC	L20587	O	CM	3584
64	0.CM.MVP518O	HIVMVP518O	L20571	O	CM	3584

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TABLE XXVII

in vitro binding of conserved HIV derived peptides to HLA-A2 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%) total	Conservation (%) B	A2-supertype binding capacity (IC50 nM) A*0201	A*0202	A*0203	A*0206	A*6802	alleles bound
1261.14	10	NEF	221	LTFGWCFKLV	55	74	294.1	48.9	185.2	57.8	6.2	5
1261.04	9	NEF	221	LTFGWCFKL	61	74	35.7	33.1	4545.5	205.6	5.6	4
1261.06	9	POL	316	YTAFTIPSI	58	68	26.3	6.1	9.1	7	16.7	5
1261.15	10	POL	774	MASDFNLPPV	39	68	62.5	22.6	55.6	33.6	18.2	5
1069.32	9	GAG	386	VLAEAMSQV	52	74	66.6	82.7	15.2	115.6	363.6	5
1261.16	10	POL	182	CTLNFPISPI	94	100	147	23.9	30.3	8.4	100	5
1261.02	9	ENV	651	LLQLTVWGI	53	63	9.8	215	43.5	24.7	645.2	4
1261.13	9	POL	448	KLVGKLNWA	95	95	59.5	12.6	5.9	39.8	3076.9	4
1211.04	9	ENV	134	KLTPLCVTL	81	95	102	126.5	66.7	185	20000	4
1261.08	9	POL	220	ALVEICTEM	23	79	217.3	187	140.8	264.3	2857.1	4
1261.11	9	VPR	59	AIIRILQQL	61	74	333.3	22.6	41.7	38.5	547.9	4
1261.09	9	POL	163	LVGPTPVNI	84	100	454.5	153.6	19.2	2846.2	67.8	4
1261.12	9	VPR	62	RILQQLLFI	56	74	19.2	1535.7	125	37	1818.2	3
1261.05	9	POL	183	TLNFPISPI	97	100	75.7	1482.8	1.1	1947.4	57.1	3
1261.03	9	GAG	271	MTNNPPIPV	31	89	166.6	7166.7	33.3	1608.7	12.1	3
1261.17	10	POL	132	KMIGGIGGFI	97	95	172.4	54.4	4.8	770.8	3333.3	3
941.03	9	POL	498	ILKEPVHGV	64	79	192.3	2388.9	6.7	37000	363.6	3
1260.10	9	POL	772	RAMASDFNL	64	79	217.3	116.2	25000	52.1	3076.9	3
1261.07	9	POL	879	KAACWWAGI	49	79	277.7	1075	83.3	160.9	2666.7	3
1211.09	10	ENV	814	SLLNATDIAV	22	68	9.8	1303	238.1	28.5	5479.4	3
1211.05	9	ENV	608	FLGAAGSTM	86	100	73.5	3583.3	1.5	4111.1	66666.7	2
25.0053	9	VPR	66	QLLFIHFRI	69	89	94.3	21500	25000	1608.7	476.2	2
25.0139	10	GAG	270	WMTNNPPIPV	31	89	98	3071.4	16.9	18500	2222.2	2
1069.33	10	POL	993	LLWKGEGAVV	95	100	111.1	632.4	25	770.8	3636.4	2
25.0142	10	NEF	219	PLTFGWCFKL	61	74	142.8	741.4	4761.9	3700	47.6	2
1069.34	9	POL	993	LLWKGEGAV	97	100	172.4	10750	21.7	1608.7	2666.7	2
25.0161	10	POL	452	KLNWASQIYA	42	84	217.3	3909.1	400	6166.7	3076.9	2
1211.082	9	GAG	79	SLYNTVATL	34	58	277.7	3583.3	50	37000	100000	2
25.0037	9	GAG	486	FLQSRPEPT	44	68	454.5	10750	32.3	18500	3076.9	2
25.0046	9	POL	91	TLWQRPLVT	61	68	270.2	21500	2500	18500	2857.1	1

TABLE XXVIII

in vitro binding of conserved HIV derived peptides to HLA-A3 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%) total	Conservation (%) B	A3-supertype binding capacity (IC50 nM) A*0301	A*1101	A*3101	A*3301	A*6801	alleles bound
1273.01	9	GAG	163	MVHQAISPR	42	58	61.1	89.6	18.0	13.8	9.5	5
1193.0200	9	POL	572	IVIWGKTPK	75	79	129.4	16.2	18.2	96.7	242.4	5
1193.03	9	POL	931	AVFIHNFKR	97	100	64.7	3.3	5.1	107.4	4.2	5
1193.01	9	POL	724	YLAWVPAHK	34	95	142.9	105.3	327.3	33.0	2.0	5
1211.32	10	POL	971	KIQNFRVYYR	81	95	343.8	28.6	2.7	341.2	210.5	5
1069.49	10	POL	929	QMAVFIHNFK	94	100	9.2	6.5	266.7	432.8	400.0	4
1273.03	10	GAG	162	QMVHQAISPR	42	58	42.3	6000.0	243.2	290.0	186.0	4
1193.09	9	POL	353	MTKILEPFR	67	84	13750.0	375.0	81.8	69.0	25.8	4
966.01	9	POL	347	AIFQSSMTK	56	79	10.0	10.0	12000.0	96666.7	242.4	3
940.03	10	NEF	100	QVPLRPMTYK	72	79	18.0	9.5	1836.7	2230.8	133.3	3
1069.43	10	ENV	48	TVYYGVPVWK	64	95	11.0	3.5	1636.4	10357.1	14.5	3
1069.48	10	POL	931	AVFIHNFKRK	91	100	114.6	20.7	1125.0	5000.0	307.7	3
1273.05	9	POL	99	TIKIGGQLK	27	63	40.7	181.8	18000.0	36250.0	72.7	3
1273.06	9	ENV	64	TLFCASDAK	81	84	118.3	11.3	10588.2	22307.7	190.5	3
1273.07	10	ENV	61	TTLFCASDAK	78	84	119.6	27.3	9473.7	14500.0	140.4	3
1273.04	9	ENV	878	RIVELLGRR	34	89	200.0	600.0	138.5	13809.5	444.4	3
1273.09	10	POL	98	VTIKIGGQLK	27	63	297.3	28.6	10588.2	11600.0	125.0	3
1273.02	9	POL	246	NTPVFAIKK	58	94.7	333.3	100.0	30000.0	48333.3	4.7	3
1150.14	9	POL	930	MAVFIHNFK	94	100	647.1	20.0	375.0	517.9	2.5	3
1273.08	9	VIF	7	VMIVWQVDR	69	95	3235.3	272.7	3.8	5.3	2424.2	3
1069.47	11	ENV	47	VTVYYGVPVWK	64	94	84.6	11.3	4615.4	36250.0	170.2	3
1069.42	11	POL	722	KVYLAWVPAHK	32	89	3.5	7.6	163.6	3580.2	8000.0	3
1069.44	9	POL	855	KLAGRWPVK	78	68	8.5	133.3	500.0	72500.0	80000.0	3

TABLE XXIX

in vitro binding of conserved HIV derived peptides to HLA-B7 supertype alleles

			1st		Conservation (%)		B7-supertype binding capacity (IC50 nM)					alleles
peptide	AA	protein	Position	sequence	total	B	B*0702	B*3501	B*5101	B*5301	B*5401	bound
1146.01	9	NEF	94	FPVRPQVPL	75	74	15.7	43.0	11.6	481.9	71.4	5
1296.01	9	ENV	259	IPIHYCAPA	56	42	423	343	153	-	3.7	4
15.0268	10	GAG	545	YPLASLRSLF	15	32	392.9	480.0	39.3	150.0	714.3	4
1261.01	9	POL	186	FPISPIETV	88	95	3437.5	1043.5	148.6	251.4	9.1	3
1296.02	9	ENV	250	CPKVSFEPI	47	79	100.0	5142.9	161.8	2447.4	100.0	3
1296.03	11	POL	893	IPYNPQSQGVV	92	89	458.3	72000.0	119.6	46500.0	66.7	3
29.0028	8	REV	75	VPLQLPPL	56	68	112.2	6000.0	0.8	46500.0	270.3	3
1292.13	9	GAG	237	HPVHAGPIA	30	74	50.0	11.6	13750.0	4428.6	4.3	3

Table XXX: A1-motif peptides

Peptide	Sequence	Protein	Conservancy Total	Conservancy Clade B	IC50 nM
1.0431	EVNIVTDSQY	HIV pol 1187	83	93	472
1.0014	FRDYVDRFY	HIV gag 298	51	96	278
2.0129	IYQYMDDLY	HIV pol 359	78	87	391
1069.27	VIYQYMDDLY	HIV pol 358	78	87	446
1069.26	VTVLDVGDAY	HIV pol 265	96	93	439

Table XXXI: A24-motif peptides

Peptide	Sequence	Protein	Conservancy Total	Conservancy Clade B	IC50 nM
25.0113	IWGCSGKLI	HIV env 69	69	91	444
25.0127	IYETYGDTW	HIV vpr 92	92	100	207
1069.60	IYQEPFKNL	HIV pol 1036	74	87	444
25.0128	PYNEWTLEL	HIV vpr 56	56	71	86
25.0123	PYNTPVFAI	HIV pol 74	74	100	387
1069.57	RYLKDQQLL	HIV env 2778	40	53	43
1069.58	RYLRDQQLL	HIV env 2778	23	32	52
1069.59	TYQIYQEPPF	HIV pol 1033	78	93	67
25.0115	VWKEATTTL	HIV env 47	47	85	400
25.0218	VWKEATTTLF	HIV env 47	47	85	44
25.0219	YWQATWIPEW	HIV pol 96	96	93	182

Table XXXII: Immunogenicity of A2-supertype cross-reactive binding peptides

Peptide	Sequence	Protein	Conservancy Total	Clade B	XRN	Immunogenicity patients	transgenic
1261.14	LTFGWCFKLV	HIV nef 221	55	74	5	0/1	0/6
1261.04	LTFGWCFKL	HIV nef 221	61	74	4	4/12	3/3
1261.06	YTAFTIPSI	HIV pol 316	58	68	5	0/1	0/6
1261.15	MASDFNLPPV	HIV pol 774	39	68	5	1/15	2/6
1069.32	VLAEAMSQV	HIV gag 386	52	74	5	6/19	3/3
1261.16	CTLNFPISPI	HIV pol 182	94	100	5	0/1	1/6
1261.02	LLQLTVWGI	HIV env 651	53	63	4	2/8	1/6
1261.13	KLVGKLNWA	HIV pol 448	95	95	4	3/15	3/3
1211.04	KLTPLCVTL	HIV env 134	85	95	4	2/12	2/6
1261.08	ALVEICTEM	HIV pol 220	23	79	4	0/2	1/6
1261.11	AIIRILQQL	HIV vpr 59	61	74	4	5/9	0/6
1261.09	LVGPTPVNI	HIV pol 163	84	100	4	1/9	1/6
1261.12	RILQQLLFI	HIV vpr 62	56	74	3	6/20	2/6
1261.05	TLNFPISPI	HIV pol 183	97	100	3	1/7	0/6
1261.03	MTNNPPIPV	HIV gag 271	31	89	3	2/17	4/6
1261.17	KMIGGIGGFI	HIV pol 132	97	95	3	2/7	0/6
941.03	ILKEPVHGV	HIV pol 498	64	79	3	8/19	3/6
1261.10	RAMASDFNL	HIV pol 772	64	79	3	2/9	0/6
1261.07	KAACWWAGI	HIV pol 879	49	79	3	1/8	0/6
1211.09	SLLNATDIAV	HIV env 814	22	68	3		

Table XXXIII: Immunogenicity of HIV-derived A3-supertype peptides

			Conservancy			Immunogenicity	
Peptide	Sequence	Protein	Total	Clade B	XRN	transgenic	patients
1211.32	KIQNFRVYYR	HIV pol 971	81	95	5	4/6	
1193.02	IVIWGKTPK	HIV pol 572	75	79	5	0/6	
1193.03	AVFIHNFKR	HIV pol 931	97	100	5	3/6	
1069.49	QMAVFIHNFK	HIV pol 929	94	100	4	3/6	
1150.14	MAVFIHNFK	HIV pol 930	94	100	3	6/6	
1069.48	AVFIHNFKRK	HIV pol 931	91	100	3	0/6	
1273.01	MVHQAISPR	HIV gag 163	42	58	5	0/6	
1273.03	QMVHQAISPR	HIV gag 162	42	58	4	0/6	
1193.01	YLAWVPAHK	HIV pol 724	34	95	5	0/6	
1069.42	KVYLAWVPAHK	HIV pol 722	32	89	3	6/6	
1193.09	MTKILEPFR	HIV pol 353	67	84	4	0/8	
966.01	AIFQSSMTK	HIV pol 347	56	79	3	5/6	1/6
940.03	QVPLRPMTYK	HIV nef 100	72	79	3	0/6	6/10
1069.44	KLAGRWPVK	HIV pol 855	78	68	3		
1273.02	NTPVFAIKK	HIV pol 246	58	95	3	0/6	
1273.08	VMIVWQVDR	HIV vif 7	69	95	3	0/6	
1273.04	RIVELLGRR	HIV env 878	34	89	3		
1273.07	TTLFCASDAK	HIV env 61	78	84	3	3/6	
1273.06	TLFCASDAK	HIV env 62	81	84	3	0/6	
1273.09	VTIKIGGQLK	HIV pol 98	27	63	3	6/6	
1273.05	TIKIGGQLK	HIV pol 99	27	63	3	0/6	
1069.43	TVYYGVPVWK	HIV env 48	64	95	3	28/33	
1069.47	VTVYYGVPVWK	HIV env 47	64	94	3	6/6	

Table XXXIV. HLA-DR screening panels

Screening Panel	Antigen	Alleles	Representative Assay		Phenotypic Frequencies					
			Allele	Alias	Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
Primary	DR1	DRB1*0101-03	DRB1*0101	(DR1)	18.5	8.4	10.7	4.5	10.1	10.4
	DR4	DRB1*0401-12	DRB1*0401	(DR4w4)	23.6	6.1	40.4	21.9	29.8	24.4
	DR7	DRB1*0701-02	DRB1*0701	(DR7)	26.2	11.1	1.0	15.0	16.6	14.0
	Panel total				59.6	24.5	49.3	38.7	51.1	44.6
Secondary	DR2	DRB1*1501-03	DRB1*1501	(DR2w2 β1)	19.9	14.8	30.9	22.0	15.0	20.5
	DR2	DRB5*0101	DRB5*0101	(DR2w2 β2)	-	-	-	-	-	-
	DR9	DRB1*09011,09012	DRB1*0901	(DR9)	3.6	4.7	24.5	19.9	6.7	11.9
	DR13	DRB1*1301-06	DRB1*1302	(DR6w19)	21.7	16.5	14.6	12.2	10.5	15.1
	Panel total				42.0	33.9	61.0	48.9	30.5	43.2
Tertiary	DR4	DRB1*0405	DRB1*0405	(DR4w15)	-	-	-	-	-	-
	DR8	DRB1*0801-5	DRB1*0802	(DR8w2)	5.5	10.9	25.0	10.7	23.3	15.1
	DR11	DRB1*1101-05	DRB1*1101	(DR5w11)	17.0	18.0	4.9	19.4	18.1	15.5
	Panel total				22.0	27.8	29.2	29.0	39.0	29.4
Quarternary	DR3	DRB1*0301-2	DRB1*0301	(DR3w17)	17.7	19.5	0.4	7.3	14.4	11.9
	DR12	DRB1*1201-02	DRB1*1201	(DR5w12)	2.8	5.5	13.1	17.6	5.7	8.9
	Panel total				20.2	24.4	13.5	24.2	19.7	20.4

Table XXXV: cross-reactive HLA-DR binding peptides

Peptide	Sequence	Protein	Binding capacity (IC50 nM)													DR Alleles bound
			DR1	DR2w201	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2	DR9	DR53	
27.0313	KRWIILGLNKIVRMY	HIV gag 298	4.2	5.1	24	188	633	404	54	124	0.36	379	49	58		12
27.0354	WEFVNTPPLVKLWYQ	HIV pol 596	7.2	222	2.1	13636	28	20	317	1355	90	15	350	39		10
27.0377	QKQITKIQNFRVYYR	HIV pol 956	2.9	3.4	80	-	357	49	53	124	25	25	75	577		11
1280.03	KVYLAWVPAHKGIGG	HIV pol 712.	8.3	25	24	-	156	165	71	12598	2500	179	196	250		9
27.0311	GEIYKRWIILGLNKI	HIV gag 294	82	138	225	-	1667	380	213	1656	98	192	63	536		9
27.0361	EKVYLAWVPAHKGIG	HIV pol 711	3.6	21	4.9	3226	9.3	27	37	6478	3500	18	31	144		9
27.0297	QHLLQLTVWGIKQLQ	HIV env 729	6.1	21	690	-	1316	345	2128	1064	350	44	907	375		8
27.0304	QGQMVHQAISPRTLN	HIV gag 171	72	65	13	17647	60	400	-	-	412	455	7313	117		8
27.0344	SPAIFQSSMTKILEP	HIV pol 335	357	217	667	-	3571	109	741	-	13	68	3267	33		8
F091.15	IKQFINMWQEVGKAMY	HIV env 566	128	217	206	-	417	271	4878	-	1000	-	350	5769	104	8
27.0341	FRKYTAFTIPSINNE	HIV pol 303	185	70	4167	-	294	136	1818	-	-	30	803	39		7
27.0364	HSNWRAMASDFNLPP	HIV pol 758	33	-	125	-	11	15	95	-	4375	472	1960	872		7
27.0373	KTAVQMAVFIHNFKR	HIV pol 915	161	650	690	-	909	452	182	18625	125	1786	1441	2586		7

A dash indicates IC50>20μM

Table XXXVI: DR3 binding peptides

Peptide	Sequence	Protein	DR3
35.0135	YRKILRQRKIDRLID	HIV vpu 31	23
35.0131	WAGIKQEFGIPYNPQ	HIV pol 874	300
35.0127	EVNIVTDSQYALGII	HIV pol 674	732
35.0125	AETFYVDGAANRETK	HIV pol 619	769
35.0133	GAVVIQDNSDIKVVP	HIV pol 989	1000

TABLE XXXVII

Immunogenicity of HIV-derived DR-supermotif peptides

Peptide	Sequence	Protein	conservation (%) total	conservation (%) clade B	DR Alleles bound	Patient Immunogenicity
27.0313	KRWIILGLNKIVRMY	HIV gag 298	85 [89][1]	94 [95]	12	3/13
27.0311	GEIYKRWIILGLNKI	HIV gag 294	58 [86]	95 [95]	9	2/13
27.0354	WEFVNTPPLVKLWYQ	HIV pol 596	79 [89]	84 [95]	10	2/13
27.0377	QKQITKIQNFRVYYR	HIV pol 956	56 [67]	95 [95]	11	3/13
1280.03	KVYLAWVPAHKGIGG	HIV pol 712	32 [34]	89 [95]	9	3/13
27.0361	EKVYLAWVPAHKGIG	HIV pol 711	32 [34]	94 [95]	9	1/13
27.0304	QGQMVHQAISPRTLN	HIV gag 171	41 [42]	52 [58]	8	4/13
27.0344	SPAIFQSSMTKILEP	HIV pol 335	52 [59]	79 [78]	8	3/13
27.0341	FRKYTAFTIPSINNE	HIV pol 303	59 [58]	68 [68]	7	3/13
27.0364	HSNWRAMASDFNLPP	HIV pol 758	48 [67]	68 [79]	7	3/13
27.0373	KTAVQMAVFIHNFKR	HIV pol 915	87 [95]	94 [100]	7	4/13

1: conservation of core region

Table XXXVIII. Candidate CTL Epitopes

Restriction	Peptide	Protein	Sequence
HLA-A2	1069.32	HIV gag 386	VLAEAMSQV
"	1261.03	HIV gag 271	MTNNPPIPV
"	1261.15	HIV pc! 774	MASDFNLPPV
"	1261.13	HIV pol 448	KLVGKLNWA
"	1261.09	HIV pol 163	LVGPTPVNI
"	941.03	HIV pol 498	ILKEPVHGV
"	1261.07	HIV pol 879	KAACWWAGI
"	1261.17	HIV pol 132	KMIGGIGGFI
"	1261.10	HIV pol 772	RAMASDFNL
"	1261.05	HIV pol 183	TLNFPISPI
"	1211.04	HIV env 134	KLTPLCVTL
"	1261.02	HIV env 651	LLQLTVWGI
"	1211.09	HIV env 163	SLLNATDIAV
"	1261.04	HIV nef 221	LTFGWCFKL
"	1261.11	HIV vpr 59	AIIRILQQL
"	1261.12	HIV vpr 62	RILQQLLFI
HLA-A3	1069.49	HIV pol 929	QMAVFIHNFK
"	1069.42	HIV pol 722	KVYLAWVPAHK
"	1211.32	HIV pol 971	KIQNFRVYYR
"	1193.09	HIV pol 353	MTKILEPFR
"	966.01	HIV pol 347	AIFQSSMTK
"	1273.09	HIV pol 98	VTIKIGGQLK
"	1273.07	HIV env 61	TTLFCASDAK
"	1069.47	HIV env 47	VTVYYGVPVWK
"	940.03	HIV nef 100	QVPLRPMTYK
"	1273.08	HIV vif 7	VMIVWQVDR
"	1273.03	HIV gag 162	QMVHQAISPR
HLA-B7	15.0268	HIV gag 545	YPLASLRSLF
"	1292.13	HIV gag 237	HPVHAGPIA
"	1261.01	HIV pol 186	FPISPIETV
"	1296.03	HIV pol 893	IPYNPQSQGVV
"	1296.01	HIV env 259	IPIHYCAPA
"	1296.02	HIV env 250	CPKVSFEPI
"	1146.01	HIV nef 94	FPVRPQVPL
"	29.0028	HIV rev 75	VPLQLPPL
HLA-A1	1.0431	HIV pol 684	EVNIVTDSQY
"	1.0014	HIV gag 317	FRDYVDRFY
"	1069.27	HIV pol 368	VIYQYMDDLY
"	1069.26	HIV pol 295	VTVLDVGDAY
HLA-A24	1069.60	HIV pol 533	IYQEPFKNL
"	25.0123	HIV pol 244	PYNTPVFAI
"	1069.59	HIV pol 530	TYQIYQEPF
"	25.0219	HIV pol 597	YWQATWIPEW
"	25.0113	HIV env 681	IWGCSGKLI
"	1069.57	HIV env 671	RYLKDQQLL
"	25.0115	HIV env 55	VWKEATTTLF
"	25.0127	HIV vpr 46	IYETYGDTW
"	25.0128	HIV vpr 14	PYNEWTLEL

Table XXXIX: HTL Candidate Epitopes

Selection Criteria	Peptide	Sequence	Protein
DR	27.0313	KRWIILGLNKIVRMY	HIV gag 298
	27.0354	WEFVNTPPLVKLWYQ	HIV pol 596
	27.0377	QKQITKIQNFRVYYR	HIV pol 956
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712
	27.0311	GEIYKRWIILGLNKI	HIV gag 294
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711
	27.0297	QHLLQLTVWGIKQLQ	HIV env 729
	27.0304	QGQMVHQAISPRTLN	HIV gag 171
	27.0344	SPAIFQSSMTKILEP	HIV pol 335
	F091.15	IKQFINMWQEVGKAMY	HIV env 566
	27.0341	FRKYTAFTIPSINNE	HIV pol 303
	27.0364	HSNWRAMASDFNLPP	HIV pol 758
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915
DR3	35.0135	YRKILRQRKIDRLID	HIV vpu 31
	35.0131	WAGIKQEFGIPYNPQ	HIV pol 874
	35.0127	EVNIVTDSQYALGII	HIV pol 674
	35.0125	AETFYVDGAANRETK	HIV pol 619
	35.0133	GAVVIQDNSDIKVVP	HIV pol 989

TABLE XL

Estimated population coverage by a panel of HIV derived HTL epitopes

Antigen	Alleles	Representative assay	No. of epitopes[2]	Population coverage (phenotypic frequency)					
				Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
DR1	DRB1*0101-03	DR1	13	18.5	8.4	10.7	4.5	10.1	10.4
DR2	DRB1*1501-03	DR2w2 ß1	12	19.9	14.8	30.9	22.0	15.0	20.5
DR2	DRB5*0101	DR2w2 ß2	12	-	-	-	-	-	-
DR3	DRB1*0301-2	DR3	5	17.7	19.5	0.40	7.3	14.4	11.9
DR4	DRB1*0401-12	DR4w4	10	23.6	6.1	40.4	21.9	29.8	24.4
DR4	DRB1*0401-12	DR4w15	13	-	-	-	-	-	-
DR7	DRB1*0701-02	DR7	11	26.2	11.1	1.0	15.0	16.6	14.0
DR8	DRB1*0801-5	DR8w2	9	5.5	10.9	25.0	10.7	23.3	15.1
DR9	DRB1*09011,09012	DR9	11	3.6	4.7	24.5	19.9	6.7	11.9
DR11	DRB1*1101-05	DR5w11	9	17.0	18.0	4.9	19.4	18.1	15.5
DR13	DRB1*1301-06	DR6w19	8	21.7	16.5	14.6	12.2	10.5	15.1
Total[1]				98.5	95.1	97.1	91.3	94.3	95.1

1. Total opulation coverage has been adjusted to acount for the presence of DRX in many ethnic populations. It has been assumed that the range of specificities represented by DRX alleles will mirror those of previously characterized HLA-DR alleles. The proportion of DRX incorporated under each motif is representative of the frequency of the motif in the remainder of the population. Total coverage has not been adjusted to account for unknown gene types.
2. Number of epitopes represents a minimal estimate, considering only the epitopes shown in Table 13. Additional alleles possibly bound by nested epitopes have not been accounted.

WHAT IS CLAIMED IS

1. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope consisting of an amino acid sequence selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VIYQYMDDLY,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVVP	WEFVNTPPLVKLWYQ,
KVYLAWVPAHKGIGG,	GEIYKRWIILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,
YRKILRQRKIDRLID,	EVNIVTDSQYALGII, and AETFYVDGAANRETK.	

2. The composition of claim 1, wherein the epitope is selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	WEFVNTPPLVKLWYQ,	KVYLAWVPAHKGIGG,
GEIYKRWIILGLNKI,	EKVYLAWVPAHKGIG,	QHLLQLTVWGIKQLQ,

QGQMVHQAISPRTLN, SPAIFQSSMTKILEP, FRKYTAFTIPSINNE, HSNWRAMASDFNLPP, KTAVQMAVFIHNFKR, YRKILRQRKIDRLID, EVNIVTDSQYALGII, and AETFYVDGAANRETK.

3. The composition of claim 1, comprising two epitopes selected from the group in claim 1.

4. The composition of claim 3, comprising three epitopes selected from the group in claim 1.

5. The composition of claim 1, wherein the composition further comprises a cytotoxic T lymphocyte (CTL) epitope selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.

6. The composition of claim 1, wherein the composition further comprises a helper T lymphocyte (HTL) epitope.

7. The composition of claim 6, wherein the HTL epitope is a pan DR binding molecule.

8. The composition of claim 1, wherein the epitope is on or within a liposome.

9. The composition of claim 1, wherein the peptide is joined to a lipid.

10. The composition of claim 1, wherein the epitope is bound to an HLA heavy chain, β2-microglobulin, and strepavidin complex, whereby a tetramer is formed.

11. The composition of claim 1, wherein the epitope is bound to an HLA molecule on an antigen presenting cell.

12. The composition of claim 1, wherein the antigen presenting cells is a dendritic cell.

13. The composition of claim 1, the composition further comprising a pharmaceutical excipient.

14. The composition of claim 1, wherein the epitope is in a unit dose form.

15. The composition of claim 1, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.

16. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VIYQYMDDLY,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVVP	WEFVNTPPLVKLWYQ,
KVYLAWVPAHKGIGG,	GEIYKRWIILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,

YRKILRQRKIDRLID, EVNIVTDSQYALGII, and AETFYVDGAANRETK, wherein the peptide comprises less than 50 contiguous amino acids that have 100% identity with a native peptide sequence.

17. The composition of claim 16, wherein at least two epitopes are linked via a spacer.

18. The composition of claim 16, further comprising a third epitope.

19. The composition of claim 18, wherein the third epitope is selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.

20. The composition of claim 16, further comprising a third epitope that is a helper T lymphocyte (HTL) epitope.

21. The composition of claim 20, wherein the HTL epitope is a panDR binding molecule.

22. The composition of claim 16, wherein the peptide is on or within a liposome.

23. The composition of claim 16, wherein the peptide is joined to a lipid.

24. The composition of claim 16, wherein the peptide further comprises at least three of the epitopes in the group of claim 16.

25. The composition of claim 16, wherein the peptide further comprises at least four of the epitopes in the group of claim 16.

26. The composition of claim 16, wherein the peptide further comprises at least five of the epitopes in the group of claim 16.

27. The composition of claim 16, wherein the peptide further comprises at least six of the epitopes in the group of claim 16.

28. The composition of claim 16, the composition further comprising a pharmaceutical excipient.

29. The composition of claim 16, further wherein the peptide is in a unit dose form.

30. The composition of claim 16, wherein the peptide is expressed from a recombinant nucleic acid that encodes the peptide.

AMENDED CLAIMS
[received by the International Bureau on 12 March 2001 (12.03.01); original claims 1-30 replaced by new claims 1-36 (6 pages)]

1. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope, said epitope consisting of an amino acid sequence selected from the group consisting of the sequences:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VIYQYMDDLY,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVVP	WEFVNTPPLVKLWYQ,
KVYLAWVPAHKGIGG,	GEIYKRWIILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,
YRKILRQRKIDRLID,	EVNIVTDSQYALGII, and AETFYVDGAANRETK.	

2. The composition of claim 1, comprising two epitopes selected from the group in claim 1.

3. The composition of claim 1, comprising three epitopes selected from the group in claim 1.

4. The composition of claim 1, wherein the composition further comprises a cytotoxic T lymphocyte (CTL) epitope selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.

5. The composition of claim 1, wherein the composition further comprises a helper T lymphocyte (HTL) epitope.

6. The composition of claim 5, wherein the HTL epitope is a pan DR binding molecule.

7. The composition of claim 1, wherein the epitope is on or within a liposome.

8. The composition of claim 1, wherein the peptide is joined to a lipid.

9. The composition of claim 1, wherein the epitope is bound to an HLA heavy chain, β2-microglobulin, and strepavidin complex, whereby a tetramer is formed.

10. The composition of claim 1, wherein the epitope is bound to an HLA molecule on an antigen presenting cell.

11. The composition of claim 1, wherein the antigen presenting cells is a dendritic cell.

12. The composition of claim 1, the composition further comprising a pharmaceutical excipient.

13. The composition of claim 1, wherein the epitope is in a unit dose form.

14. The composition of claim 1, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.

15. An expression vector comprising a recombinant nucleic acid molecule encoding a prepared epitope set out in claim 1.

16. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VIYQYMDDLY,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVVP	WEFVNTPPLVKLWYQ,
KVYLAWVPAHKGIGG,	GEIYKRWIILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,

YRKILRQRKIDRLID, EVNIVTDSQYALGII, and AETFYVDGAANRETK, wherein the peptide comprises less than 50 contiguous amino acids that have 100% identity with a native peptide sequence.

17. The composition of claim 16, wherein at least two epitopes are linked via a spacer.

18. The composition of claim 16, further comprising a third epitope.

19. The composition of claim 18, wherein the third epitope is selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.

20. The composition of claim 16, further comprising a third epitope that is a helper T lymphocyte (HTL) epitope.

21. The composition of claim 20, wherein the HTL epitope is a panDR binding molecule.

22. The composition of claim 16, wherein the peptide is on or within a liposome.

23. The composition of claim 16, wherein the peptide is joined to a lipid.

24. The composition of claim 16, wherein the peptide further comprises at least three of the epitopes in the group of claim 16.

25. The composition of claim 16, wherein the peptide further comprises at least four of the epitopes in the group of claim 16.

26. The composition of claim 16, wherein the peptide further comprises at least five of the epitopes in the group of claim 16.

27. The composition of claim 16, wherein the peptide further comprises at least six of the epitopes in the group of claim 16.

28. The composition of claim 16, the composition further comprising a pharmaceutical excipient.

29. The composition of claim 16, further wherein the peptide is in a unit dose form.

30. The composition of claim 16, wherein the peptide is expressed from a recombinant nucleic acid that encodes the peptide.

31. An expression vector comprising a recombinant nucleic acid encoding a prepared peptide as set out in claim 16.

32. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope, said epitope consisting of an amino acid sequence selected from the group consisting of the sequences set forth in Tables VII-XX.

33. A composition of claim 32, wherein the composition comprises a further epitope consisting of an amino acid sequence selected from the group consisting of the sequences set forth in Tables VII-XX.

34. The composition of claim 32, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.

35. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of the sequences set out in Tables VII-XX.

36. The composition of claim 35, wherein the prepared peptide is expressed from a recombinant nucleic acid moleucle that encodes the peptide.

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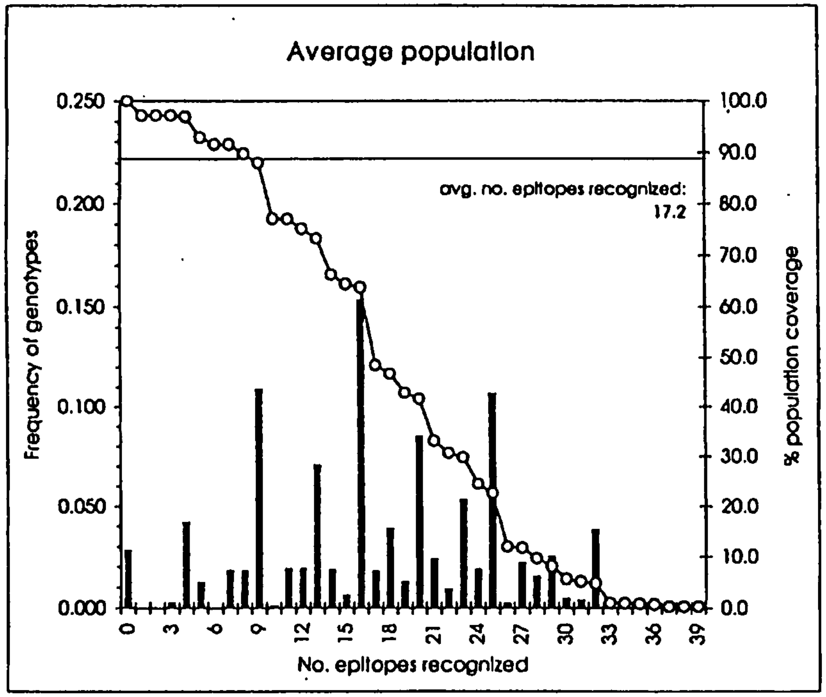
Figure 1



Plot of total frequency of genotypes as a function of the number of candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hit population cluster in proportion to the relative frequency of the cluster within the HLA specified population.

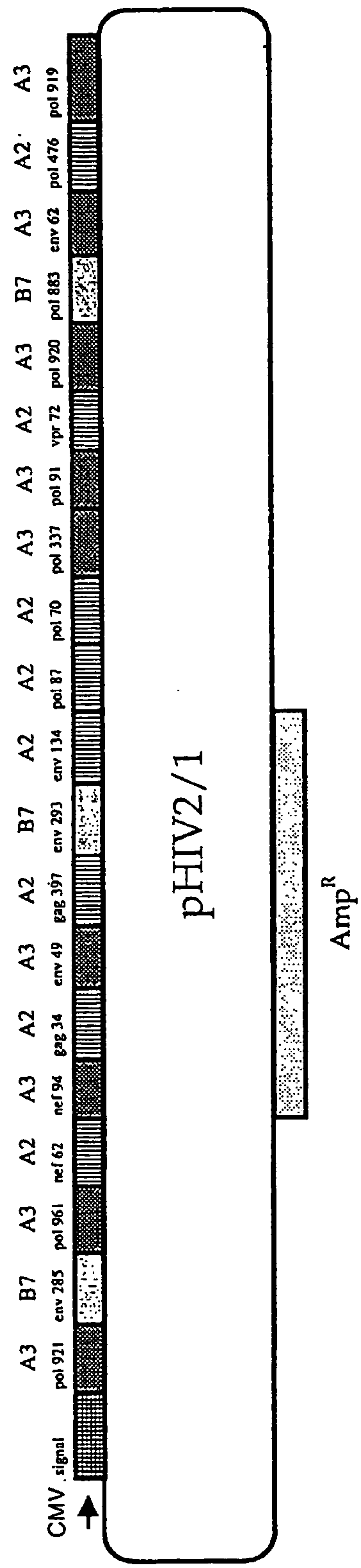

CMV
signal
A3 pol 921
B7 env 285
A3 pol 961
A2 nef 62
A3 nef 94
A2 gag 34
A3 env 49
A2 gag 397
B7 env 293
A2 env 134
A2 pol 87
A2 pol 70
A3 pol 337
A3 pol 91
A2 vpr 72
A3 pol 920
B7 pol 883
A3 env 62
A2 pol 476
A3 pol 919
pHIV2/1
Amp^R

FIGURE 2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/27766

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A61K 38/08, 38/10, 38/16, 39/295, 39/21; C07K 7/00, 9/00, 14/155
US CL : 530/328,327,326,325,324; 424/188.1, 208.1
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/328,327,326,325,324; 424/188.1, 208.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, WEST 2.0 search terms: author names, hiv, peptid?, hla, mhc, t cell, vaccine, polyvalent, ctl

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	RAMMENSEE et al. MHC ligands and peptide motifs: first listing. Immunogenetics. 1995, Vol 41, pages 178-228, see entire document.	1-30
Y	US 5,683,701 (MCMICHAEL et al.) 04 November 1997, see entire document.	1-30
Y	WO 94/20127A1 (CYTEL COEPORATION) 15 September 1994, see entire document.	1-30
Y	US PATENT 5,756,666 A (TAKIGUCHI et al.) 26 May 1998, see entir4 document.	1-30

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 DECEMBER 2000	12 JAN 2001

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